

Ian B Dodd

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

3,467
citations

201658

27
h-index

149686

56
g-index

63
all docs

63
docs citations

63
times ranked

3141
citing authors

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

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19	Why Do Phage Play Dice?. <i>Journal of Virology</i> , 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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 349-354.	7.1	47
21	Control of gene expression in the temperate coliphage 186. <i>Journal of Molecular Biology</i> , 1990, 214, 27-37.	4.2	44
22	A Simple Histone Code Opens Many Paths to Epigenetics. <i>PLoS Computational Biology</i> , 2012, 8, e1002643.	3.2	44
23	Road rules for traffic on DNA—systematic analysis of transcriptional roadblocking in vivo. <i>Nucleic Acids Research</i> , 2014, 42, 8861-8872.	14.5	44
24	Action at a distance in CI repressor regulation of the bacteriophage 186 genetic switch. <i>Molecular Microbiology</i> , 2002, 45, 697-710.	2.5	43
25	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.	14.5	37
26	Enhancer-like long-range transcriptional activation by λ CI-mediated DNA looping. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2922-2927.	7.1	34
27	Economy of Operon Formation: Cotranscription Minimizes Shortfall in Protein Complexes. <i>MBio</i> , 2010, 1, .	4.1	31
28	The Structural Basis of Cooperative Regulation at an Alternate Genetic Switch. <i>Molecular Cell</i> , 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. <i>Molecular Microbiology</i> , 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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4449-57.	7.1	25
31	The role of repressor kinetics in relief of transcriptional interference between convergent promoters. <i>Nucleic Acids Research</i> , 2016, 44, 6625-6638.	14.5	25
32	Directing traffic on DNA—How transcription factors relieve or induce transcriptional interference. <i>Transcription</i> , 2017, 8, 120-125.	3.1	25
33	Defining the SOS Operon of Coliphage 186. <i>Virology</i> , 1996, 219, 105-114.	2.4	23
34	Functional Alignment of Regulatory Networks: A Study of Temperate Phages. <i>PLoS Computational Biology</i> , 2005, 1, e74.	3.2	23
35	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.	2.4	22
36	DNA Binding by the Coliphage 186 Repressor Protein CI. <i>Journal of Biological Chemistry</i> , 1996, 271, 11532-11540.	3.4	22

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37	The Late-Expressed Region of the Temperate Coliphage 186 Genome. <i>Virology</i> , 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. <i>Journal of Biological Chemistry</i> , 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. <i>Nucleic Acids Research</i> , 2013, 41, 5746-5756.	14.5	22
40	Bacteriophage P4 Vis protein is needed for prophage excision. <i>Virology</i> , 2004, 322, 82-92.	2.4	21
41	Modelling Transcriptional Interference and DNA Looping in Gene Regulation. <i>Journal of Molecular Biology</i> , 2007, 369, 1200-1213.	4.2	21
42	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.	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> . <i>Epigenetics</i> , 2015, 10, 293-302.	2.7	17
44	Minimal Gene Regulatory Circuits for a Lysis-Lysogeny Choice in the Presence of Noise. <i>PLoS ONE</i> , 2010, 5, e15037.	2.5	16
45	Minimal Gene Regulatory Circuits that Can Count like Bacteriophage Lambda. <i>Journal of Molecular Biology</i> , 2009, 394, 681-693.	4.2	12
46	The prediction of helix-turn-helix DNA-binding regions in proteins. A reply to Yudkin. <i>Protein Engineering, Design and Selection</i> , 1988, 2, 174-175.	2.1	11
47	Nucleosome dynamics and maintenance of epigenetic states of CpG islands. <i>Physical Review E</i> , 2016, 93, 062417.	2.1	11
48	Network models of phage-bacteria coevolution. <i>Physical Review E</i> , 2006, 74, 066105.	2.1	9
49	Efficient chromosomal-scale DNA looping in <i>Escherichia coli</i> using multiple DNA-looping elements. <i>Nucleic Acids Research</i> , 2017, 45, 5074-5085.	14.5	7
50	The loopometer: a quantitative <i>in vivo</i> assay for DNA-looping proteins. <i>Nucleic Acids Research</i> , 2021, 49, e39-e39.	14.5	6
51	Promoter Activation by CII, a Potent Transcriptional Activator from Bacteriophage 186. <i>Journal of Biological Chemistry</i> , 2014, 289, 32094-32108.	3.4	5
52	RNA polymerase pausing at a protein roadblock can enhance transcriptional interference by promoter occlusion. <i>FEBS Letters</i> , 2019, 593, 903-917.	2.8	5
53	Bacteriophage lambda repressor mediates the formation of a complex enhancer-like structure. <i>Transcription</i> , 2013, 4, 201-205.	3.1	3
54	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.	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, In Vitro, and In Vivo 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