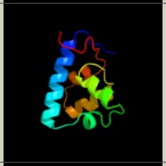
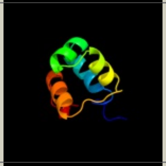
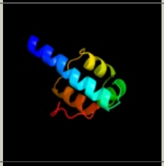
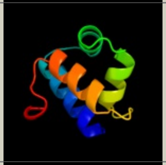
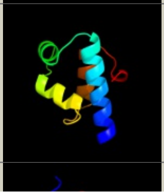
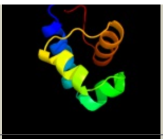
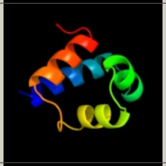
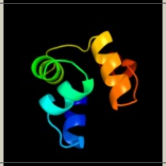
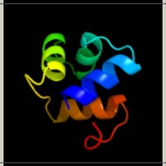
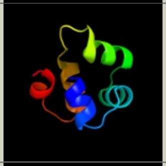
Phyre$^2$

| | |
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P00816 |
| Date | Thu Jan 5 10:56:55 GMT 2012 |
| Unique Job ID | ec5ed00a7f6c55f3 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2iv1J_ | Alignment |  | 100.0 | 99 | **PDB header:**lyase<br>**Chain:** J: **PDB Molecule:**cyanate hydratase;<br>**PDBTitle:** site directed mutagenesis of key residues involved in the2 catalytic mechanism of cyanase |
| 2 | d1dwka2 | Alignment |  | 100.0 | 97 | **Fold:**Cyanase C-terminal domain<br>**Superfamily:**Cyanase C-terminal domain<br>**Family:**Cyanase C-terminal domain |
| 3 | d1dwka1 | Alignment |  | 100.0 | 98 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**Cyanase N-terminal domain |
| 4 | c1y9qA_ | Alignment |  | 97.1 | 14 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcriptional regulator, hth_3 family;<br>**PDBTitle:** crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae |
| 5 | d1y7ya1 | Alignment |  | 97.1 | 17 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**SinR domain-like |
| 6 | d1adra_ | Alignment |  | 97.0 | 13 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**Phage repressors |
| 7 | c3clcC_ | Alignment |  | 97.0 | 11 | **PDB header:**transcription regulator/dna<br>**Chain:** C: **PDB Molecule:**regulatory protein;<br>**PDBTitle:** crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator |
| 8 | c3f6wE_ | Alignment |  | 97.0 | 16 | **PDB header:**dna binding protein<br>**Chain:** E: **PDB Molecule:**xre-family like protein;<br>**PDBTitle:** xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000 |
| 9 | d2b5aa1 | Alignment |  | 97.0 | 18 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**SinR domain-like |
| 10 | c2bnoA_ | Alignment |  | 97.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**epoxidase;<br>**PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis. |
| 11 | c2ewtA_ | Alignment |  | 96.9 | 10 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**putative dna-binding protein;<br>**PDBTitle:** crystal structure of the dna-binding domain of bldd |

| | | | | | | |
|---|---|---|---|---|---|---|
| 12 | c3ivpD_ | Alignment |  | 96.9 | 14 | **PDB header:**dna binding protein<br>**Chain:** D: **PDB Molecule:**putative transposon-related dna-binding protein;<br>**PDBTitle:** the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630. |
| 13 | c3f52A_ | Alignment |  | 96.8 | 16 | **PDB header:**transcription activator<br>**Chain:** A: **PDB Molecule:**clp gene regulator (clgr);<br>**PDBTitle:** crystal structure of the clp gene regulator clgr from c. glutamicum |
| 14 | d2o38a1 | Alignment |  | 96.8 | 24 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**NE1354 |
| 15 | c2o38A_ | Alignment |  | 96.8 | 24 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein;<br>**PDBTitle:** putative xre family transcriptional regulator |
| 16 | c3cecA_ | Alignment |  | 96.7 | 23 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**putative antidote protein of plasmid maintenance system;<br>**PDBTitle:** crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution |
| 17 | c3op9A_ | Alignment |  | 96.7 | 15 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**pli0006 protein;<br>**PDBTitle:** crystal structure of transcriptional regulator from listeria innocua |
| 18 | d1y9qa1 | Alignment |  | 96.7 | 14 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**Probable transcriptional regulator VC1968, N-terminal domain |
| 19 | c3kxaD_ | Alignment |  | 96.7 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** D: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** crystal structure of ngo0477 from neisseria gonorrhoeae |
| 20 | d1rioa_ | Alignment |  | 96.7 | 25 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**Phage repressors |
| 21 | c3eusB_ | Alignment | not modelled | 96.6 | 12 | **PDB header:**dna binding protein<br>**Chain:** B: **PDB Molecule:**dna-binding protein;<br>**PDBTitle:** the crystal structure of the dna binding protein from silicibacter2 pomeroyi |
| 22 | d1llib_ | Alignment | not modelled | 96.6 | 24 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**Phage repressors |
| 23 | d2icta1 | Alignment | not modelled | 96.6 | 25 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**SinR domain-like |
| 24 | d2r1jl1 | Alignment | not modelled | 96.6 | 10 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**Phage repressors |
| 25 | c2kpjA_ | Alignment | not modelled | 96.6 | 9 | **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 |
| 26 | c3dnvB_ | Alignment | not modelled | 96.5 | 17 | **PDB header:**transcription/dna<br>**Chain:** B: **PDB Molecule:**hth-type transcriptional regulator hipb;<br>**PDBTitle:** mdt protein |
| 27 | d2ofya1 | Alignment | not modelled | 96.5 | 19 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**SinR domain-like |
| 28 | c3bdnB_ | Alignment | not modelled | 96.4 | 27 | **PDB header:**transcription/dna<br>**Chain:** B: **PDB Molecule:**lambda repressor;<br>**PDBTitle:** crystal structure of the lambda repressor |
| | | | | | | **PDB header:**transcription regulator |

| | | | | | | |
|---|---|---|---|---|---|---|
| 29 | c1b0nA_ | Alignment | not modelled | 96.4 | 20 | **Chain:** A: **PDB Molecule:**protein (sinr protein);<br>**PDBTitle:** sinr protein/sini protein complex |
| 30 | c3b7hA_ | Alignment | not modelled | 96.4 | 15 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**prophage lp1 protein 11;<br>**PDBTitle:** crystal structure of the prophage lp1 protein 11 |
| 31 | d1x57a1 | Alignment | not modelled | 96.3 | 11 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**EDF1-like |
| 32 | d1lmb3_ | Alignment | not modelled | 96.3 | 25 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**Phage repressors |
| 33 | d1b0na2 | Alignment | not modelled | 96.3 | 20 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**SinR domain-like |
| 34 | c3pxpA_ | Alignment | not modelled | 96.3 | 13 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**helix-turn-helix domain protein;<br>**PDBTitle:** crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution |
| 35 | c3mlfC_ | Alignment | not modelled | 96.3 | 7 | **PDB header:**transcription regulator<br>**Chain:** C: **PDB Molecule:**transcriptional regulator;<br>**PDBTitle:** putative transcriptional regulator from staphylococcus aureus. |
| 36 | c2wusR_ | Alignment | not modelled | 96.3 | 13 | **PDB header:**structural protein<br>**Chain:** R: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** bacterial actin mreb assembles in complex with cell shape2 protein rodz |
| 37 | c3trbA_ | Alignment | not modelled | 96.3 | 21 | **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 |
| 38 | c3t76A_ | Alignment | not modelled | 96.2 | 11 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcriptional regulator vanug;<br>**PDBTitle:** crystal structure of transcriptional regulator vanug, form ii |
| 39 | d2a6ca1 | Alignment | not modelled | 96.2 | 14 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**NE1354 |
| 40 | c2ebyA_ | Alignment | not modelled | 96.1 | 25 | **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 |
| 41 | d1utxa_ | Alignment | not modelled | 96.1 | 16 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**SinR domain-like |
| 42 | d1sq8a_ | Alignment | not modelled | 96.1 | 16 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**Phage repressors |
| 43 | d2croa_ | Alignment | not modelled | 96.1 | 12 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**Phage repressors |
| 44 | d1r69a_ | Alignment | not modelled | 96.0 | 14 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**Phage repressors |
| 45 | c3fymA_ | Alignment | not modelled | 95.9 | 10 | **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 |
| 46 | c3omtA_ | Alignment | not modelled | 95.8 | 9 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae. |
| 47 | c3bs3A_ | Alignment | not modelled | 95.8 | 18 | **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 |
| 48 | c3lisB_ | Alignment | not modelled | 95.6 | 16 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**csp231i c protein;<br>**PDBTitle:** crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form) |
| 49 | c2xcjB_ | Alignment | not modelled | 95.1 | 20 | **PDB header:**viral protein<br>**Chain:** B: **PDB Molecule:**c protein;<br>**PDBTitle:** crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2 |
| 50 | c2jvlA_ | Alignment | not modelled | 94.4 | 18 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**trmbf1;<br>**PDBTitle:** nmr structure of the c-terminal domain of mbf1 of trichoderma reesei |
| 51 | c2ef8A_ | Alignment | not modelled | 94.1 | 21 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**putative transcription factor;<br>**PDBTitle:** crystal structure of c.ecot38is |
| 52 | d1nera_ | Alignment | not modelled | 92.7 | 17 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**Phage repressors |
| 53 | c3fmyA_ | Alignment | not modelled | 90.4 | 17 | **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) |
| 54 | c2fjrB_ | Alignment | not modelled | 87.9 | 12 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**repressor protein ci;<br>**PDBTitle:** crystal structure of bacteriophage 186 |
| 55 | c2ppxA_ | Alignment | not modelled | 85.0 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein atu1735;<br>**PDBTitle:** crystal structure of a hth xre-family like protein from |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
|  |  |  |  |  |  | agrobacterium2 tumefaciens |
| 56 | d2ppxa1 | Alignment | not modelled | 85.0 | 12 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**SinR domain-like |
| 57 | d1efaa1 | Alignment | not modelled | 78.2 | 18 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |
| 58 | d1lcda_ | Alignment | not modelled | 77.7 | 18 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |
| 59 | d2bjca1 | Alignment | not modelled | 76.6 | 20 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |
| 60 | c1zx4B_ | Alignment | not modelled | 74.8 | 25 | **PDB header:**translation<br>**Chain:** B: **PDB Molecule:**plasmid partition par b protein;<br>**PDBTitle:** structure of parb bound to dna |
| 61 | c3gn5B_ | Alignment | not modelled | 72.6 | 15 | **PDB header:**dna binding protein<br>**Chain:** B: **PDB Molecule:**hth-type transcriptional regulator mqsa (ygit/b3021);<br>**PDBTitle:** structure of the e. coli protein mqsa (ygit/b3021) |
| 62 | c2qfcB_ | Alignment | not modelled | 71.3 | 15 | **PDB header:**transcription regulation<br>**Chain:** B: **PDB Molecule:**plcr protein;<br>**PDBTitle:** crystal structure of bacillus thuringiensis plcr complexed with papr |
| 63 | d2hsga1 | Alignment | not modelled | 71.2 | 13 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |
| 64 | d1ggaa2 | Alignment | not modelled | 69.6 | 22 | **Fold:**FwdE/GAPDH domain-like<br>**Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain<br>**Family:**GAPDH-like |
| 65 | c2l8nA_ | Alignment | not modelled | 67.4 | 16 | **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 |
| 66 | d1vz0a1 | Alignment | not modelled | 67.2 | 28 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**KorB DNA-binding domain-like<br>**Family:**KorB DNA-binding domain-like |
| 67 | d1qpza1 | Alignment | not modelled | 67.1 | 11 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |
| 68 | c2lcvA_ | Alignment | not modelled | 66.5 | 16 | **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 |
| 69 | c3pv9D_ | Alignment | not modelled | 64.8 | 16 | **PDB header:**immune system<br>**Chain:** D: **PDB Molecule:**putative uncharacterized protein ph1245;<br>**PDBTitle:** structure of ph1245, a cas1 from pyrococcus horikoshii |
| 70 | d1or7a1 | Alignment | not modelled | 64.2 | 18 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**Sigma4 domain |
| 71 | d1v6ga2 | Alignment | not modelled | 61.8 | 43 | **Fold:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Superfamily:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Family:**LIM domain |
| 72 | d1uxca_ | Alignment | not modelled | 60.0 | 18 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |
| 73 | c1or7A_ | Alignment | not modelled | 59.9 | 18 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**rna polymerase sigma-e factor;<br>**PDBTitle:** crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea |
| 74 | d1ku7a_ | Alignment | not modelled | 53.8 | 8 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**Sigma4 domain |
| 75 | c3rmiA_ | Alignment | not modelled | 53.5 | 21 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**chorismate mutase protein;<br>**PDBTitle:** crystal structure of chorismate mutase from bartonella henselae str.2 houston-1 in complex with malate |
| 76 | c3h5tA_ | Alignment | not modelled | 51.4 | 20 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcriptional regulator, laci family;<br>**PDBTitle:** crystal structure of a transcriptional regulator, lacl2 family protein from corynebacterium glutamicum |
| 77 | c2axzC_ | Alignment | not modelled | 50.9 | 4 | **PDB header:**transcription<br>**Chain:** C: **PDB Molecule:**prgx;<br>**PDBTitle:** crystal structure of prgx/ccf10 complex |
| 78 | c3mkyP_ | Alignment | not modelled | 50.6 | 18 | **PDB header:**dna binding protein/dna<br>**Chain:** P: **PDB Molecule:**protein sopb;<br>**PDBTitle:** structure of sopb(155-323)-18mer dna complex, i23 form |
| 79 | d2gtvx1 | Alignment | not modelled | 50.4 | 11 | **Fold:**Chorismate mutase II<br>**Superfamily:**Chorismate mutase II<br>**Family:**monomeric chorismate mutase |
| 80 | d1ttya_ | Alignment | not modelled | 50.1 | 8 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**Sigma4 domain |
| 81 | c3r1fO_ | Alignment | not modelled | 49.5 | 9 | **PDB header:**transcription<br>**Chain:** O: **PDB Molecule:**esx-1 secretion-associated regulator espr;<br>**PDBTitle:** crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis |
|  |  |  |  |  |  | **Fold:**DNA/RNA-binding 3-helical bundle |

| | | | | | | |
|---|---|---|---|---|---|---|
| 82 | d2p7vb1 | Alignment | not modelled | 49.0 | 8 | **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**Sigma4 domain |
| 83 | c2o8xA_ | Alignment | not modelled | 48.7 | 21 | **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 |
| 84 | d1uxda_ | Alignment | not modelled | 48.4 | 18 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |
| 85 | c3t72o_ | Alignment | not modelled | 48.0 | 9 | **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 |
| 86 | d1ku3a_ | Alignment | not modelled | 47.6 | 9 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**Sigma4 domain |
| 87 | d1r71a_ | Alignment | not modelled | 47.1 | 23 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**KorB DNA-binding domain-like<br>**Family:**KorB DNA-binding domain-like |
| 88 | d1rp3a2 | Alignment | not modelled | 47.0 | 9 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**Sigma4 domain |
| 89 | d1k3ta2 | Alignment | not modelled | 46.8 | 24 | **Fold:**FwdE/GAPDH domain-like<br>**Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain<br>**Family:**GAPDH-like |
| 90 | c3bd1B_ | Alignment | not modelled | 46.4 | 9 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**cro protein;<br>**PDBTitle:** structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1 |
| 91 | d2cg4a1 | Alignment | not modelled | 44.3 | 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 |
| 92 | d1i1ga1 | Alignment | not modelled | 44.1 | 25 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain |
| 93 | c2kiqA_ | Alignment | not modelled | 44.0 | 17 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcription elongation regulator 1;<br>**PDBTitle:** solution structure of the ff domain 2 of human transcription2 elongation factor ca150 |
| 94 | d1gv2a2 | Alignment | not modelled | 43.1 | 19 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Myb/SANT domain |
| 95 | c2llkA_ | Alignment | not modelled | 42.4 | 16 | **PDB header:**cell cycle, transcription<br>**Chain:** A: **PDB Molecule:**cyclin-d-binding myb-like transcription factor 1;<br>**PDBTitle:** solution nmr structure of the n-terminal myb-like 1 domain of the2 human cyclin-d-binding transcription factor 1 (hdmp1), northeast3 structural genomics consortium (nesg) target id hr8011a |
| 96 | d2csba5 | Alignment | not modelled | 41.2 | 31 | **Fold:**Topoisomerase V catalytic domain-like<br>**Superfamily:**Topoisomerase V catalytic domain-like<br>**Family:**Topoisomerase V catalytic domain-like |
| 97 | c2gbbA_ | Alignment | not modelled | 41.1 | 22 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**putative chorismate mutase;<br>**PDBTitle:** crystal structure of secreted chorismate mutase from2 yersinia pestis |
| 98 | c3kjxD_ | Alignment | not modelled | 39.5 | 20 | **PDB header:**transcription regulator<br>**Chain:** D: **PDB Molecule:**transcriptional regulator, laci family;<br>**PDBTitle:** crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi |
| 99 | d2fp1a1 | Alignment | not modelled | 39.1 | 26 | **Fold:**Chorismate mutase II<br>**Superfamily:**Chorismate mutase II<br>**Family:**Secreted chorismate mutase-like |
| 100 | c1zgwA_ | Alignment | not modelled | 37.7 | 10 | **PDB header:**transcription regulator/dna<br>**Chain:** A: **PDB Molecule:**ada polyprotein;<br>**PDBTitle:** nmr structure of e. coli ada protein in complex with dna |
| 101 | c1rp3G_ | Alignment | not modelled | 36.9 | 11 | **PDB header:**transcription<br>**Chain:** G: **PDB Molecule:**rna polymerase sigma factor sigma-28 (flia);<br>**PDBTitle:** cocrystal structure of the flagellar sigma/anti-sigma2 complex, sigma-28/flgm |
| 102 | d1tc3c_ | Alignment | not modelled | 36.1 | 18 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Recombinase DNA-binding domain |
| 103 | c1u78A_ | Alignment | not modelled | 36.0 | 17 | **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 |
| 104 | d1k78a1 | Alignment | not modelled | 35.8 | 12 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Paired domain |
| 105 | d2vkea1 | Alignment | not modelled | 35.4 | 24 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 106 | c1r71B_ | Alignment | not modelled | 35.1 | 21 | **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 |
| 107 | c3lfxE_ | Alignment | not modelled | 34.9 | 20 | **PDB header:**structural genomics, unknown function<br>**Chain:** E: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** structure of tm1797, a cas1 protein from thermotoga |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | | | maritima |
| 108 | c2cfxD_ | Alignment | not modelled | 34.7 | 24 | **PDB header:**transcription<br>**Chain:** D: **PDB Molecule:**hth-type transcriptional regulator lrpc;<br>**PDBTitle:** structure of b.subtilis lrpc |
| 109 | d2j0pa1 | Alignment | not modelled | 33.9 | 21 | **Fold:**Heme iron utilization protein-like<br>**Superfamily:**Heme iron utilization protein-like<br>**Family:**HemS/ChuS-like |
| 110 | d1xsva_ | Alignment | not modelled | 33.3 | 24 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**YlxM/p13-like |
| 111 | c2e71A_ | Alignment | not modelled | 32.8 | 16 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcription elongation regulator 1;<br>**PDBTitle:** solution structure of the second ff domain of human2 transcription factor ca150 |
| 112 | c3hugA_ | Alignment | not modelled | 32.5 | 24 | **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 |
| 113 | d1s7oa_ | Alignment | not modelled | 31.9 | 27 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**YlxM/p13-like |
| 114 | c3m6zA_ | Alignment | not modelled | 31.7 | 31 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**topoisomerase v;<br>**PDBTitle:** crystal structure of an n-terminal 44 kda fragment of topoisomerase v2 in the presence of guanidium hydrochloride |
| 115 | c3i4pA_ | Alignment | not modelled | 31.6 | 24 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcriptional regulator, asnc family;<br>**PDBTitle:** crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens |
| 116 | d1d5ya1 | Alignment | not modelled | 31.6 | 12 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**AraC type transcriptional activator |
| 117 | c3mzyA_ | Alignment | not modelled | 30.8 | 15 | **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 |
| 118 | c3osgA_ | Alignment | not modelled | 29.5 | 13 | **PDB header:**transcription/dna<br>**Chain:** A: **PDB Molecule:**myb21;<br>**PDBTitle:** the structure of protozoan parasite trichomonas vaginalis myb2 in2 complex with mre-1-12 dna |
| 119 | c2v9vA_ | Alignment | not modelled | 29.3 | 17 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor;<br>**PDBTitle:** crystal structure of moorella thermoacetica selb(377-511) |
| 120 | c2vprA_ | Alignment | not modelled | 29.3 | 16 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**tetracycline resistance repressor protein;<br>**PDBTitle:** tet repressor class h in complex with 5a,6-2 anhydrotetracycline-mg |