

Michael B Eisen

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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	Molecular portraits of human breast tumours. <i>Nature</i> , 2000 , 406, 747-52	50.4	11221
143	Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. <i>Nature</i> , 2000 , 403, 503-11	50.4	7592
142	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
141	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
140	Systematic variation in gene expression patterns in human cancer cell lines. <i>Nature Genetics</i> , 2000 , 24, 227-35	36.3	1739
139	The transcriptional program in the response of human fibroblasts to serum. <i>Science</i> , 1999 , 283, 83-7	33.3	1713
138	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007 , 450, 203-18	50.4	1586
137	A gene expression database for the molecular pharmacology of cancer. <i>Nature Genetics</i> , 2000 , 24, 236-44	36.3	1173
136	In vivo enhancer analysis of human conserved non-coding sequences. <i>Nature</i> , 2006 , 444, 499-502	50.4	911
135	DNA arrays for analysis of gene expression. <i>Methods in Enzymology</i> , 1999 , 303, 179-205	1.7	747
134	Genome-wide analysis of DNA copy-number changes using cDNA microarrays. <i>Nature Genetics</i> , 1999 , 23, 41-6	36.3	712
133	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
132	Discovery of functional elements in 12 <i>Drosophila</i> genomes using evolutionary signatures. <i>Nature</i> , 2007 , 450, 219-32	50.4	506
131	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, 757-62	11.5	482
130	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
129	The Stanford Microarray Database. <i>Nucleic Acids Research</i> , 2001 , 29, 152-5	20.1	337
128	Gene expression informatics--it's all in your mine. <i>Nature Genetics</i> , 1999 , 21, 51-5	36.3	316

127	Gene shaving as a method for identifying distinct sets of genes with similar expression patterns. <i>Genome Biology</i> , 2000 , 1, RESEARCH0003	18.3	304
126	Noise minimization in eukaryotic gene expression. <i>PLoS Biology</i> , 2004 , 2, e137	9.7	303
125	Exploring the conditional coregulation of yeast gene expression through fuzzy k-means clustering. <i>Genome Biology</i> , 2002 , 3, RESEARCH0059	18.3	273
124	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	18.3	270
123	Widespread discordance of gene trees with species tree in Drosophila: evidence for incomplete lineage sorting. <i>PLoS Genetics</i> , 2006 , 2, e173	6	265
122	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
121	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	6	227
120	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
119	Sepsid even-skipped enhancers are functionally conserved in Drosophila despite lack of sequence conservation. <i>PLoS Genetics</i> , 2008 , 4, e1000106	6	221
118	A quantitative spatiotemporal atlas of gene expression in the Drosophila blastoderm. <i>Cell</i> , 2008 , 133, 364-74	56.2	218
117	Large-scale identification of secreted and membrane-associated gene products using DNA microarrays. <i>Nature Genetics</i> , 2000 , 25, 58-62	36.3	213
116	Large-scale turnover of functional transcription factor binding sites in Drosophila. <i>PLoS Computational Biology</i> , 2006 , 2, e130	5	195
115	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
114	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
113	Association of cohesin and Nipped-B with transcriptionally active regions of the Drosophila melanogaster genome. <i>Chromosoma</i> , 2008 , 117, 89-102	2.8	180
112	NELF and GAGA factor are linked to promoter-proximal pausing at many genes in Drosophila. <i>Molecular and Cellular Biology</i> , 2008 , 28, 3290-300	4.8	176
111	Conservation and evolution of cis-regulatory systems in ascomycete fungi. <i>PLoS Biology</i> , 2004 , 2, e398	9.7	174
110	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

109	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	18.3	171
108	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
107	Population genetic variation in gene expression is associated with phenotypic variation in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology</i> , 2004 , 5, R26	18.3	159
106	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
105	Rapid quantitative profiling of complex microbial populations. <i>Nucleic Acids Research</i> , 2006 , 34, e5	20.1	145
104	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
103	Control of embryonic stem cell lineage commitment by core promoter factor, TAF3. <i>Cell</i> , 2011 , 146, 720-31	36.2	132
102	Aging and gene expression in the primate brain. <i>PLoS Biology</i> , 2005 , 3, e274	9.7	131
101	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
100	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
99	Establishment of regions of genomic activity during the <i>Drosophila</i> maternal to zygotic transition. <i>ELife</i> , 2014 , 3,	8.9	123
98	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
97	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
96	Position specific variation in the rate of evolution in transcription factor binding sites. <i>BMC Evolutionary Biology</i> , 2003 , 3, 19	3	114
95	Serendipitous discovery of Wolbachia genomes in multiple <i>Drosophila</i> species. <i>Genome Biology</i> , 2005 , 6, R23	18.3	108
94	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, 17618-23	11.5	103
93	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
92	The genome of the crustacean a model for animal development, regeneration, immunity and lignocellulose digestion. <i>ELife</i> , 2016 , 5,	8.9	100

91	Comparative validation of the <i>D. melanogaster</i> modENCODE transcriptome annotation. <i>Genome Research</i> , 2014 , 24, 1209-23	9.7	95
90	Impact of chromatin structures on DNA processing for genomic analyses. <i>PLoS ONE</i> , 2009 , 4, e6700	3.7	95
89	Gene family innovation, conservation and loss on the animal stem lineage. <i>ELife</i> , 2018 , 7,	8.9	94
88	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
87	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
86	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
85	Benchmarking tools for the alignment of functional noncoding DNA. <i>BMC Bioinformatics</i> , 2004 , 5, 6	3.6	85
84	Dense Bicoid hubs accentuate binding along the morphogen gradient. <i>Genes and Development</i> , 2017 , 31, 1784-1794	12.6	84
83	Rapid Global Spread of wRi-like <i>Wolbachia</i> across Multiple <i>Drosophila</i> . <i>Current Biology</i> , 2018 , 28, 963-971	16.8	79
82	Dynamic multifactor hubs interact transiently with sites of active transcription in embryos. <i>ELife</i> , 2018 , 7,	8.9	75
81	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
80	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
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	<i>Drosophila</i> embryogenesis scales uniformly across temperature in developmentally diverse species. <i>PLoS Genetics</i> , 2014 , 10, e1004293	6	67
77	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
76	GATA: a graphic alignment tool for comparative sequence analysis. <i>BMC Bioinformatics</i> , 2005 , 6, 9	3.6	58
75	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
74	All motifs are NOT created equal: structural properties of transcription factor-DNA interactions and the inference of sequence specificity 2005 , 6, P7		51

73	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
72	Association mapping from sequencing reads using -mers. <i>ELife</i> , 2018 , 7,	8.9	48
71	Automatic image analysis for gene expression patterns of fly embryos. <i>BMC Cell Biology</i> , 2007 , 8 Suppl 1, S7		47
70	An essential role for zygotic expression in the pre-cellular <i>Drosophila</i> embryo. <i>PLoS Genetics</i> , 2013 , 9, e1003428	6	44
69	Identification of direct T-box target genes in the developing zebrafish mesoderm. <i>Development (Cambridge)</i> , 2009 , 136, 749-60	6.6	43
68	Transcriptional Activation of the Zygotic Genome in <i>Drosophila</i> . <i>Current Topics in Developmental Biology</i> , 2015 , 113, 85-112	5.3	42
67	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
66	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
65	Phylogenetically and spatially conserved word pairs associated with gene-expression changes in yeasts. <i>Genome Biology</i> , 2003 , 4, R43	18.3	40
64	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
63	Why PLoS became a publisher. <i>PLoS Biology</i> , 2003 , 1, E36	9.7	36
62	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
61	Big genomes facilitate the comparative identification of regulatory elements. <i>PLoS ONE</i> , 2009 , 4, e4688	3.7	33
60	Robust manipulation of the behavior of by a fungal pathogen in the laboratory. <i>ELife</i> , 2018 , 7,	8.9	33
59	Improving transcriptome assembly through error correction of high-throughput sequence reads. <i>PeerJ</i> , 2013 , 1, e113	3.1	32
58	Silent but not static: accelerated base-pair substitution in silenced chromatin of budding yeasts. <i>PLoS Genetics</i> , 2008 , 4, e1000247	6	30
57	Dual functions of TAF7L in adipocyte differentiation. <i>ELife</i> , 2013 , 2, e00170	8.9	29
56	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

55	The fitness landscapes of cis-acting binding sites in different promoter and environmental contexts. <i>PLoS Genetics</i> , 2010 , 6, e1001042	6	25
54	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
53	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
52	The ecology of the <i>Drosophila</i> -yeast mutualism in wineries. <i>PLoS ONE</i> , 2018 , 13, e0196440	3.7	21
51	Probing the informational and regulatory plasticity of a transcription factor DNA-binding domain. <i>PLoS Genetics</i> , 2012 , 8, e1002614	6	20
50	Design of a combinatorial DNA microarray for protein-DNA interaction studies. <i>BMC Bioinformatics</i> , 2006 , 7, 429	3.6	20
49	Identifying cis-regulatory sequences by word profile similarity. <i>PLoS ONE</i> , 2009 , 4, e6901	3.7	20
48	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
47	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
46	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
45	Single Molecule Imaging in Live Embryos Using Lattice Light-Sheet Microscopy. <i>Methods in Molecular Biology</i> , 2018 , 1814, 541-559	1.4	18
44	Low-cost, low-input RNA-seq protocols perform nearly as well as high-input protocols. <i>PeerJ</i> , 2015 , 3, e869	3.1	17
43	Sex Bias and Maternal Contribution to Gene Expression Divergence in <i>Drosophila</i> Blastoderm Embryos. <i>PLoS Genetics</i> , 2015 , 11, e1005592	6	15
42	Sex-specific embryonic gene expression in species with newly evolved sex chromosomes. <i>PLoS Genetics</i> , 2014 , 10, e1004159	6	15
41	Primate-specific evolution of an LDLR enhancer. <i>Genome Biology</i> , 2006 , 7, R68	18.3	15
40	Flexible promoter architecture requirements for coactivator recruitment. <i>BMC Molecular Biology</i> , 2006 , 7, 16	4.5	15
39	Genome-wide measurement of spatial expression in patterning mutants of. <i>F1000Research</i> , 2017 , 6, 41	3.6	15
38	Convergent evolution of gene expression in two high-toothed stickleback populations. <i>PLoS Genetics</i> , 2018 , 14, e1007443	6	14

37	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
36	<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
35	Plan U: Universal access to scientific and medical research via funder preprint mandates. <i>PLoS Biology</i> , 2019 , 17, e3000273	9.7	11
34	Kinetic sculpting of the seven stripes of the <i>Drosophila</i> gene. <i>ELife</i> , 2020 , 9,	8.9	9
33	Entomophthovirus: An insect-derived iflavivirus that infects a behavior manipulating fungal pathogen of dipterans		9
32	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
31	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
30	Determining physical constraints in transcriptional initiation complexes using DNA sequence analysis. <i>PLoS ONE</i> , 2007 , 2, e1199	3.7	7
29	Kinetic sculpting of the seven stripes of the <i>Drosophila</i> even-skipped gene		6
28	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
27	A model for sequential evolution of ligands by exponential enrichment (SELEX) data. <i>Annals of Applied Statistics</i> , 2012 , 6,	2.1	5
26	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
25	PLoS Medicine—A Medical Journal for the Internet Age. <i>PLoS Medicine</i> , 2004 , 1, e31	11.6	5
24	DNA dealt wrong hand on cover. <i>Nature</i> , 2010 , 467, 401	50.4	4
23	Regulation of gene expression by the intracellular second messengers IP3 and diacylglycerol. <i>Genesis</i> , 1988 , 9, 351-8		4
22	Impact of essential workers in the context of social distancing for epidemic control. <i>PLoS ONE</i> , 2021 , 16, e0255680	3.7	4
21	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
20	Establishment of regions of genomic activity during the <i>Drosophila</i> maternal to zygotic transition		3

19	Association Mapping from Sequencing Reads Using K-mers		3
18	Or22 allelic variation alone does not explain differences in discrimination of yeast-produced volatiles by <i>D. melanogaster</i>		3
17	Dynamic multifactor hubs interact transiently with sites of active transcription in <i>Drosophila</i> embryos		3
16	Zelda potentiates transcription factor binding to zygotic enhancers by increasing local chromatin accessibility during early <i>Drosophila melanogaster</i> embryogenesis		3
15	Atlas ³ , patterns from every cell. <i>Science</i> , 2017 , 358, 172-173	33.3	2
14	Structural variation among wild and industrial strains of <i>Penicillium chrysogenum</i> . <i>PLoS ONE</i> , 2014 , 9, e96784	3.7	2
13	Spatial promoter recognition signatures may enhance transcription factor specificity in yeast. <i>PLoS ONE</i> , 2013 , 8, e53778	3.7	2
12	PointCloudXplore: a visualization tool for 3D gene expression data		2
11	Chronic ethanol ingestion impairs <i>Drosophila melanogaster</i> health in a microbiome-dependent manner		2
10	Oxygen changes drive non-uniform scaling in <i>Drosophila melanogaster</i> embryogenesis. <i>F1000Research</i> , 2015 , 4, 1102	3.6	2
9	Dense Bicoid Hubs Accentuate Binding along the Morphogen Gradient		2
8	Robust manipulation of the behavior of <i>Drosophila melanogaster</i> by a fungal pathogen in the laboratory		1
7	Impact of essential workers in the context of social distancing for epidemic control		1
6	The ancestral animal genetic toolkit revealed by diverse choanoflagellate transcriptomes		1
5	Mutation of sequences flanking and separating transcription factor binding sites in a <i>Drosophila</i> enhancer significantly alter its output		1
4	A chromatin extension model for insulator function based on comparison of high-resolution chromatin conformation capture and polytene banding maps		1
3	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		1
2	Exploring the genetic basis of variation in gene predictions with a synthetic association study. <i>PLoS ONE</i> , 2010 , 5, e11645	3.7	

1 Open access: the sooner the better. *Science*, **2009**, 325, 266; author reply 266-7

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