

Michael B Eisen

List of Publications by Year in descending order

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Version: 2024-02-01

135
papers

55,720
citations

13854

67
h-index

11928

134
g-index

176
all docs

176
docs citations

176
times ranked

51121
citing authors

#	ARTICLE	IF	CITATIONS
1	Rapid global phaseout of animal agriculture has the potential to stabilize greenhouse gas levels for 30 years and offset 68 percent of CO2 emissions this century. , 2022, 1, e0000010.		62
2	Single-nucleus RNA-sequencing in pre-cellularization <i>Drosophila melanogaster</i> embryos. PLoS ONE, 2022, 17, e0270471.	1.1	5
3	A phylogeny for the <i>Drosophila montium</i> species group: A model clade for comparative analyses. Molecular Phylogenetics and Evolution, 2021, 158, 107061.	1.2	19
4	Rigorous review and editorial oversight of clinical preprints. ELife, 2021, 10, .	2.8	2
5	Impact of essential workers in the context of social distancing for epidemic control. PLoS ONE, 2021, 16, e0255680.	1.1	13
6	Whole Genome Sequences of 23 Species from the <i>Drosophila montium</i> Species Group (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 10, 1443-1455.	0.8	16
7	Publishing in the time of COVID-19. ELife, 2020, 9, .	2.8	54
8	We need to act now. ELife, 2020, 9, .	2.8	9
9	Kinetic sculpting of the seven stripes of the <i>Drosophila</i> even-skipped gene. ELife, 2020, 9, .	2.8	32
10	Implementing a "publish, then review" model of publishing. ELife, 2020, 9, .	2.8	25
11	Plan U: Universal access to scientific and medical research via funder preprint mandates. PLoS Biology, 2019, 17, e3000273.	2.6	28
12	Rapid Global Spread of wRi-like Wolbachia across Multiple <i>Drosophila</i> . Current Biology, 2018, 28, 963-971.e8.	1.8	127
13	Convergent evolution of gene expression in two high-toothed stickleback populations. PLoS Genetics, 2018, 14, e1007443.	1.5	32
14	Association mapping from sequencing reads using k-mers. ELife, 2018, 7, .	2.8	88
15	Single Molecule Imaging in Live Embryos Using Lattice Light-Sheet Microscopy. Methods in Molecular Biology, 2018, 1814, 541-559.	0.4	24
16	Gene family innovation, conservation and loss on the animal stem lineage. ELife, 2018, 7, .	2.8	149
17	Patterns of chromatin accessibility along the anterior-posterior axis in the early <i>Drosophila</i> embryo. PLoS Genetics, 2018, 14, e1007367.	1.5	38
18	The ecology of the <i>Drosophila</i> -yeast mutualism in wineries. PLoS ONE, 2018, 13, e0196440.	1.1	34

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19	Robust manipulation of the behavior of <i>Drosophila melanogaster</i> by a fungal pathogen in the laboratory. <i>ELife</i> , 2018, 7, .	2.8	58
20	Dynamic multifactor hubs interact transiently with sites of active transcription in <i>Drosophila</i> embryos. <i>ELife</i> , 2018, 7, .	2.8	149
21	Patterns of Genome-Wide Diversity and Population Structure in the <i>Drosophila athabasca</i> Species Complex. <i>Molecular Biology and Evolution</i> , 2017, 34, 1912-1923.	3.5	17
22	Atlas of gene expression, patterns from every cell. <i>Science</i> , 2017, 358, 172-173.	6.0	5
23	A molecular atlas of the developing ectoderm defines neural, neural crest, placode, and nonneural progenitor identity in vertebrates. <i>PLoS Biology</i> , 2017, 15, e2004045.	2.6	44
24	Dense Bicoid hubs accentuate binding along the morphogen gradient. <i>Genes and Development</i> , 2017, 31, 1784-1794.	2.7	161
25	Genome-wide measurement of spatial expression in patterning mutants of <i>Drosophila melanogaster</i> . <i>F1000Research</i> , 2017, 6, 41.	0.8	27
26	Convergence of topological domain boundaries, insulators, and polytene interbands revealed by high-resolution mapping of chromatin contacts in the early <i>Drosophila melanogaster</i> embryo. <i>ELife</i> , 2017, 6, .	2.8	81
27	Stable Host Gene Expression in the Gut of Adult <i>Drosophila melanogaster</i> with Different Bacterial Mono-Associations. <i>PLoS ONE</i> , 2016, 11, e0167357.	1.1	23
28	The genome of the crustacean <i>Parhyale hawaiiensis</i> , a model for animal development, regeneration, immunity and lignocellulose digestion. <i>ELife</i> , 2016, 5, .	2.8	130
29	Ten Years of <i>PLoS Computational Biology</i> : A Decade of Appreciation and Innovation. <i>PLoS Computational Biology</i> , 2015, 11, e1004317.	1.5	1
30	Sex Bias and Maternal Contribution to Gene Expression Divergence in <i>Drosophila</i> Blastoderm Embryos. <i>PLoS Genetics</i> , 2015, 11, e1005592.	1.5	26
31	Low-cost, low-input RNA-seq protocols perform nearly as well as high-input protocols. <i>PeerJ</i> , 2015, 3, e869.	0.9	24
32	Transcriptional Activation of the Zygotic Genome in <i>Drosophila</i> . <i>Current Topics in Developmental Biology</i> , 2015, 113, 85-112.	1.0	58
33	Oxygen changes drive non-uniform scaling in <i>Drosophila melanogaster</i> embryogenesis. <i>F1000Research</i> , 2015, 4, 1102.	0.8	5
34	Structural Variation among Wild and Industrial Strains of <i>Penicillium chrysogenum</i> . <i>PLoS ONE</i> , 2014, 9, e96784.	1.1	5
35	<i>Drosophila</i> Embryogenesis Scales Uniformly across Temperature in Developmentally Diverse Species. <i>PLoS Genetics</i> , 2014, 10, e1004293.	1.5	109
36	Sex-Specific Embryonic Gene Expression in Species with Newly Evolved Sex Chromosomes. <i>PLoS Genetics</i> , 2014, 10, e1004159.	1.5	25

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37	Comparative validation of the <i>D. melanogaster</i> modENCODE transcriptome annotation. <i>Genome Research</i> , 2014, 24, 1209-1223.	2.4	147
38	<i>Saccharomyces cerevisiae</i> mitochondria are required for optimal attractiveness to <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2014, 9, e113899.	1.1	19
39	Establishment of regions of genomic activity during the <i>Drosophila</i> maternal to zygotic transition. <i>ELife</i> , 2014, 3, .	2.8	170
40	Characterization of the transcriptome, nucleotide sequence polymorphism, and natural selection in the desert adapted mouse <i>Peromyscus eremicus</i> . <i>PeerJ</i> , 2014, 2, e642.	0.9	34
41	Insights into the evolution of Darwin's finches from comparative analysis of the <i>Geospiza magnirostris</i> genome sequence. <i>BMC Genomics</i> , 2013, 14, 95.	1.2	38
42	A second-generation assembly of the <i>Drosophila simulans</i> genome provides new insights into patterns of lineage-specific divergence. <i>Genome Research</i> , 2013, 23, 89-98.	2.4	157
43	An Essential Role for Zygotic Expression in the Pre-Cellular <i>Drosophila</i> Embryo. <i>PLoS Genetics</i> , 2013, 9, e1003428.	1.5	57
44	Extensive Divergence of Transcription Factor Binding in <i>Drosophila</i> Embryos with Highly Conserved Gene Expression. <i>PLoS Genetics</i> , 2013, 9, e1003748.	1.5	93
45	Dual functions of TAF7L in adipocyte differentiation. <i>ELife</i> , 2013, 2, e00170.	2.8	41
46	Spatial Promoter Recognition Signatures May Enhance Transcription Factor Specificity in Yeast. <i>PLoS ONE</i> , 2013, 8, e53778.	1.1	2
47	Sequencing mRNA from Cryo-Sliced <i>Drosophila</i> Embryos to Determine Genome-Wide Spatial Patterns of Gene Expression. <i>PLoS ONE</i> , 2013, 8, e71820.	1.1	64
48	Mice Infected with Low-Virulence Strains of <i>Toxoplasma gondii</i> Lose Their Innate Aversion to Cat Urine, Even after Extensive Parasite Clearance. <i>PLoS ONE</i> , 2013, 8, e75246.	1.1	106
49	Improving transcriptome assembly through error correction of high-throughput sequence reads. <i>PeerJ</i> , 2013, 1, e113.	0.9	38
50	The Enigmatic Conservation of a Rap1 Binding Site in the <i>Saccharomyces cerevisiae</i> HMR-E Silencer. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1555-1562.	0.8	5
51	Probing the Informational and Regulatory Plasticity of a Transcription Factor DNA-Binding Domain. <i>PLoS Genetics</i> , 2012, 8, e1002614.	1.5	23
52	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.	3.3	141
53	A model for sequential evolution of ligands by exponential enrichment (SELEX) data. <i>Annals of Applied Statistics</i> , 2012, 6, .	0.5	6
54	The Awesome Power of Yeast Evolutionary Genetics: New Genome Sequences and Strain Resources for the <i>Saccharomyces sensu stricto</i> Genus. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 11-25.	0.8	348

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55	The role of chromatin accessibility in directing the widespread, overlapping patterns of Drosophila transcription factor binding. <i>Genome Biology</i> , 2011, 12, R34.	13.9	199
56	Control of Embryonic Stem Cell Lineage Commitment by Core Promoter Factor, TAF3. <i>Cell</i> , 2011, 146, 720-731.	13.5	155
57	Noncanonical Compensation of Zygotic X Transcription in Early Drosophila melanogaster Development Revealed through Single-Embryo RNA-Seq. <i>PLoS Biology</i> , 2011, 9, e1000590.	2.6	195
58	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.	1.5	150
59	Zelda Binding in the Early Drosophila melanogaster Embryo Marks Regions Subsequently Activated at the Maternal-to-Zygotic Transition. <i>PLoS Genetics</i> , 2011, 7, e1002266.	1.5	306
60	A Conserved Developmental Patterning Network Produces Quantitatively Different Output in Multiple Species of Drosophila. <i>PLoS Genetics</i> , 2011, 7, e1002346.	1.5	51
61	Coupling visualization and data analysis for knowledge discovery from multi-dimensional scientific data. <i>Procedia Computer Science</i> , 2010, 1, 1757-1764.	1.2	8
62	DNA dealt wrong hand on cover. <i>Nature</i> , 2010, 467, 401-401.	13.7	9
63	Exploring the Genetic Basis of Variation in Gene Predictions with a Synthetic Association Study. <i>PLoS ONE</i> , 2010, 5, e11645.	1.1	0
64	The Fitness Landscapes of cis-Acting Binding Sites in Different Promoter and Environmental Contexts. <i>PLoS Genetics</i> , 2010, 6, e1001042.	1.5	32
65	Binding Site Turnover Produces Pervasive Quantitative Changes in Transcription Factor Binding between Closely Related Drosophila Species. <i>PLoS Biology</i> , 2010, 8, e1000343.	2.6	184
66	Evolutionary Mirages: Selection on Binding Site Composition Creates the Illusion of Conserved Grammars in Drosophila Enhancers. <i>PLoS Genetics</i> , 2010, 6, e1000829.	1.5	70
67	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.	1.9	28
68	Big Genomes Facilitate the Comparative Identification of Regulatory Elements. <i>PLoS ONE</i> , 2009, 4, e4688.	1.1	41
69	Open Access: The Sooner the Better. <i>Science</i> , 2009, 325, 266-266.	6.0	0
70	Identification of direct T-box target genes in the developing zebrafish mesoderm. <i>Development (Cambridge)</i> , 2009, 136, 749-760.	1.2	48
71	A condensin-like dosage compensation complex acts at a distance to control expression throughout the genome. <i>Genes and Development</i> , 2009, 23, 602-618.	2.7	99
72	Genome-wide Analysis of Alternative Pre-mRNA Splicing and RNA-Binding Specificities of the Drosophila hnRNP A/B Family Members. <i>Molecular Cell</i> , 2009, 33, 438-449.	4.5	79

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73	Developmental roles of 21 <i>Drosophila</i> 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.	13.9	313
74	Genome-Wide Transcriptional Response of <i>Silurana (Xenopus) tropicalis</i> to Infection with the Deadly Chytrid Fungus. <i>PLoS ONE</i> , 2009, 4, e6494.	1.1	84
75	Impact of Chromatin Structures on DNA Processing for Genomic Analyses. <i>PLoS ONE</i> , 2009, 4, e6700.	1.1	115
76	Identifying Cis-Regulatory Sequences by Word Profile Similarity. <i>PLoS ONE</i> , 2009, 4, e6901.	1.1	22
77	Association of cohesin and Nipped-B with transcriptionally active regions of the <i>Drosophila melanogaster</i> genome. <i>Chromosoma</i> , 2008, 117, 89-102.	1.0	194
78	Global gene expression profiles for life stages of the deadly amphibian pathogen <i>Batrachochytrium dendrobatidis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 17034-17039.	3.3	101
79	A Quantitative Spatiotemporal Atlas of Gene Expression in the <i>Drosophila</i> Blastoderm. <i>Cell</i> , 2008, 133, 364-374.	13.5	263
80	Silent but Not Static: Accelerated Base-Pair Substitution in Silenced Chromatin of Budding Yeasts. <i>PLoS Genetics</i> , 2008, 4, e1000247.	1.5	32
81	NELF and GAGA Factor Are Linked to Promoter-Proximal Pausing at Many Genes in <i>Drosophila</i> . <i>Molecular and Cellular Biology</i> , 2008, 28, 3290-3300.	1.1	198
82	Tools for neuroanatomy and neurogenetics in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 9715-9720.	3.3	902
83	A Careful Look at Binding Site Reorganization in the even-skipped Enhancers of <i>Drosophila</i> and Sepsids. <i>PLoS Genetics</i> , 2008, 4, e1000268.	1.5	28
84	Transcription Factors Bind Thousands of Active and Inactive Regions in the <i>Drosophila</i> Blastoderm. <i>PLoS Biology</i> , 2008, 6, e27.	2.6	428
85	Sepsid even-skipped Enhancers Are Functionally Conserved in <i>Drosophila</i> Despite Lack of Sequence Conservation. <i>PLoS Genetics</i> , 2008, 4, e1000106.	1.5	262
86	Automatic image analysis for gene expression patterns of fly embryos. <i>BMC Cell Biology</i> , 2007, 8, S7.	3.0	58
87	Discovery of functional elements in 12 <i>Drosophila</i> genomes using evolutionary signatures. <i>Nature</i> , 2007, 450, 219-232.	13.7	573
88	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	13.7	1,886
89	Determining Physical Constraints in Transcriptional Initiation Complexes Using DNA Sequence Analysis. <i>PLoS ONE</i> , 2007, 2, e1199.	1.1	8
90	Three-dimensional morphology and gene expression in the <i>Drosophila</i> blastoderm at cellular resolution I: data acquisition pipeline. <i>Genome Biology</i> , 2006, 7, R123.	13.9	121

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91	Primate-specific evolution of an LDLR enhancer. <i>Genome Biology</i> , 2006, 7, R68.	13.9	16
92	Rapid quantitative profiling of complex microbial populations. <i>Nucleic Acids Research</i> , 2006, 34, e5-e5.	6.5	158
93	Flexible promoter architecture requirements for coactivator recruitment. <i>BMC Molecular Biology</i> , 2006, 7, 16.	3.0	19
94	In vivo enhancer analysis of human conserved non-coding sequences. <i>Nature</i> , 2006, 444, 499-502.	13.7	1,072
95	Detecting the limits of regulatory element conservation and divergence estimation using pairwise and multiple alignments. <i>BMC Bioinformatics</i> , 2006, 7, 376.	1.2	46
96	Design of a combinatorial DNA microarray for protein-DNA interaction studies. <i>BMC Bioinformatics</i> , 2006, 7, 429.	1.2	24
97	Widespread Discordance of Gene Trees with Species Tree in <i>Drosophila</i> : Evidence for Incomplete Lineage Sorting. <i>PLoS Genetics</i> , 2006, 2, e173.	1.5	319
98	Large-Scale Turnover of Functional Transcription Factor Binding Sites in <i>Drosophila</i> . <i>PLoS Computational Biology</i> , 2006, 2, e130.	1.5	231
99	GATA: a graphic alignment tool for comparative sequence analysis. <i>BMC Bioinformatics</i> , 2005, 6, 9.	1.2	70
100	Aging and Gene Expression in the Primate Brain. <i>PLoS Biology</i> , 2005, 3, e274.	2.6	160
101	Identification of oligonucleotide sequences that direct the movement of the <i>Escherichia coli</i> FtsK translocase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 17618-17623.	3.3	109
102	Functional genomic analysis of the rates of protein evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5483-5488.	3.3	255
103	Title is missing!. <i>Genome Biology</i> , 2005, 6, P7.	13.9	63
104	Serendipitous discovery of <i>Wolbachia</i> genomes in multiple <i>Drosophila</i> species. <i>Genome Biology</i> , 2005, 6, R23.	13.9	126
105	<i>PLoS Computational Biology: A New Community Journal</i> . <i>PLoS Computational Biology</i> , 2005, 1, e4.	1.5	7
106	Coevolution of gene expression among interacting proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9033-9038.	3.3	221
107	Conservation and Evolution of Cis-Regulatory Systems in Ascomycete Fungi. <i>PLoS Biology</i> , 2004, 2, e398.	2.6	207
108	<i>PLoS Medicine</i> – A Medical Journal for the Internet Age. <i>PLoS Medicine</i> , 2004, 1, e31.	3.9	8

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109	Noise Minimization in Eukaryotic Gene Expression. PLoS Biology, 2004, 2, e137.	2.6	370
110	Benchmarking tools for the alignment of functional noncoding DNA. BMC Bioinformatics, 2004, 5, 6.	1.2	99
111	MONKEY: identifying conserved transcription-factor binding sites in multiple alignments using a binding site-specific evolutionary model. Genome Biology, 2004, 5, R98.	13.9	134
112	Computational identification of developmental enhancers: conservation and function of transcription factor binding-site clusters in Drosophila melanogaster and Drosophila pseudoobscura. Genome Biology, 2004, 5, R61.	13.9	184
113	Population genetic variation in gene expression is associated with phenotypic variation in Saccharomyces cerevisiae. Genome Biology, 2004, 5, R26.	13.9	200
114	Position specific variation in the rate of evolution in transcription factor binding sites. BMC Evolutionary Biology, 2003, 3, 19.	3.2	130
115	Phylogenetically and spatially conserved word pairs associated with gene-expression changes in yeasts. Genome Biology, 2003, 4, R43.	13.9	44
116	Why PLoS Became a Publisher. PLoS Biology, 2003, 1, e36.	2.6	76
117	Exploiting transcription factor binding site clustering to identify cis-regulatory modules involved in pattern formation in the Drosophila genome. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 757-762.	3.3	541
118	Exploring the conditional coregulation of yeast gene expression through fuzzy k-means clustering. Genome Biology, 2002, 3, research0059.1.	13.9	362
119	The Stanford Microarray Database. Nucleic Acids Research, 2001, 29, 152-155.	6.5	415
120	Systematic variation in gene expression patterns in human cancer cell lines. Nature Genetics, 2000, 24, 227-235.	9.4	1,946
121	A gene expression database for the molecular pharmacology of cancer. Nature Genetics, 2000, 24, 236-244.	9.4	1,357
122	Large-scale identification of secreted and membrane-associated gene products using DNA microarrays. Nature Genetics, 2000, 25, 58-62.	9.4	241
123	Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. Nature, 2000, 403, 503-511.	13.7	8,977
124	Molecular portraits of human breast tumours. Nature, 2000, 406, 747-752.	13.7	13,397
125	The yeast mitochondrial transport proteins: new sequences and consensus residues, lack of direct relation between consensus residues and transmembrane helices, expression patterns of the transport protein genes, and protein-protein interactions with other proteins. Biochimica Et Biophysica Acta - Biomembranes, 2000, 1467, 207-218.	1.4	42
126	'Gene shaving' as a method for identifying distinct sets of genes with similar expression patterns. Genome Biology, 2000, 1, research0003.1.	13.9	392

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127	Genomic Expression Programs in the Response of Yeast Cells to Environmental Changes. <i>Molecular Biology of the Cell</i> , 2000, 11, 4241-4257.	0.9	4,281
128	Genome-wide analysis of DNA copy-number changes using cDNA microarrays. <i>Nature Genetics</i> , 1999, 23, 41-46.	9.4	928
129	Gene expression informatics â€”it's all in your mine. <i>Nature Genetics</i> , 1999, 21, 51-55.	9.4	375
130	The Transcriptional Program in the Response of Human Fibroblasts to Serum. <i>Science</i> , 1999, 283, 83-87.	6.0	1,895
131	[12] DNA arrays for analysis of gene expression. <i>Methods in Enzymology</i> , 1999, 303, 179-205.	0.4	896
132	Comprehensive Identification of Cell Cycleâ€”regulated Genes of the Yeast <i>Saccharomyces cerevisiae</i> by Microarray Hybridization. <i>Molecular Biology of the Cell</i> , 1998, 9, 3273-3297.	0.9	4,372
133	Binding of the Influenza A Virus to Cell-Surface Receptors: Structures of Five Hemagglutininâ€”Sialyloligosaccharide Complexes Determined by X-Ray Crystallography. <i>Virology</i> , 1997, 232, 19-31.	1.1	196
134	HOOK: A program for finding novel molecular architectures that satisfy the chemical and steric requirements of a macromolecule binding site. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 19, 199-221.	1.5	213
135	Regulation of gene expression by the intracellular second messengers IP3 and diacylglycerol. <i>Genesis</i> , 1988, 9, 351-358.	3.3	5