

Michael B Eisen

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

144
papers

46,481
citations

67
h-index

176
g-index

176
ext. papers

51,770
ext. citations

11.6
avg, IF

6.65
L-index

#	Paper	IF	Citations
144	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		8
143	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	4.1	6
142	Impact of essential workers in the context of social distancing for epidemic control. <i>PLoS ONE</i> , 2021 , 16, e0255680	3.7	4
141	Whole Genome Sequences of 23 Species from the Species Group (Diptera: Drosophilidae): A Resource for Testing Evolutionary Hypotheses. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 1443-1455	3.2	7
140	Kinetic sculpting of the seven stripes of the <i>Drosophila</i> gene. <i>ELife</i> , 2020 , 9,	8.9	9
139	Plan U: Universal access to scientific and medical research via funder preprint mandates. <i>PLoS Biology</i> , 2019 , 17, e3000273	9.7	11
138	Rapid Global Spread of wRi-like Wolbachia across Multiple <i>Drosophila</i> . <i>Current Biology</i> , 2018 , 28, 963-971	6.8	79
137	Patterns of chromatin accessibility along the anterior-posterior axis in the early <i>Drosophila</i> embryo. <i>PLoS Genetics</i> , 2018 , 14, e1007367	6	19
136	The ecology of the <i>Drosophila</i> -yeast mutualism in wineries. <i>PLoS ONE</i> , 2018 , 13, e0196440	3.7	21
135	Robust manipulation of the behavior of by a fungal pathogen in the laboratory. <i>ELife</i> , 2018 , 7,	8.9	33
134	Dynamic multifactor hubs interact transiently with sites of active transcription in embryos. <i>ELife</i> , 2018 , 7,	8.9	75
133	Convergent evolution of gene expression in two high-toothed stickleback populations. <i>PLoS Genetics</i> , 2018 , 14, e1007443	6	14
132	Association mapping from sequencing reads using -mers. <i>ELife</i> , 2018 , 7,	8.9	48
131	Single Molecule Imaging in Live Embryos Using Lattice Light-Sheet Microscopy. <i>Methods in Molecular Biology</i> , 2018 , 1814, 541-559	1.4	18
130	Gene family innovation, conservation and loss on the animal stem lineage. <i>ELife</i> , 2018 , 7,	8.9	94
129	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	8.3	13
128	Atlas ³ , patterns from every cell. <i>Science</i> , 2017 , 358, 172-173	33.3	2

127	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	9.7	27
126	Genome-wide measurement of spatial expression in patterning mutants of. <i>F1000Research</i> , 2017 , 6, 41	3.6	15
125	Convergence of topological domain boundaries, insulators, and polytene interbands revealed by high-resolution mapping of chromatin contacts in the early embryo. <i>ELife</i> , 2017 , 6,	8.9	56
124	Dense Bicoid hubs accentuate binding along the morphogen gradient. <i>Genes and Development</i> , 2017 , 31, 1784-1794	12.6	84
123	The genome of the crustacean a model for animal development, regeneration, immunity and lignocellulose digestion. <i>ELife</i> , 2016 , 5,	8.9	100
122	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	3.7	19
121	Sex Bias and Maternal Contribution to Gene Expression Divergence in <i>Drosophila</i> Blastoderm Embryos. <i>PLoS Genetics</i> , 2015 , 11, e1005592	6	15
120	Low-cost, low-input RNA-seq protocols perform nearly as well as high-input protocols. <i>PeerJ</i> , 2015 , 3, e869	3.1	17
119	Transcriptional Activation of the Zygotic Genome in <i>Drosophila</i> . <i>Current Topics in Developmental Biology</i> , 2015 , 113, 85-112	5.3	42
118	Oxygen changes drive non-uniform scaling in <i>Drosophila melanogaster</i> embryogenesis. <i>F1000Research</i> , 2015 , 4, 1102	3.6	2
117	Comparative validation of the <i>D. melanogaster</i> modENCODE transcriptome annotation. <i>Genome Research</i> , 2014 , 24, 1209-23	9.7	95
116	Structural variation among wild and industrial strains of <i>Penicillium chrysogenum</i> . <i>PLoS ONE</i> , 2014 , 9, e96784	3.7	2
115	<i>Drosophila</i> embryogenesis scales uniformly across temperature in developmentally diverse species. <i>PLoS Genetics</i> , 2014 , 10, e1004293	6	67
114	Sex-specific embryonic gene expression in species with newly evolved sex chromosomes. <i>PLoS Genetics</i> , 2014 , 10, e1004159	6	15
113	<i>Saccharomyces cerevisiae</i> mitochondria are required for optimal attractiveness to <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2014 , 9, e113899	3.7	13
112	Establishment of regions of genomic activity during the <i>Drosophila</i> maternal to zygotic transition. <i>ELife</i> , 2014 , 3,	8.9	123
111	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	3.1	20
110	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	4.5	33

109	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	9.7	120
108	An essential role for zygotic expression in the pre-cellular <i>Drosophila</i> embryo. <i>PLoS Genetics</i> , 2013 , 9, e1003428	6	44
107	Extensive divergence of transcription factor binding in <i>Drosophila</i> embryos with highly conserved gene expression. <i>PLoS Genetics</i> , 2013 , 9, e1003748	6	70
106	Dual functions of TAF7L in adipocyte differentiation. <i>ELife</i> , 2013 , 2, e00170	8.9	29
105	Spatial promoter recognition signatures may enhance transcription factor specificity in yeast. <i>PLoS ONE</i> , 2013 , 8, e53778	3.7	2
104	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	3.7	50
103	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	3.7	88
102	Improving transcriptome assembly through error correction of high-throughput sequence reads. <i>PeerJ</i> , 2013 , 1, e113	3.1	32
101	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, 1555-62	3.2	3
100	Probing the informational and regulatory plasticity of a transcription factor DNA-binding domain. <i>PLoS Genetics</i> , 2012 , 8, e1002614	6	20
99	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, 21330-5	11.5	117
98	A model for sequential evolution of ligands by exponential enrichment (SELEX) data. <i>Annals of Applied Statistics</i> , 2012 , 6,	2.1	5
97	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	18.3	164
96	Control of embryonic stem cell lineage commitment by core promoter factor, TAF3. <i>Cell</i> , 2011 , 146, 720-31	36.2	132
95	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	9.7	141
94	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	3.2	231
93	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	6	130
92	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	6	227

91	A conserved developmental patterning network produces quantitatively different output in multiple species of <i>Drosophila</i> . <i>PLoS Genetics</i> , 2011 , 7, e1002346	6	40
90	DNA dealt wrong hand on cover. <i>Nature</i> , 2010 , 467, 401	50.4	4
89	Exploring the genetic basis of variation in gene predictions with a synthetic association study. <i>PLoS ONE</i> , 2010 , 5, e11645	3.7	
88	The fitness landscapes of cis-acting binding sites in different promoter and environmental contexts. <i>PLoS Genetics</i> , 2010 , 6, e1001042	6	25
87	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	9.7	154
86	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	6	64
85	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	24
84	Coupling visualization and data analysis for knowledge discovery from multi-dimensional scientific data. <i>Procedia Computer Science</i> , 2010 , 1, 1757-1764	1.6	5
83	Big genomes facilitate the comparative identification of regulatory elements. <i>PLoS ONE</i> , 2009 , 4, e4688	3.7	33
82	Open access: the sooner the better. <i>Science</i> , 2009 , 325, 266; author reply 266-7	33.3	
81	Identification of direct T-box target genes in the developing zebrafish mesoderm. <i>Development (Cambridge)</i> , 2009 , 136, 749-60	6.6	43
80	A condensin-like dosage compensation complex acts at a distance to control expression throughout the genome. <i>Genes and Development</i> , 2009 , 23, 602-18	12.6	85
79	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, 438-49	17.6	70
78	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	18.3	270
77	Genome-wide transcriptional response of <i>Silurana (Xenopus) tropicalis</i> to infection with the deadly chytrid fungus. <i>PLoS ONE</i> , 2009 , 4, e6494	3.7	71
76	Impact of chromatin structures on DNA processing for genomic analyses. <i>PLoS ONE</i> , 2009 , 4, e6700	3.7	95
75	Identifying cis-regulatory sequences by word profile similarity. <i>PLoS ONE</i> , 2009 , 4, e6901	3.7	20
74	A quantitative spatiotemporal atlas of gene expression in the <i>Drosophila</i> blastoderm. <i>Cell</i> , 2008 , 133, 364-74	56.2	218

73	Silent but not static: accelerated base-pair substitution in silenced chromatin of budding yeasts. <i>PLoS Genetics</i> , 2008 , 4, e1000247	6	30
72	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, 3290-300	4.8	176
71	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, 9715-20	11.5	688
70	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	6	25
69	Transcription factors bind thousands of active and inactive regions in the <i>Drosophila</i> blastoderm. <i>PLoS Biology</i> , 2008 , 6, e27	9.7	360
68	Sepsid even-skipped enhancers are functionally conserved in <i>Drosophila</i> despite lack of sequence conservation. <i>PLoS Genetics</i> , 2008 , 4, e1000106	6	221
67	Association of cohesin and Nipped-B with transcriptionally active regions of the <i>Drosophila melanogaster</i> genome. <i>Chromosoma</i> , 2008 , 117, 89-102	2.8	180
66	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, 17034-9	11.5	89
65	Automatic image analysis for gene expression patterns of fly embryos. <i>BMC Cell Biology</i> , 2007 , 8 Suppl 1, S7		47
64	Discovery of functional elements in 12 <i>Drosophila</i> genomes using evolutionary signatures. <i>Nature</i> , 2007 , 450, 219-32	50.4	506
63	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007 , 450, 203-18	50.4	1586
62	Determining physical constraints in transcriptional initiation complexes using DNA sequence analysis. <i>PLoS ONE</i> , 2007 , 2, e1199	3.7	7
61	Detecting the limits of regulatory element conservation and divergence estimation using pairwise and multiple alignments. <i>BMC Bioinformatics</i> , 2006 , 7, 376	3.6	41
60	Design of a combinatorial DNA microarray for protein-DNA interaction studies. <i>BMC Bioinformatics</i> , 2006 , 7, 429	3.6	20
59	Widespread discordance of gene trees with species tree in <i>Drosophila</i> : evidence for incomplete lineage sorting. <i>PLoS Genetics</i> , 2006 , 2, e173	6	265
58	Large-scale turnover of functional transcription factor binding sites in <i>Drosophila</i> . <i>PLoS Computational Biology</i> , 2006 , 2, e130	5	195
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	18.3	100
56	Primate-specific evolution of an LDLR enhancer. <i>Genome Biology</i> , 2006 , 7, R68	18.3	15

55	Rapid quantitative profiling of complex microbial populations. <i>Nucleic Acids Research</i> , 2006 , 34, e5	20.1	145
54	Flexible promoter architecture requirements for coactivator recruitment. <i>BMC Molecular Biology</i> , 2006 , 7, 16	4.5	15
53	In vivo enhancer analysis of human conserved non-coding sequences. <i>Nature</i> , 2006 , 444, 499-502	50.4	911
52	All motifs are NOT created equal: structural properties of transcription factor-DNA interactions and the inference of sequence specificity 2005 , 6, P7		51
51	Serendipitous discovery of Wolbachia genomes in multiple Drosophila species. <i>Genome Biology</i> , 2005 , 6, R23	18.3	108
50	GATA: a graphic alignment tool for comparative sequence analysis. <i>BMC Bioinformatics</i> , 2005 , 6, 9	3.6	58
49	Aging and gene expression in the primate brain. <i>PLoS Biology</i> , 2005 , 3, e274	9.7	131
48	Identification of oligonucleotide sequences that direct the movement of the Escherichia coli FtsK translocase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 17618-23	11.5	103
47	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, 5483-8	11.5	226
46	Coevolution of gene expression among interacting proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 9033-8	11.5	171
45	Conservation and evolution of cis-regulatory systems in ascomycete fungi. <i>PLoS Biology</i> , 2004 , 2, e398	9.7	174
44	PLoS Medicine—A Medical Journal for the Internet Age. <i>PLoS Medicine</i> , 2004 , 1, e31	11.6	5
43	Noise minimization in eukaryotic gene expression. <i>PLoS Biology</i> , 2004 , 2, e137	9.7	303
42	Benchmarking tools for the alignment of functional noncoding DNA. <i>BMC Bioinformatics</i> , 2004 , 5, 6	3.6	85
41	MONKEY: identifying conserved transcription-factor binding sites in multiple alignments using a binding site-specific evolutionary model. <i>Genome Biology</i> , 2004 , 5, R98	18.3	123
40	Computational identification of developmental enhancers: conservation and function of transcription factor binding-site clusters in Drosophila melanogaster and Drosophila pseudoobscura. <i>Genome Biology</i> , 2004 , 5, R61	18.3	171
39	Population genetic variation in gene expression is associated with phenotypic variation in Saccharomyces cerevisiae. <i>Genome Biology</i> , 2004 , 5, R26	18.3	159
38	Why PLoS became a publisher. <i>PLoS Biology</i> , 2003 , 1, E36	9.7	36

37	Position specific variation in the rate of evolution in transcription factor binding sites. <i>BMC Evolutionary Biology</i> , 2003 , 3, 19	3	114
36	Phylogenetically and spatially conserved word pairs associated with gene-expression changes in yeasts. <i>Genome Biology</i> , 2003 , 4, R43	18.3	40
35	Exploiting transcription factor binding site clustering to identify cis-regulatory modules involved in pattern formation in the Drosophila genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 757-62	11.5	482
34	Exploring the conditional coregulation of yeast gene expression through fuzzy k-means clustering. <i>Genome Biology</i> , 2002 , 3, RESEARCH0059	18.3	273
33	The Stanford Microarray Database. <i>Nucleic Acids Research</i> , 2001 , 29, 152-5	20.1	337
32	Systematic variation in gene expression patterns in human cancer cell lines. <i>Nature Genetics</i> , 2000 , 24, 227-35	36.3	1739
31	A gene expression database for the molecular pharmacology of cancer. <i>Nature Genetics</i> , 2000 , 24, 236-44	36.3	1173
30	Large-scale identification of secreted and membrane-associated gene products using DNA microarrays. <i>Nature Genetics</i> , 2000 , 25, 58-62	36.3	213
29	Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. <i>Nature</i> , 2000 , 403, 503-11	50.4	7592
28	Molecular portraits of human breast tumours. <i>Nature</i> , 2000 , 406, 747-52	50.4	11221
27	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. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2000 , 1467, 207-18	3.8	40
26	Gene shaving: a method for identifying distinct sets of genes with similar expression patterns. <i>Genome Biology</i> , 2000 , 1, RESEARCH0003	18.3	304
25	Genomic expression programs in the response of yeast cells to environmental changes. <i>Molecular Biology of the Cell</i> , 2000 , 11, 4241-57	3.5	3708
24	Genome-wide analysis of DNA copy-number changes using cDNA microarrays. <i>Nature Genetics</i> , 1999 , 23, 41-6	36.3	712
23	Gene expression informatics--it's all in your mine. <i>Nature Genetics</i> , 1999 , 21, 51-5	36.3	316
22	The transcriptional program in the response of human fibroblasts to serum. <i>Science</i> , 1999 , 283, 83-7	33.3	1713
21	DNA arrays for analysis of gene expression. <i>Methods in Enzymology</i> , 1999 , 303, 179-205	1.7	747
20	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, 3273-97	3.5	3710

19	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	3.6	182
18	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	4.2	182
17	Regulation of gene expression by the intracellular second messengers IP3 and diacylglycerol. <i>Genesis</i> , 1988 , 9, 351-8		4
16	PointCloudXplore: a visualization tool for 3D gene expression data		2
15	Robust manipulation of the behavior of <i>Drosophila melanogaster</i> by a fungal pathogen in the laboratory		1
14	Impact of essential workers in the context of social distancing for epidemic control		1
13	Establishment of regions of genomic activity during the <i>Drosophila</i> maternal to zygotic transition		3
12	Association Mapping from Sequencing Reads Using K-mers		3
11	Or22 allelic variation alone does not explain differences in discrimination of yeast-produced volatiles by <i>D. melanogaster</i>		3
10	The ancestral animal genetic toolkit revealed by diverse choanoflagellate transcriptomes		1
9	Chronic ethanol ingestion impairs <i>Drosophila melanogaster</i> health in a microbiome-dependent manner		2
8	Kinetic sculpting of the seven stripes of the <i>Drosophila</i> even-skipped gene		6
7	Entomophthovirus: An insect-derived iflavirus that infects a behavior manipulating fungal pathogen of dipterans		9
6	Dynamic multifactor hubs interact transiently with sites of active transcription in <i>Drosophila</i> embryos		3
5	Mutation of sequences flanking and separating transcription factor binding sites in a <i>Drosophila</i> enhancer significantly alter its output		1
4	Zelda potentiates transcription factor binding to zygotic enhancers by increasing local chromatin accessibility during early <i>Drosophila melanogaster</i> embryogenesis		3
3	A chromatin extension model for insulator function based on comparison of high-resolution chromatin conformation capture and polytene banding maps		1
2	Dense Bicoid Hubs Accentuate Binding along the Morphogen Gradient		2

1 Convergence of topological domain boundaries, insulators, and polytene interbands revealed by high-resolution mapping of chromatin contacts in the early *Drosophila melanogaster* embryo

1