

Mark D Biggin

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

4,506
citations

218677

26
h-index

189892

50
g-index

58
all docs

58
docs citations

58
times ranked

4793
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcription factors that activate the Ultrabithorax promoter in developmentally staged extracts. <i>Cell</i> , 1988, 53, 699-711.	28.9	477
2	Transcription Factors Bind Thousands of Active and Inactive Regions in the Drosophila Blastoderm. <i>PLoS Biology</i> , 2008, 6, e27.	5.6	428
3	Developmental roles of 21 Drosophila transcription factors are determined by quantitative differences in binding to an overlapping set of thousands of genomic regions. <i>Genome Biology</i> , 2009, 10, R80.	9.6	313
4	Animal Transcription Networks as Highly Connected, Quantitative Continua. <i>Developmental Cell</i> , 2011, 21, 611-626.	7.0	275
5	A Quantitative Spatiotemporal Atlas of Gene Expression in the Drosophila Blastoderm. <i>Cell</i> , 2008, 133, 364-374.	28.9	263
6	System wide analyses have underestimated protein abundances and the importance of transcription in mammals. <i>PeerJ</i> , 2014, 2, e270.	2.0	255
7	Large-Scale Turnover of Functional Transcription Factor Binding Sites in Drosophila. <i>PLoS Computational Biology</i> , 2006, 2, e130.	3.2	231
8	The role of chromatin accessibility in directing the widespread, overlapping patterns of Drosophila transcription factor binding. <i>Genome Biology</i> , 2011, 12, R34.	9.6	199
9	Binding Site Turnover Produces Pervasive Quantitative Changes in Transcription Factor Binding between Closely Related Drosophila Species. <i>PLoS Biology</i> , 2010, 8, e1000343.	5.6	184
10	Dynamic reprogramming of chromatin accessibility during Drosophila embryo development. <i>Genome Biology</i> , 2011, 12, R43.	9.6	174
11	A purified Drosophila homeodomain protein represses transcription in vitro. <i>Cell</i> , 1989, 58, 433-440.	28.9	157
12	Statistics requantitates the central dogma. <i>Science</i> , 2015, 347, 1066-1067.	12.6	155
13	Zeste encodes a sequence-specific transcription factor that activates the Ultrabithorax promoter in vitro. <i>Cell</i> , 1988, 53, 713-722.	28.9	152
14	Quantitative Models of the Mechanisms That Control Genome-Wide Patterns of Transcription Factor Binding during Early Drosophila Development. <i>PLoS Genetics</i> , 2011, 7, e1001290.	3.5	150
15	DNA regions bound at low occupancy by transcription factors do not drive patterned reporter gene expression in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 21330-21335.	7.1	141
16	Three-dimensional morphology and gene expression in the Drosophila blastoderm at cellular resolution I: data acquisition pipeline. <i>Genome Biology</i> , 2006, 7, R123.	9.6	121
17	Transcription factors and the control of Drosophila development. <i>Trends in Genetics</i> , 1989, 5, 377-383.	6.7	95
18	Three-dimensional morphology and gene expression in the Drosophila blastoderm at cellular resolution II: dynamics. <i>Genome Biology</i> , 2006, 7, R124.	9.6	94

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19	The specificity of protein-DNA crosslinking by formaldehyde: in vitro and in <i>Drosophila</i> embryos. <i>Nucleic Acids Research</i> , 2000, 28, 4e-4.	14.5	62
20	High-Throughput SELEX Determination of DNA Sequences Bound by Transcription Factors In Vitro. <i>Methods in Molecular Biology</i> , 2012, 786, 51-63.	0.9	52
21	Zeste maintains repression of <i>Ubx</i> transgenes: support for a new model of Polycomb repression. <i>Development (Cambridge)</i> , 2002, 129, 1339-1343.	2.5	52
22	A Conserved Developmental Patterning Network Produces Quantitatively Different Output in Multiple Species of <i>Drosophila</i> . <i>PLoS Genetics</i> , 2011, 7, e1002346.	3.5	51
23	A Tagless Strategy for Identification of Stable Protein Complexes Genome-wide by Multidimensional Orthogonal Chromatographic Separation and iTRAQ Reagent Tracking. <i>Journal of Proteome Research</i> , 2008, 7, 1836-1849.	3.7	46
24	Visual Exploration of Three-Dimensional Gene Expression Using Physical Views and Linked Abstract Views. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 296-309.	3.0	30
25	Survey of large protein complexes in <i>D. vulgaris</i> reveals great structural diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16580-16585.	7.1	29
26	Integrating Data Clustering and Visualization for the Analysis of 3D Gene Expression Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2010, 7, 64-79.	3.0	28
27	Quantitating translational control: mRNA abundance-dependent and independent contributions and the mRNA sequences that specify them. <i>Nucleic Acids Research</i> , 2017, 45, 11821-11836.	14.5	28
28	To bind or not to bind. <i>Nature Genetics</i> , 2001, 28, 303-304.	21.4	22
29	High-throughput Isolation and Characterization of Untagged Membrane Protein Complexes: Outer Membrane Complexes of <i>Desulfovibrio vulgaris</i> . <i>Journal of Proteome Research</i> , 2012, 11, 5720-5735.	3.7	22
30	Measurement of in Vivo DNA Binding by Sequence-Specific Transcription Factors Using UV Cross-Linking. <i>Methods</i> , 1997, 11, 215-224.	3.8	20
31	Exploiting regulatory heterogeneity to systematically identify enhancers with high accuracy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 900-908.	7.1	20
32	Transcriptional regulation in <i>Drosophila</i> : the post-genome challenge. <i>Functional and Integrative Genomics</i> , 2001, 1, 223-234.	3.5	18
33	Octomeric pyruvate-ferredoxin oxidoreductase from <i>Desulfovibrio vulgaris</i> . <i>Journal of Structural Biology</i> , 2007, 159, 9-18.	2.8	16
34	Bacterial Interactomes: Interacting Protein Partners Share Similar Function and Are Validated in Independent Assays More Frequently Than Previously Reported. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1539-1555.	3.8	16
35	Accessibility of transcriptionally inactive genes is specifically reduced at homeoprotein-DNA binding sites in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2000, 28, 2839-2846.	14.5	13
36	Automated Iterative MS/MS Acquisition: A Tool for Improving Efficiency of Protein Identification Using a LC-MALDI MS Workflow. <i>Analytical Chemistry</i> , 2011, 83, 6286-6293.	6.5	13

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37	Quantitative Tagless Copurification: A Method to Validate and Identify Protein-Protein Interactions. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2186-2202.	3.8	12
38	Volumetric Semantic Segmentation Using Pyramid Context Features. , 2013, 2013, 3448-3455.		10
39	Automatic channel unmixing for high-throughput quantitative analysis of fluorescence images. <i>Optics Express</i> , 2007, 15, 12306.	3.4	9
40	Nonparametric identification of regulatory interactions from spatial and temporal gene expression data. <i>BMC Bioinformatics</i> , 2010, 11, 413.	2.6	9
41	Building quantitative, three-dimensional atlases of gene expression and morphology at cellular resolution. <i>Wiley Interdisciplinary Reviews: Developmental Biology</i> , 2013, 2, 767-779.	5.9	9
42	Ultraviolet cross-linking assay to measure sequence-specific DNA binding in vivo. <i>Methods in Enzymology</i> , 1999, 304, 496-515.	1.0	8
43	Coupling visualization and data analysis for knowledge discovery from multi-dimensional scientific data. <i>Procedia Computer Science</i> , 2010, 1, 1757-1764.	2.0	8
44	An In Vivo UV Crosslinking Assay That Detects DNA Binding by Sequence-Specific Transcription Factors. , 1999, 119, 497-508.		6
45	A model for sequential evolution of ligands by exponential enrichment (SELEX) data. <i>Annals of Applied Statistics</i> , 2012, 6, .	1.1	6
46	Quantitative Models of the Mechanisms that Control Genome-Wide Patterns of Animal Transcription Factor Binding. <i>Methods in Cell Biology</i> , 2012, 110, 263-283.	1.1	6
47	Genome-Wide In Vivo Cross-linking of Sequence-Specific Transcription Factors. <i>Methods in Molecular Biology</i> , 2012, 809, 3-26.	0.9	6
48	MyoD, a Lesson in Widespread DNA Binding. <i>Developmental Cell</i> , 2010, 18, 505-506.	7.0	5
49	A multichannel gel electrophoresis and continuous fraction collection apparatus for high-throughput protein separation and characterization. <i>Electrophoresis</i> , 2010, 31, 440-447.	2.4	4
50	Mapping Organism Expression Levels at Cellular Resolution in Developing Drosophila. <i>Microscopy and Microanalysis</i> , 2001, 7, 10-11.	0.4	1
51	A Multichannel Gel Electrophoresis and Continuous Fraction Collection Apparatus for High-Throughput Protein Separation and Characterization. <i>Methods in Molecular Biology</i> , 2012, 869, 373-384.	0.9	1
52	A Multichannel Gel Electrophoresis and Continuous Fraction Collection Apparatus for High-Throughput Protein Separation and Characterization. <i>Methods in Molecular Biology</i> , 2019, 1855, 437-448.	0.9	1
53	Mapping organism expression levels at cellular resolution in developing Drosophila. <i>Microscopy and Microanalysis</i> , 2002, 8, 1044-1045.	0.4	0
54	Visually Relating Gene Expression and in vivo DNA Binding Data. , 2011, , .		0

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55	Nonparametric Variable Selection and Modeling for Spatial and Temporal Regulatory Networks. Methods in Cell Biology, 2012, 110, 243-261.	1.1	0