# Phyre2

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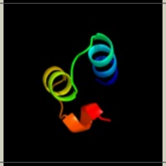
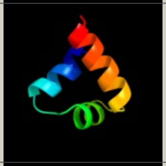
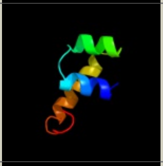
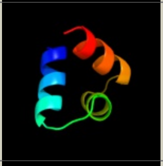
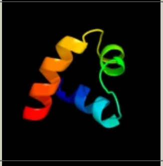
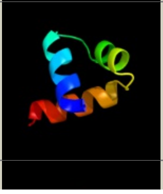
| Description | P39387 |
| Date | Thu Jan 5 12:00:19 GMT 2012 |
| Unique Job ID | 07bf3903d66093ad |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1a9xa1 | Alignment |  | 92.8 | 14 | **Fold:**Carbamoyl phosphate synthetase, large subunit connection domain<br>**Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain<br>**Family:**Carbamoyl phosphate synthetase, large subunit connection domain |
| 2 | c2x48B_ | Alignment |  | 86.3 | 16 | **PDB header:**viral protein<br>**Chain:** B: **PDB Molecule:**cag38821;<br>**PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1 |
| 3 | d1p4wa_ | Alignment |  | 80.8 | 13 | **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) |
| 4 | d1trra_ | Alignment |  | 76.6 | 19 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**TrpR-like<br>**Family:**Trp repressor, TrpR |
| 5 | d1yioa1 | Alignment |  | 76.1 | 13 | **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) |
| 6 | c1x3uA_ | Alignment |  | 76.0 | 13 | **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 |
| 7 | c2krfB_ | Alignment |  | 74.2 | 10 | **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 |
| 8 | d1fsea_ | Alignment |  | 73.5 | 13 | **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) |
| 9 | c1h0mD_ | Alignment |  | 72.7 | 13 | **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 |
| 10 | c2jpcA_ | Alignment |  | 72.5 | 15 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**ssrb;<br>**PDBTitle:** ssrb dna binding protein |
| 11 | d1a04a1 | Alignment |  | 71.5 | 10 | **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) |

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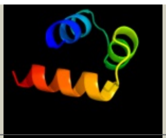
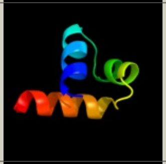
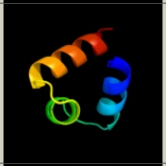
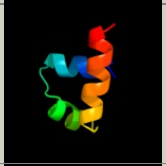
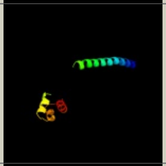
| 12 | c3cloC_ | Alignment |  | 70.0 | 15 | **PDB header:**transcription regulator<br>**Chain:** C: **PDB Molecule:**transcriptional regulator;<br>**PDBTitle:** crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution |
| 13 | c2q0oA_ | Alignment |  | 68.2 | 13 | **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 |
| 14 | c1zljE_ | Alignment |  | 67.2 | 21 | **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 |
| 15 | c2rnjA_ | Alignment |  | 65.2 | 10 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**response regulator protein vrar;<br>**PDBTitle:** nmr structure of the s. aureus vrar dna binding domain |
| 16 | d1l3la1 | Alignment |  | 65.1 | 13 | **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) |
| 17 | c3sztB_ | Alignment |  | 63.4 | 8 | **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 |
| 18 | c2gm4B_ | Alignment |  | 63.3 | 15 | **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 |
| 19 | d1d5ya1 | Alignment |  | 62.0 | 13 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**AraC type transcriptional activator |
| 20 | d1vz0a1 | Alignment |  | 60.2 | 21 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**KorB DNA-binding domain-like<br>**Family:**KorB DNA-binding domain-like |
| 21 | d1s6la1 | Alignment | not modelled | 59.0 | 26 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**MerB N-terminal domain-like |
| 22 | c2avuF_ | Alignment | not modelled | 55.9 | 20 | **PDB header:**transcription activator<br>**Chain:** F: **PDB Molecule:**flagellar transcriptional activator flhc;<br>**PDBTitle:** structure of the escherichia coli flhdc complex, a2 prokaryotic heteromeric regulator of transcription |
| 23 | d2avue1 | Alignment | not modelled | 55.7 | 20 | **Fold:**FlhC-like<br>**Superfamily:**FlhC-like<br>**Family:**FlhC-like |
| 24 | d1jhga_ | Alignment | not modelled | 55.3 | 17 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**TrpR-like<br>**Family:**Trp repressor, TrpR |
| 25 | c1r71B_ | Alignment | not modelled | 52.8 | 18 | **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 |
| 26 | c3c3wB_ | Alignment | not modelled | 52.0 | 21 | **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 |
| 27 | d1r71a_ | Alignment | not modelled | 51.0 | 18 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**KorB DNA-binding domain-like<br>**Family:**KorB DNA-binding domain-like |
| 28 | d1bl0a1 | Alignment | not modelled | 50.5 | 12 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**AraC type transcriptional activator |
| 29 | c3qp5C | Alignment | not modelled | 50.5 | 10 | **PDB header:**transcription<br>**Chain:** C: **PDB Molecule:**cvir transcriptional regulator; |

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| 29 | c3qp5C_ | Alignment | not modelled | 50.5 | 10 | **PDBTitle:** crystal structure of cvir bound to antagonist chlorolactone (cl) |
| 30 | c1m6vE_ | Alignment | not modelled | 49.5 | 13 | **PDB header:**ligase<br>**Chain:** E: **PDB Molecule:**carbamoyl phosphate synthetase large chain;<br>**PDBTitle:** crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase |
| 31 | c1u78A_ | Alignment | not modelled | 42.9 | 9 | **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 |
| 32 | d2p7vb1 | Alignment | not modelled | 41.8 | 10 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**Sigma4 domain |
| 33 | c1rnlA_ | Alignment | not modelled | 41.5 | 10 | **PDB header:**signal transduction protein<br>**Chain:** A: **PDB Molecule:**nitrate/nitrite response regulator protein narl;<br>**PDBTitle:** the nitrate/nitrite response regulator protein narl from narl |
| 34 | c3fymA_ | Alignment | not modelled | 39.7 | 17 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** the 1a structure of ymfm, a putative dna-binding membrane2 protein from staphylococcus aureus |
| 35 | c3d6zA_ | Alignment | not modelled | 35.6 | 22 | **PDB header:**transcription regulator/dna<br>**Chain:** A: **PDB Molecule:**multidrug-efflux transporter 1 regulator;<br>**PDBTitle:** crystal structure of r275e mutant of bmrr bound to dna and rhodamine |
| 36 | d1q1ha_ | Alignment | not modelled | 35.3 | 24 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Transcription factor E/IIe-alpha, N-terminal domain |
| 37 | c1q1hA_ | Alignment | not modelled | 35.3 | 24 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcription factor e;<br>**PDBTitle:** an extended winged helix domain in general transcription2 factor e/iie alpha |
| 38 | d2phcb1 | Alignment | not modelled | 34.9 | 29 | **Fold:**Cyclophilin-like<br>**Superfamily:**Cyclophilin-like<br>**Family:**PH0987 C-terminal domain-like |
| 39 | c3t76A_ | Alignment | not modelled | 34.3 | 16 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcriptional regulator vanug;<br>**PDBTitle:** crystal structure of transcriptional regulator vanug, form ii |
| 40 | d1ku3a_ | Alignment | not modelled | 32.4 | 10 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**Sigma4 domain |
| 41 | d2cyya1 | Alignment | not modelled | 31.9 | 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 |
| 42 | c3klnC_ | Alignment | not modelled | 31.7 | 15 | **PDB header:**transcription<br>**Chain:** C: **PDB Molecule:**transcriptional regulator, luxr family;<br>**PDBTitle:** vibrio cholerae vpst |
| 43 | c2r0qF_ | Alignment | not modelled | 31.2 | 10 | **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 |
| 44 | d1ttya_ | Alignment | not modelled | 31.2 | 7 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**Sigma4 domain |
| 45 | d1ku7a_ | Alignment | not modelled | 29.4 | 10 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**Sigma4 domain |
| 46 | c3t72o_ | Alignment | not modelled | 29.0 | 10 | **PDB header:**transcription/dna<br>**Chain:** O: **PDB Molecule:**pho box dna (strand 1);<br>**PDBTitle:** phob(e)-sigma70(4)-(rnap-betha-flap-tip-helix)-dna transcription2 activation sub-complex |
| 47 | d1smyf2 | Alignment | not modelled | 28.9 | 13 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**Sigma4 domain |
| 48 | d1ic8a2 | Alignment | not modelled | 28.9 | 15 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**POU-specific domain |
| 49 | c3mzyA_ | Alignment | not modelled | 28.7 | 10 | **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 |
| 50 | c3trbA_ | Alignment | not modelled | 28.1 | 17 | **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 |
| 51 | c2z99A_ | Alignment | not modelled | 27.8 | 15 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** crystal structure of scpb from mycobacterium tuberculosis |
| 52 | c2o8xA_ | Alignment | not modelled | 27.0 | 12 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**probable rna polymerase sigma-c factor;<br>**PDBTitle:** crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc |
| 53 | d1fxza2 | Alignment | not modelled | 26.6 | 24 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**RmlC-like cupins<br>**Family:**Germin/Seed storage 7S protein |
| 54 | d2cg4a1 | Alignment | not modelled | 26.3 | 21 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain |

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|---|---|---|---|---|---|---|
| 55 | d2et1a1 | Alignment | not modelled | 26.1 | 13 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**RmlC-like cupins<br>**Family:**Germin/Seed storage 7S protein |
| 56 | c2zp2B_ | Alignment | not modelled | 25.8 | 38 | **PDB header:**transferase inhibitor<br>**Chain:** B: **PDB Molecule:**kinase a inhibitor;<br>**PDBTitle:** c-terminal domain of kipi from bacillus subtilis |
| 57 | c2k9lA_ | Alignment | not modelled | 25.1 | 24 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon;<br>**PDBTitle:** structure of the core binding domain of sigma54 |
| 58 | c2do6A_ | Alignment | not modelled | 24.9 | 17 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b;<br>**PDBTitle:** solution structure of rsgi ruh-065, a uba domain from human2 cdna |
| 59 | d2iv2x2 | Alignment | not modelled | 24.8 | 29 | **Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Family:**Formate dehydrogenase/DMSO reductase, domains 1-3 |
| 60 | c2cg4B_ | Alignment | not modelled | 24.7 | 21 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**regulatory protein asnc;<br>**PDBTitle:** structure of e.coli asnc |
| 61 | c2jnhA_ | Alignment | not modelled | 23.5 | 16 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b;<br>**PDBTitle:** solution structure of the uba domain from cbl-b |
| 62 | c2d9sA_ | Alignment | not modelled | 23.5 | 20 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**cbl e3 ubiquitin protein ligase;<br>**PDBTitle:** solution structure of rsgi ruh-049, a uba domain from mouse2 cdna |
| 63 | d2cfxa1 | Alignment | not modelled | 22.9 | 14 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain |
| 64 | c2e1cA_ | Alignment | not modelled | 22.9 | 32 | **PDB header:**transcription/dna<br>**Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph1519;<br>**PDBTitle:** structure of putative hth-type transcriptional regulator ph1519/dna2 complex |
| 65 | c3itcA_ | Alignment | not modelled | 22.6 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**renal dipeptidase;<br>**PDBTitle:** crystal structure of sco3058 with bound citrate and glycerol |
| 66 | c2ragB_ | Alignment | not modelled | 22.2 | 21 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**dipeptidase;<br>**PDBTitle:** crystal structure of aminohydrolase from caulobacter crescentus |
| 67 | d1s7oa_ | Alignment | not modelled | 22.1 | 12 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**YlxM/p13-like |
| 68 | c2ejxA_ | Alignment | not modelled | 22.1 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**st0812;<br>**PDBTitle:** crystal structure of the hypothetical protein st0812 from2 sulfolobus tokodaii |
| 69 | c3korD_ | Alignment | not modelled | 22.1 | 15 | **PDB header:**transcription<br>**Chain:** D: **PDB Molecule:**possible trp repressor;<br>**PDBTitle:** crystal structure of a putative trp repressor from staphylococcus2 aureus |
| 70 | c2vbzA_ | Alignment | not modelled | 22.0 | 24 | **PDB header:**dna-binding protein<br>**Chain:** A: **PDB Molecule:**transcriptional regulatory protein;<br>**PDBTitle:** feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan |
| 71 | d1rp3a1 | Alignment | not modelled | 21.9 | 21 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**Sigma3 domain |
| 72 | d1z6ra1 | Alignment | not modelled | 21.7 | 14 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**ROK associated domain |
| 73 | c2v79B_ | Alignment | not modelled | 21.7 | 15 | **PDB header:**dna-binding protein<br>**Chain:** B: **PDB Molecule:**dna replication protein dnad;<br>**PDBTitle:** crystal structure of the n-terminal domain of dnad from2 bacillus subtilis |
| 74 | c2l4aA_ | Alignment | not modelled | 21.6 | 24 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**leucine responsive regulatory protein;<br>**PDBTitle:** nmr structure of the dna-binding domain of e.coli lrp |
| 75 | c3b7hA_ | Alignment | not modelled | 21.6 | 16 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**prophage lp1 protein 11;<br>**PDBTitle:** crystal structure of the prophage lp1 protein 11 |
| 76 | d2jioa2 | Alignment | not modelled | 20.5 | 21 | **Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Family:**Formate dehydrogenase/DMSO reductase, domains 1-3 |
| 77 | c1h0hA_ | Alignment | not modelled | 20.5 | 19 | **PDB header:**dehydrogenase<br>**Chain:** A: **PDB Molecule:**formate dehydrogenase (large subunit);<br>**PDBTitle:** tungsten containing formate dehydrogenase from2 desulfovibrio gigas |
| 78 | c1vz0B_ | Alignment | not modelled | 20.3 | 21 | **PDB header:**nuclear protein<br>**Chain:** B: **PDB Molecule:**chromosome partitioning protein parb;<br>**PDBTitle:** chromosome segregation protein spo0j from thermus2 thermophilus |
| 79 | c2phcB_ | Alignment | not modelled | 20.2 | 29 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein ph0987;<br>**PDBTitle:** crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii |
| 80 | c3c1dA_ | Alignment | not modelled | 20.0 | 15 | **PDB header:**recombination, dna binding protein<br>**Chain:** A: **PDB Molecule:**regulatory protein recx;<br>**PDBTitle:** x-ray crystal structure of recx |
| | | | | | | **Fold:**DNA/RNA-binding 3-helical bundle |

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| 81 | d1l0oc_ | Alignment | not modelled | 19.9 | 15 | **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**Sigma4 domain |
| 82 | c1l0oC_ | Alignment | not modelled | 19.9 | 15 | **PDB header:**protein binding<br>**Chain:** C: **PDB Molecule:**sigma factor;<br>**PDBTitle:** crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf |
| 83 | c2ivfA_ | Alignment | not modelled | 19.9 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**ethylbenzene dehydrogenase alpha-subunit;<br>**PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum |
| 84 | d1y9qa1 | Alignment | not modelled | 19.5 | 16 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**Probable transcriptional regulator VC1968, N-terminal domain |
| 85 | d1dpua_ | Alignment | not modelled | 19.5 | 10 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**C-terminal domain of RPA32 |
| 86 | c1dpuA_ | Alignment | not modelled | 19.5 | 10 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**replication protein a (rpa32) c-terminal domain;<br>**PDBTitle:** solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88) |
| 87 | c2iv2X_ | Alignment | not modelled | 19.2 | 30 | **PDB header:**oxidoreductase<br>**Chain:** X: **PDB Molecule:**formate dehydrogenase h;<br>**PDBTitle:** reinterpretation of reduced form of formate dehydrogenase h2 from e. coli |
| 88 | d1xsva_ | Alignment | not modelled | 19.2 | 15 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**YlxM/p13-like |
| 89 | d1h0ha2 | Alignment | not modelled | 19.2 | 19 | **Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Family:**Formate dehydrogenase/DMSO reductase, domains 1-3 |
| 90 | c2jvlA_ | Alignment | not modelled | 18.8 | 13 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**trmbf1;<br>**PDBTitle:** nmr structure of the c-terminal domain of mbf1 of trichoderma reesei |
| 91 | c2vn2B_ | Alignment | not modelled | 18.8 | 15 | **PDB header:**replication<br>**Chain:** B: **PDB Molecule:**chromosome replication initiation protein;<br>**PDBTitle:** crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426 |
| 92 | c3hugA_ | Alignment | not modelled | 18.6 | 9 | **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 |
| 93 | c2cfxD_ | Alignment | not modelled | 18.3 | 14 | **PDB header:**transcription<br>**Chain:** D: **PDB Molecule:**hth-type transcriptional regulator lrpc;<br>**PDBTitle:** structure of b.subtilis lrpc |
| 94 | c2w7nA_ | Alignment | not modelled | 18.1 | 16 | **PDB header:**transcription/dna<br>**Chain:** A: **PDB Molecule:**trfb transcriptional repressor protein;<br>**PDBTitle:** crystal structure of kora bound to operator dna: insight2 into repressor cooperation in rp4 gene regulation |
| 95 | c2dbbA_ | Alignment | not modelled | 17.8 | 11 | **PDB header:**transcriptional regulator<br>**Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph0061;<br>**PDBTitle:** crystal structure of ph0061 |
| 96 | d1r69a_ | Alignment | not modelled | 17.4 | 16 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**Phage repressors |
| 97 | d2ga1a1 | Alignment | not modelled | 17.4 | 31 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Alr1493-like |
| 98 | c2kw0A_ | Alignment | not modelled | 17.2 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**ccmh protein;<br>**PDBTitle:** solution structure of n-terminal domain of ccmh from escherichia.coli |
| 99 | d2a6ca1 | Alignment | not modelled | 16.9 | 11 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**NE1354 |