

# Ian B Dodd

## List of Publications by Year in descending order

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Version: 2024-02-01

60  
papers

3,467  
citations

230014

27  
h-index

169272

56  
g-index

63  
all docs

63  
docs citations

63  
times ranked

3560  
citing authors

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | The loopometer: a quantitative <i>in vivo</i> assay for DNA-looping proteins. <i>Nucleic Acids Research</i> , 2021, 49, e39-e39.   | 6.5 | 6         |
| 2  | The pIT5 Plasmid Series, an Improved Toolkit for Repeated Genome Integration in <i>E. coli</i> . <i>ACS Synthetic Biology</i> , 2021, 10, 1633-1639.   | 1.9 | 1         |
| 3  | Analysis of Infection Time Courses Shows CII Levels Determine the Frequency of Lysogeny in Phage 186. <i>Pharmaceuticals</i> , 2021, 14, 998.  | 1.7 | 1         |
| 4  | Instability of CII is needed for efficient switching between lytic and lysogenic development in bacteriophage 186. <i>Nucleic Acids Research</i> , 2020, 48, 12030-12041.  | 6.5 | 3         |
| 5  | A quantitative binding model for the Apl protein, the dual purpose recombination-directionality factor and lysis-lysogeny regulator of bacteriophage 186. <i>Nucleic Acids Research</i> , 2020, 48, 8914-8926.   | 6.5 | 1         |
| 6  | RNA polymerase pausing at a protein roadblock can enhance transcriptional interference by promoter occlusion. <i>FEBS Letters</i> , 2019, 593, 903-917.  | 1.3 | 5         |
| 7  | Positive and Negative Control of Enhancer-Promoter Interactions by Other DNA Loops Generates Specificity and Tunability. <i>Cell Reports</i> , 2019, 26, 2419-2433.e3.   | 2.9 | 19        |
| 8  | Directing traffic on DNA—How transcription factors relieve or induce transcriptional interference. <i>Transcription</i> , 2017, 8, 120-125.  | 1.7 | 25        |
| 9  | Efficient chromosomal-scale DNA looping in <i>Escherichia coli</i> using multiple DNA-looping elements. <i>Nucleic Acids Research</i> , 2017, 45, 5074-5085.   | 6.5 | 7         |
| 10 | Programmable DNA looping using engineered bivalent dCas9 complexes. <i>Nature Communications</i> , 2017, 8, 1628.  | 5.8 | 60        |
| 11 | Modeling Bistable Chromatin States. , 2017, , 145-168.   |     | 2         |
| 12 | Nucleosome dynamics and maintenance of epigenetic states of CpG islands. <i>Physical Review E</i> , 2016, 93, 062417.  | 0.8 | 11        |
| 13 | The role of repressor kinetics in relief of transcriptional interference between convergent promoters. <i>Nucleic Acids Research</i> , 2016, 44, 6625-6638.  | 6.5 | 25        |
| 14 | DNA methylation in human epigenomes depends on local topology of CpG sites. <i>Nucleic Acids Research</i> , 2016, 44, 5123-5132.   | 6.5 | 153       |
| 15 | Cooperative stabilization of the SIR complex provides robust epigenetic memory in a model of SIR silencing in <i>Saccharomyces cerevisiae</i> . <i>Epigenetics</i> , 2015, 10, 293-302.  | 1.3 | 17        |
| 16 | Road rules for traffic on DNA—systematic analysis of transcriptional roadblocking <i>in vivo</i> . <i>Nucleic Acids Research</i> , 2014, 42, 8861-8872.  | 6.5 | 44        |
| 17 | Quantitation of the DNA tethering effect in long-range DNA looping <i>in vivo</i> and <i>in vitro</i> using the Lac and $\lambda$ repressors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 349-354. | 3.3 | 47        |
| 18 | Promoter Activation by CII, a Potent Transcriptional Activator from Bacteriophage 186. <i>Journal of Biological Chemistry</i> , 2014, 289, 32094-32108.  | 1.6 | 5         |

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|----|---|-----|-----------|
| 19 | Collaboration between CpG sites is needed for stable somatic inheritance of DNA methylation states. <i>Nucleic Acids Research</i> , 2014, 42, 2235-2244.  | 6.5 | 83        |
| 20 | Quantitation of interactions between two DNA loops demonstrates loop domain insulation in <i>E. coli</i> cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4449-57. | 3.3 | 25        |
| 21 | In Silico, InÂVivo, and InÂVivo Estimation of J-Factors for LAC Repressor-Mediated DNA Loop Formation. <i>Biophysical Journal</i> , 2013, 104, 174a-175a.   | 0.2 | 0         |
| 22 | Enhancer-like long-range transcriptional activation by CI-mediated DNA looping. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2922-2927.                                | 3.3 | 34        |
| 23 | One-Step Cloning and Chromosomal Integration of DNA. <i>ACS Synthetic Biology</i> , 2013, 2, 537-541.   | 1.9 | 189       |
| 24 | Bacteriophage lambda repressor mediates the formation of a complex enhancer-like structure. <i>Transcription</i> , 2013, 4, 201-205.  | 1.7 | 3         |
| 25 | Single molecule analysis of DNA wrapping and looping by a circular 14mer wheel of the bacteriophage 186 CI repressor. <i>Nucleic Acids Research</i> , 2013, 41, 5746-5756.  | 6.5 | 22        |
| 26 | A Simple Histone Code Opens Many Paths to Epigenetics. <i>PLoS Computational Biology</i> , 2012, 8, e1002643.   | 1.5 | 44        |
| 27 | Barriers and Silencers: A Theoretical Toolkit for Control and Containment of Nucleosome-Based Epigenetic States. <i>Journal of Molecular Biology</i> , 2011, 414, 624-637.  | 2.0 | 50        |
| 28 | Identification of residues in the N-terminal PAS domains important for dimerization of Arnt and AhR. <i>Nucleic Acids Research</i> , 2011, 39, 3695-3709.   | 6.5 | 37        |
| 29 | Minimal Gene Regulatory Circuits for a Lysis-Lysogeny Choice in the Presence of Noise. <i>PLoS ONE</i> , 2010, 5, e15037.   | 1.1 | 16        |
| 30 | Theory for the stability and regulation of epigenetic landscapes. <i>Physical Biology</i> , 2010, 7, 026010.  | 0.8 | 56        |
| 31 | Economy of Operon Formation: Cotranscription Minimizes Shortfall in Protein Complexes. <i>MBio</i> , 2010, 1, .   | 1.8 | 31        |
| 32 | Why Do Phage Play Dice?. <i>Journal of Virology</i> , 2009, 83, 11416-11420.  | 1.5 | 49        |
| 33 | Minimal Gene Regulatory Circuits that Can Count like Bacteriophage Lambda. <i>Journal of Molecular Biology</i> , 2009, 394, 681-693.  | 2.0 | 12        |
| 34 | Potent Transcriptional Interference by Pausing of RNA Polymerases over a Downstream Promoter. <i>Molecular Cell</i> , 2009, 34, 545-555.  | 4.5 | 81        |
| 35 | The Generation of Promoter-Mediated Transcriptional Noise in Bacteria. <i>PLoS Computational Biology</i> , 2008, 4, e1000109.   | 1.5 | 52        |
| 36 | Ultrasensitive gene regulation by positive feedback loops in nucleosome modification. <i>Molecular Systems Biology</i> , 2008, 4, 182.  | 3.2 | 58        |

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|----|---|------|-----------|
| 37 | Cro's role in the $\lambda$ -Cro bistable switch is critical for $\lambda$ 's transition from lysogeny to lytic development. <i>Genes and Development</i> , 2007, 21, 2461-2472.      | 2.7  | 84        |
| 38 | Theoretical Analysis of Epigenetic Cell Memory by Nucleosome Modification. <i>Cell</i> , 2007, 129, 813-822.  | 13.5 | 413       |
| 39 | Modelling Transcriptional Interference and DNA Looping in Gene Regulation. <i>Journal of Molecular Biology</i> , 2007, 369, 1200-1213.  | 2.0  | 21        |
| 40 | The Structural Basis of Cooperative Regulation at an Alternate Genetic Switch. <i>Molecular Cell</i> , 2006, 21, 605-615.   | 4.5  | 30        |
| 41 | Network models of phage-bacteria coevolution. <i>Physical Review E</i> , 2006, 74, 066105.  | 0.8  | 9         |
| 42 | Functional Alignment of Regulatory Networks: A Study of Temperate Phages. <i>PLoS Computational Biology</i> , 2005, 1, e74.   | 1.5  | 23        |
| 43 | A Mathematical Model for Transcriptional Interference by RNA Polymerase Traffic in <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2005, 346, 399-409.                | 2.0  | 96        |
| 44 | Revisited gene regulation in bacteriophage $\lambda$ . <i>Current Opinion in Genetics and Development</i> , 2005, 15, 145-152.  | 1.5  | 121       |
| 45 | Bacteriophage P4 <i>Vis</i> protein is needed for prophage excision. <i>Virology</i> , 2004, 322, 82-92.  | 1.1  | 21        |
| 46 | Cooperativity in long-range gene regulation by the $\lambda$ CI repressor. <i>Genes and Development</i> , 2004, 18, 344-354.  | 2.7  | 161       |
| 47 | The Helix-Turn-Helix Motif of the Coliphage 186 Immunity Repressor Binds to Two Distinct Recognition Sequences. <i>Journal of Biological Chemistry</i> , 2002, 277, 3186-3194.        | 1.6  | 22        |
| 48 | Action at a distance in CI repressor regulation of the bacteriophage 186 genetic switch. <i>Molecular Microbiology</i> , 2002, 45, 697-710.   | 1.2  | 43        |
| 49 | Octamerization of lambda CI repressor is needed for effective repression of PRM and efficient switching from lysogeny. <i>Genes and Development</i> , 2001, 15, 3013-3022.            | 2.7  | 159       |
| 50 | The Late-Expressed Region of the Temperate Coliphage 186 Genome. <i>Virology</i> , 1998, 248, 117-130.  | 1.1  | 22        |
| 51 | Defining the SOS Operon of Coliphage 186. <i>Virology</i> , 1996, 219, 105-114.   | 1.1  | 23        |
| 52 | The <i>Escherichia coli</i> Retrons Ec67 and Ec86 Replace DNA between the cos Site and a Transcription Terminator of a 186-Related Prophage. <i>Virology</i> , 1996, 219, 115-124.    | 1.1  | 22        |
| 53 | DNA Binding by the Coliphage 186 Repressor Protein CI. <i>Journal of Biological Chemistry</i> , 1996, 271, 11532-11540.   | 1.6  | 22        |
| 54 | The Cro-like $\lambda$ CI repressor of coliphage 186 is required for prophage excision and binds near the phage attachment site. <i>Molecular Microbiology</i> , 1993, 10, 1139-1150. | 1.2  | 29        |

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|----|--|-----|-----------|
| 55 | Improved detection of helix-turn-helix DNA-binding motifs in protein sequences. Nucleic Acids Research, 1990, 18, 5019-5026.                           | 6.5 | 562       |
| 56 | Control of gene expression in the temperate coliphage 186. Journal of Molecular Biology, 1990, 214, 27-37.   | 2.0 | 44        |
| 57 | The prediction of helix-turn-helix DNA-binding regions in proteins. A reply to Yudkin. Protein Engineering, Design and Selection, 1988, 2, 174-175.    | 1.0 | 11        |
| 58 | Systematic method for the detection of potential $\lambda$ Cro-like DNA-binding regions in proteins. Journal of Molecular Biology, 1987, 194, 557-564. | 2.0 | 204       |
| 59 | Control of gene expression in the P2-related template coliphages. Journal of Molecular Biology, 1986, 191, 199-209.                                    | 2.0 | 50        |
| 60 | Control of Enhancer-Promoter Contact by Alternative DNA Loops. SSRN Electronic Journal, 0, , .   | 0.4 | 0         |