

Michael B Eisen

List of Publications by Year in descending order

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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	Molecular portraits of human breast tumours. <i>Nature</i> , 2000, 406, 747-752.	13.7	13,397
2	Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. <i>Nature</i> , 2000, 403, 503-511.	13.7	8,977
3	Comprehensive Identification of Cell Cycle-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
4	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
5	Systematic variation in gene expression patterns in human cancer cell lines. <i>Nature Genetics</i> , 2000, 24, 227-235.	9.4	1,946
6	The Transcriptional Program in the Response of Human Fibroblasts to Serum. <i>Science</i> , 1999, 283, 83-87.	6.0	1,895
7	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	13.7	1,886
8	A gene expression database for the molecular pharmacology of cancer. <i>Nature Genetics</i> , 2000, 24, 236-244.	9.4	1,357
9	In vivo enhancer analysis of human conserved non-coding sequences. <i>Nature</i> , 2006, 444, 499-502.	13.7	1,072
10	Genome-wide analysis of DNA copy-number changes using cDNA microarrays. <i>Nature Genetics</i> , 1999, 23, 41-46.	9.4	928
11	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
12	[12] DNA arrays for analysis of gene expression. <i>Methods in Enzymology</i> , 1999, 303, 179-205.	0.4	896
13	Discovery of functional elements in 12 <i>Drosophila</i> genomes using evolutionary signatures. <i>Nature</i> , 2007, 450, 219-232.	13.7	573
14	Exploiting transcription factor binding site clustering to identify cis-regulatory modules involved in pattern formation in the <i>Drosophila</i> genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 757-762.	3.3	541
15	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
16	The Stanford Microarray Database. <i>Nucleic Acids Research</i> , 2001, 29, 152-155.	6.5	415
17	'Gene shaving' as a method for identifying distinct sets of genes with similar expression patterns. <i>Genome Biology</i> , 2000, 1, research0003.1.	13.9	392
18	Gene expression informatics - it's all in your mine. <i>Nature Genetics</i> , 1999, 21, 51-55.	9.4	375

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19	Noise Minimization in Eukaryotic Gene Expression. <i>PLoS Biology</i> , 2004, 2, e137.	2.6	370
20	Exploring the conditional coregulation of yeast gene expression through fuzzy k-means clustering. <i>Genome Biology</i> , 2002, 3, research0059.1.	13.9	362
21	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
22	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
23	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
24	Zelda Binding in the Early <i>Drosophila melanogaster</i> Embryo Marks Regions Subsequently Activated at the Maternal-to-Zygotic Transition. <i>PLoS Genetics</i> , 2011, 7, e1002266.	1.5	306
25	A Quantitative Spatiotemporal Atlas of Gene Expression in the <i>Drosophila</i> Blastoderm. <i>Cell</i> , 2008, 133, 364-374.	13.5	263
26	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
27	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
28	Large-scale identification of secreted and membrane-associated gene products using DNA microarrays. <i>Nature Genetics</i> , 2000, 25, 58-62.	9.4	241
29	Large-Scale Turnover of Functional Transcription Factor Binding Sites in <i>Drosophila</i> . <i>PLoS Computational Biology</i> , 2006, 2, e130.	1.5	231
30	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
31	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
32	Conservation and Evolution of Cis-Regulatory Systems in Ascomycete Fungi. <i>PLoS Biology</i> , 2004, 2, e398.	2.6	207
33	Population genetic variation in gene expression is associated with phenotypic variation in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology</i> , 2004, 5, R26.	13.9	200
34	The role of chromatin accessibility in directing the widespread, overlapping patterns of <i>Drosophila</i> transcription factor binding. <i>Genome Biology</i> , 2011, 12, R34.	13.9	199
35	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
36	Binding of the Influenza A Virus to Cell-Surface Receptors: Structures of Five Hemagglutinin-Sialyloligosaccharide Complexes Determined by X-Ray Crystallography. <i>Virology</i> , 1997, 232, 19-31.	1.1	196

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37	Noncanonical Compensation of Zygotic X Transcription in Early <i>Drosophila melanogaster</i> Development Revealed through Single-Embryo RNA-Seq. <i>PLoS Biology</i> , 2011, 9, e1000590.	2.6	195
38	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
39	Computational identification of developmental enhancers: conservation and function of transcription factor binding-site clusters in <i>Drosophila melanogaster</i> and <i>Drosophila pseudoobscura</i> . <i>Genome Biology</i> , 2004, 5, R61.	13.9	184
40	Binding Site Turnover Produces Pervasive Quantitative Changes in Transcription Factor Binding between Closely Related <i>Drosophila</i> Species. <i>PLoS Biology</i> , 2010, 8, e1000343.	2.6	184
41	Establishment of regions of genomic activity during the <i>Drosophila</i> maternal to zygotic transition. <i>ELife</i> , 2014, 3, .	2.8	170
42	Dense Bicoid hubs accentuate binding along the morphogen gradient. <i>Genes and Development</i> , 2017, 31, 1784-1794.	2.7	161
43	Aging and Gene Expression in the Primate Brain. <i>PLoS Biology</i> , 2005, 3, e274.	2.6	160
44	Rapid quantitative profiling of complex microbial populations. <i>Nucleic Acids Research</i> , 2006, 34, e5-e5.	6.5	158
45	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
46	Control of Embryonic Stem Cell Lineage Commitment by Core Promoter Factor, TAF3. <i>Cell</i> , 2011, 146, 720-731.	13.5	155
47	Quantitative Models of the Mechanisms That Control Genome-Wide Patterns of Transcription Factor Binding during Early <i>Drosophila</i> Development. <i>PLoS Genetics</i> , 2011, 7, e1001290.	1.5	150
48	Gene family innovation, conservation and loss on the animal stem lineage. <i>ELife</i> , 2018, 7, .	2.8	149
49	Dynamic multifactor hubs interact transiently with sites of active transcription in <i>Drosophila</i> embryos. <i>ELife</i> , 2018, 7, .	2.8	149
50	Comparative validation of the <i>D. melanogaster</i> modENCODE transcriptome annotation. <i>Genome Research</i> , 2014, 24, 1209-1223.	2.4	147
51	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
52	MONKEY: identifying conserved transcription-factor binding sites in multiple alignments using a binding site-specific evolutionary model. <i>Genome Biology</i> , 2004, 5, R98.	13.9	134
53	Position specific variation in the rate of evolution in transcription factor binding sites. <i>BMC Evolutionary Biology</i> , 2003, 3, 19.	3.2	130
54	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

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55	Rapid Global Spread of wRi-like Wolbachia across Multiple <i>Drosophila</i> . <i>Current Biology</i> , 2018, 28, 963-971.e8.	1.8	127
56	Serendipitous discovery of Wolbachia genomes in multiple <i>Drosophila</i> species. <i>Genome Biology</i> , 2005, 6, R23.	13.9	126
57	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
58	Impact of Chromatin Structures on DNA Processing for Genomic Analyses. <i>PLoS ONE</i> , 2009, 4, e6700.	1.1	115
59	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
60	<i>Drosophila</i> Embryogenesis Scales Uniformly across Temperature in Developmentally Diverse Species. <i>PLoS Genetics</i> , 2014, 10, e1004293.	1.5	109
61	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
62	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
63	Benchmarking tools for the alignment of functional noncoding DNA. <i>BMC Bioinformatics</i> , 2004, 5, 6.	1.2	99
64	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
65	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
66	Association mapping from sequencing reads using k-mers. <i>ELife</i> , 2018, 7, .	2.8	88
67	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
68	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
69	Genome-wide Analysis of Alternative Pre-mRNA Splicing and RNA-Binding Specificities of the <i>Drosophila</i> hnRNP A/B Family Members. <i>Molecular Cell</i> , 2009, 33, 438-449.	4.5	79
70	Why PLoS Became a Publisher. <i>PLoS Biology</i> , 2003, 1, e36.	2.6	76
71	GATA: a graphic alignment tool for comparative sequence analysis. <i>BMC Bioinformatics</i> , 2005, 6, 9.	1.2	70
72	Evolutionary Mirages: Selection on Binding Site Composition Creates the Illusion of Conserved Grammars in <i>Drosophila</i> Enhancers. <i>PLoS Genetics</i> , 2010, 6, e1000829.	1.5	70

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73	Sequencing mRNA from Cryo-Sliced Drosophila Embryos to Determine Genome-Wide Spatial Patterns of Gene Expression. PLoS ONE, 2013, 8, e71820.	1.1	64
74	Title is missing!. Genome Biology, 2005, 6, P7.	13.9	63
75	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
76	Automatic image analysis for gene expression patterns of fly embryos. BMC Cell Biology, 2007, 8, S7.	3.0	58
77	Transcriptional Activation of the Zygotic Genome in Drosophila. Current Topics in Developmental Biology, 2015, 113, 85-112.	1.0	58
78	Robust manipulation of the behavior of Drosophila melanogaster by a fungal pathogen in the laboratory. ELife, 2018, 7, .	2.8	58
79	An Essential Role for Zygotic Expression in the Pre-Cellular Drosophila Embryo. PLoS Genetics, 2013, 9, e1003428.	1.5	57
80	Publishing in the time of COVID-19. ELife, 2020, 9, .	2.8	54
81	A Conserved Developmental Patterning Network Produces Quantitatively Different Output in Multiple Species of Drosophila. PLoS Genetics, 2011, 7, e1002346.	1.5	51
82	Identification of direct T-box target genes in the developing zebrafish mesoderm. Development (Cambridge), 2009, 136, 749-760.	1.2	48
83	Detecting the limits of regulatory element conservation and divergence estimation using pairwise and multiple alignments. BMC Bioinformatics, 2006, 7, 376.	1.2	46
84	Phylogenetically and spatially conserved word pairs associated with gene-expression changes in yeasts. Genome Biology, 2003, 4, R43.	13.9	44
85	A molecular atlas of the developing ectoderm defines neural, neural crest, placode, and nonneural progenitor identity in vertebrates. PLoS Biology, 2017, 15, e2004045.	2.6	44
86	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
87	Big Genomes Facilitate the Comparative Identification of Regulatory Elements. PLoS ONE, 2009, 4, e4688.	1.1	41
88	Dual functions of TAF7L in adipocyte differentiation. ELife, 2013, 2, e00170.	2.8	41
89	Insights into the evolution of Darwin's finches from comparative analysis of the Geospiza magnirostris genome sequence. BMC Genomics, 2013, 14, 95.	1.2	38
90	Patterns of chromatin accessibility along the anterior-posterior axis in the early Drosophila embryo. PLoS Genetics, 2018, 14, e1007367.	1.5	38

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91	Improving transcriptome assembly through error correction of high-throughput sequence reads. PeerJ, 2013, 1, e113.	0.9	38
92	The ecology of the Drosophila-yeast mutualism in wineries. PLoS ONE, 2018, 13, e0196440.	1.1	34
93	Characterization of the transcriptome, nucleotide sequence polymorphism, and natural selection in the desert adapted mouse <i>Peromyscus eremicus</i> . PeerJ, 2014, 2, e642.	0.9	34
94	Silent but Not Static: Accelerated Base-Pair Substitution in Silenced Chromatin of Budding Yeasts. PLoS Genetics, 2008, 4, e1000247.	1.5	32
95	The Fitness Landscapes of cis-Acting Binding Sites in Different Promoter and Environmental Contexts. PLoS Genetics, 2010, 6, e1001042.	1.5	32
96	Convergent evolution of gene expression in two high-toothed stickleback populations. PLoS Genetics, 2018, 14, e1007443.	1.5	32
97	Kinetic sculpting of the seven stripes of the Drosophila even-skipped gene. ELife, 2020, 9, .	2.8	32
98	A Careful Look at Binding Site Reorganization in the even-skipped Enhancers of Drosophila and Sepsids. PLoS Genetics, 2008, 4, e1000268.	1.5	28
99	Integrating Data Clustering and Visualization for the Analysis of 3D Gene Expression Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 64-79.	1.9	28
100	Plan U: Universal access to scientific and medical research via funder preprint mandates. PLoS Biology, 2019, 17, e3000273.	2.6	28
101	Genome-wide measurement of spatial expression in patterning mutants of Drosophila melanogaster. F1000Research, 2017, 6, 41.	0.8	27
102	Sex Bias and Maternal Contribution to Gene Expression Divergence in Drosophila Blastoderm Embryos. PLoS Genetics, 2015, 11, e1005592.	1.5	26
103	Sex-Specific Embryonic Gene Expression in Species with Newly Evolved Sex Chromosomes. PLoS Genetics, 2014, 10, e1004159.	1.5	25
104	Implementing a "publish, then review" model of publishing. ELife, 2020, 9, .	2.8	25
105	Design of a combinatorial DNA microarray for protein-DNA interaction studies. BMC Bioinformatics, 2006, 7, 429.	1.2	24
106	Low-cost, low-input RNA-seq protocols perform nearly as well as high-input protocols. PeerJ, 2015, 3, e869.	0.9	24
107	Single Molecule Imaging in Live Embryos Using Lattice Light-Sheet Microscopy. Methods in Molecular Biology, 2018, 1814, 541-559.	0.4	24
108	Probing the Informational and Regulatory Plasticity of a Transcription Factor DNA-Binding Domain. PLoS Genetics, 2012, 8, e1002614.	1.5	23

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109	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
110	Identifying Cis-Regulatory Sequences by Word Profile Similarity. <i>PLoS ONE</i> , 2009, 4, e6901.	1.1	22
111	Flexible promoter architecture requirements for coactivator recruitment. <i>BMC Molecular Biology</i> , 2006, 7, 16.	3.0	19
112	A phylogeny for the <i>Drosophila montium</i> species group: A model clade for comparative analyses. <i>Molecular Phylogenetics and Evolution</i> , 2021, 158, 107061.	1.2	19
113	<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
114	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
115	Primate-specific evolution of an LDLR enhancer. <i>Genome Biology</i> , 2006, 7, R68.	13.9	16
116	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
117	Impact of essential workers in the context of social distancing for epidemic control. <i>PLoS ONE</i> , 2021, 16, e0255680.	1.1	13
118	DNA dealt wrong hand on cover. <i>Nature</i> , 2010, 467, 401-401.	13.7	9
119	We need to act now. <i>ELife</i> , 2020, 9, .	2.8	9
120	PLoS Medicine – A Medical Journal for the Internet Age. <i>PLoS Medicine</i> , 2004, 1, e31.	3.9	8
121	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
122	Determining Physical Constraints in Transcriptional Initiation Complexes Using DNA Sequence Analysis. <i>PLoS ONE</i> , 2007, 2, e1199.	1.1	8
123	PLoS Computational Biology: A New Community Journal. <i>PLoS Computational Biology</i> , 2005, 1, e4.	1.5	7
124	A model for sequential evolution of ligands by exponential enrichment (SELEX) data. <i>Annals of Applied Statistics</i> , 2012, 6, .	0.5	6
125	Regulation of gene expression by the intracellular second messengers IP3 and diacylglycerol. <i>Genesis</i> , 1988, 9, 351-358.	3.3	5
126	The Enigmatic Conservation of a Rap1 Binding Site in the <i>Saccharomyces cerevisiae</i> HMRE Silencer. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1555-1562.	0.8	5

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127	Structural Variation among Wild and Industrial Strains of <i>Penicillium chrysogenum</i> . PLoS ONE, 2014, 9, e96784.	1.1	5
128	Atlas of t, patterns from every cell. Science, 2017, 358, 172-173.	6.0	5
129	Oxygen changes drive non-uniform scaling in <i>Drosophila melanogaster</i> embryogenesis. F1000Research, 2015, 4, 1102.	0.8	5
130	Single-nucleus RNA-sequencing in pre-cellularization <i>Drosophila melanogaster</i> embryos. PLoS ONE, 2022, 17, e0270471.	1.1	5
131	Spatial Promoter Recognition Signatures May Enhance Transcription Factor Specificity in Yeast. PLoS ONE, 2013, 8, e53778.	1.1	2
132	Rigorous review and editorial oversight of clinical preprints. ELife, 2021, 10, .	2.8	2
133	Ten Years of PLoS Computational Biology: A Decade of Appreciation and Innovation. PLoS Computational Biology, 2015, 11, e1004317.	1.5	1
134	Open Access: The Sooner the Better. Science, 2009, 325, 266-266.	6.0	0
135	Exploring the Genetic Basis of Variation in Gene Predictions with a Synthetic Association Study. PLoS ONE, 2010, 5, e11645.	1.1	0