Ian B Dodd

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Improved detection of helix-turn-helix DNA-binding motifs in protein sequences. Nucleic Acids Research, 1990, 18, 5019-5026.	14.5	562
2	Theoretical Analysis of Epigenetic Cell Memory by Nucleosome Modification. Cell, 2007, 129, 813-822.	28.9	413
3	Systematic method for the detection of potential λ Cro-like DNA-binding regions in proteins. Journal of Molecular Biology, 1987, 194, 557-564.	4.2	204
4	One-Step Cloning and Chromosomal Integration of DNA. ACS Synthetic Biology, 2013, 2, 537-541.	3.8	189
5	Cooperativity in long-range gene regulation by the λ CI repressor. Genes and Development, 2004, 18, 344-354.	5.9	161
6	Octamerization of lambda CI repressor is needed for effective repression of PRM and efficient switching from lysogeny. Genes and Development, 2001, 15, 3013-3022.	5.9	159
7	DNA methylation in human epigenomes depends on local topology of CpG sites. Nucleic Acids Research, 2016, 44, 5123-5132.	14.5	153
8	Revisited gene regulation in bacteriophage λ. Current Opinion in Genetics and Development, 2005, 15, 145-152.	3.3	121
9	A Mathematical Model for Transcriptional Interference by RNA Polymerase Traffic in Escherichia coli. Journal of Molecular Biology, 2005, 346, 399-409.	4.2	96
10	Cro's role in the Cl–Cro bistable switch is critical for λ's transition from lysogeny to lytic development. Genes and Development, 2007, 21, 2461-2472.	5.9	84
11	Collaboration between CpG sites is needed for stable somatic inheritance of DNA methylation states. Nucleic Acids Research, 2014, 42, 2235-2244.	14.5	83
12	Potent Transcriptional Interference by Pausing of RNA Polymerases over a Downstream Promoter. Molecular Cell, 2009, 34, 545-555.	9.7	81
13	Programmable DNA looping using engineered bivalent dCas9 complexes. Nature Communications, 2017, 8, 1628.	12.8	60
14	Ultrasensitive gene regulation by positive feedback loops in nucleosome modification. Molecular Systems Biology, 2008, 4, 182.	7.2	58
15	Theory for the stability and regulation of epigenetic landscapes. Physical Biology, 2010, 7, 026010.	1.8	56
16	The Generation of Promoter-Mediated Transcriptional Noise in Bacteria. PLoS Computational Biology, 2008, 4, e1000109.	3.2	52
17	Control of gene expression in the P2-related template coliphages. Journal of Molecular Biology, 1986, 191, 199-209.	4.2	50
18	Barriers and Silencers: A Theoretical Toolkit for Control and Containment of Nucleosome-Based Epigenetic States. Journal of Molecular Biology, 2011, 414, 624-637.	4.2	50

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19	Why Do Phage Play Dice?. Journal of Virology, 2009, 83, 11416-11420.	3.4	49
20	Quantitation of the DNA tethering effect in long-range DNA looping in vivo and in vitro using the Lac and λ repressors. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 349-354.	7.1	47
21	Control of gene expression in the temperate coliphage 186. Journal of Molecular Biology, 1990, 214, 27-37.	4.2	44
22	A Simple Histone Code Opens Many Paths to Epigenetics. PLoS Computational Biology, 2012, 8, e1002643.	3.2	44
23	Road rules for traffic on DNA—systematic analysis of transcriptional roadblocking <i>in vivo</i> . Nucleic Acids Research, 2014, 42, 8861-8872.	14.5	44
24	Action at a distance in CI repressor regulation of the bacteriophage 186 genetic switch. Molecular Microbiology, 2002, 45, 697-710.	2.5	43
25	Identification of residues in the N-terminal PAS domains important for dimerization of Arnt and AhR. Nucleic Acids Research, 2011, 39, 3695-3709.	14.5	37
26	Enhancer-like long-range transcriptional activation by λ CI-mediated DNA looping. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2922-2927.	7.1	34
27	Economy of Operon Formation: Cotranscription Minimizes Shortfall in Protein Complexes. MBio, 2010, 1, .	4.1	31
28	The Structural Basis of Cooperative Regulation at an Alternate Genetic Switch. Molecular Cell, 2006, 21, 605-615.	9.7	30
29	The Cro-like Apl repressor of coliphage 186 is required for prophage excision and binds near the phage attachment site. Molecular Microbiology, 1993, 10, 1139-1150.	2.5	29
30	Quantitation of interactions between two DNA loops demonstrates loop domain insulation in <i>E. coli</i> cells. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4449-57.	7.1	25
31	The role of repressor kinetics in relief of transcriptional interference between convergent promoters. Nucleic Acids Research, 2016, 44, 6625-6638.	14.5	25
32	Directing traffic on DNA—How transcription factors relieve or induce transcriptional interference. Transcription, 2017, 8, 120-125.	3.1	25
33	Defining the SOS Operon of Coliphage 186. Virology, 1996, 219, 105-114.	2.4	23
34	Functional Alignment of Regulatory Networks: A Study of Temperate Phages. PLoS Computational Biology, 2005, 1, e74.	3.2	23
35	TheEscherichia coliRetrons Ec67 and Ec86 Replace DNA between thecosSite and a Transcription Terminator of a 186-Related Prophage. Virology, 1996, 219, 115-124.	2.4	22
36	DNA Binding by the Coliphage 186 Repressor Protein Cl. Journal of Biological Chemistry, 1996, 271, 11532-11540.	3.4	22

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37	The Late-Expressed Region of the Temperate Coliphage 186 Genome. Virology, 1998, 248, 117-130.	2.4	22
38	The Helix-Turn-Helix Motif of the Coliphage 186 Immunity Repressor Binds to Two Distinct Recognition Sequences. Journal of Biological Chemistry, 2002, 277, 3186-3194.	3.4	22
39	Single molecule analysis of DNA wrapping and looping by a circular 14mer wheel of the bacteriophage 186 CI repressor. Nucleic Acids Research, 2013, 41, 5746-5756.	14.5	22
40	Bacteriophage P4 Vis protein is needed for prophage excision. Virology, 2004, 322, 82-92.	2.4	21
41	Modelling Transcriptional Interference and DNA Looping in Gene Regulation. Journal of Molecular Biology, 2007, 369, 1200-1213.	4.2	21
42	Positive and Negative Control of Enhancer-Promoter Interactions by Other DNA Loops Generates Specificity and Tunability. Cell Reports, 2019, 26, 2419-2433.e3.	6.4	19
43	Cooperative stabilization of the SIR complex provides robust epigenetic memory in a model of SIR silencing in <i>Saccharomyces cerevisiae</i> . Epigenetics, 2015, 10, 293-302.	2.7	17
44	Minimal Gene Regulatory Circuits for a Lysis-Lysogeny Choice in the Presence of Noise. PLoS ONE, 2010, 5, e15037.	2.5	16
45	Minimal Gene Regulatory Circuits that Can Count like Bacteriophage Lambda. Journal of Molecular Biology, 2009, 394, 681-693.	4.2	12
46	The prediction of helix-turn-helix DNA-binding regions in proteins. A reply to Yudkin. Protein Engineering, Design and Selection, 1988, 2, 174-175.	2.1	11
47	Nucleosome dynamics and maintenance of epigenetic states of CpG islands. Physical Review E, 2016, 93, 062417.	2.1	11
48	Network models of phage-bacteria coevolution. Physical Review E, 2006, 74, 066105.	2.1	9
49	Efficient chromosomal-scale DNA looping in Escherichia coli using multiple DNA-looping elements. Nucleic Acids Research, 2017, 45, 5074-5085.	14.5	7
50	The loopometer: a quantitative <i>in vivo</i> assay for DNA-looping proteins. Nucleic Acids Research, 2021, 49, e39-e39.	14.5	6
51	Promoter Activation by CII, a Potent Transcriptional Activator from Bacteriophage 186. Journal of Biological Chemistry, 2014, 289, 32094-32108.	3.4	5
52	RNA polymerase pausing at a protein roadblock can enhance transcriptional interference by promoter occlusion. FEBS Letters, 2019, 593, 903-917.	2.8	5
53	Bacteriophage lambda repressor mediates the formation of a complex enhancer-like structure. Transcription, 2013, 4, 201-205.	3.1	3
54	Instability of CII is needed for efficient switching between lytic and lysogenic development in bacteriophage 186. Nucleic Acids Research, 2020, 48, 12030-12041.	14.5	3

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55	Modeling Bistable Chromatin States. , 2017, , 145-168.		2
56	A quantitative binding model for the Apl protein, the dual purpose recombination-directionality factor and lysis-lysogeny regulator of bacteriophage 186. Nucleic Acids Research, 2020, 48, 8914-8926.	14.5	1
57	The pIT5 Plasmid Series, an Improved Toolkit for Repeated Genome Integration in <i>E. coli</i> . ACS Synthetic Biology, 2021, 10, 1633-1639.	3.8	1
58	Analysis of Infection Time Courses Shows CII Levels Determine the Frequency of Lysogeny in Phage 186. Pharmaceuticals, 2021, 14, 998.	3.8	1
59	In Silico, InÂVitro, and InÂVivo Estimation of J-Factors for LAC Repressor-Mediated DNA Loop Formation. Biophysical Journal, 2013, 104, 174a-175a.	0.5	0
60	Control of Enhancer-Promoter Contact by Alternative DNA Loops. SSRN Electronic Journal, 0, , .	0.4	0