

Eileen E M Furlong

List of Publications by Citations

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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.

81

papers

6,830

citations

38

h-index

82

g-index

88

ext. papers

8,735

ext. citations

15.8

avg, IF

6.3

L-index

#	Paper	IF	Citations
81	Transcription factors: from enhancer binding to developmental control. <i>Nature Reviews Genetics</i> , 2012 , 13, 613-26	30.1	1156
80	Gene expression during the life cycle of <i>Drosophila melanogaster</i> . <i>Science</i> , 2002 , 297, 2270-5	33.3	740
79	Tissue-specific analysis of chromatin state identifies temporal signatures of enhancer activity during embryonic development. <i>Nature Genetics</i> , 2012 , 44, 148-56	36.3	370
78	Enhancer loops appear stable during development and are associated with paused polymerase. <i>Nature</i> , 2014 , 512, 96-100	50.4	332
77	Combinatorial binding predicts spatio-temporal cis-regulatory activity. <i>Nature</i> , 2009 , 462, 65-70	50.4	294
76	Developmental enhancers and chromosome topology. <i>Science</i> , 2018 , 361, 1341-1345	33.3	239
75	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016 , 167, 1145-1149	56.2	232
74	A core transcriptional network for early mesoderm development in <i>Drosophila melanogaster</i> . <i>Genes and Development</i> , 2007 , 21, 436-49	12.6	231
73	The cis-regulatory dynamics of embryonic development at single-cell resolution. <i>Nature</i> , 2018 , 555, 538-544	54.4	199
72	A transcription factor collective defines cardiac cell fate and reflects lineage history. <i>Cell</i> , 2012 , 148, 473-86	56.2	191
71	A temporal map of transcription factor activity: mef2 directly regulates target genes at all stages of muscle development. <i>Developmental Cell</i> , 2006 , 10, 797-807	10.2	185
70	Dynamic regulation by polycomb group protein complexes controls pattern formation and the cell cycle in <i>Drosophila</i> . <i>Developmental Cell</i> , 2008 , 15, 877-89	10.2	158
69	Highly rearranged chromosomes reveal uncoupling between genome topology and gene expression. <i>Nature Genetics</i> , 2019 , 51, 1272-1282	36.3	145
68	Conservation of transcription factor binding specificities across 600 million years of bilateria evolution. <i>ELife</i> , 2015 , 4,	8.9	140
67	The degree of enhancer or promoter activity is reflected by the levels and directionality of eRNA transcription. <i>Genes and Development</i> , 2018 , 32, 42-57	12.6	125
66	Shadow Enhancers Are Pervasive Features of Developmental Regulatory Networks. <i>Current Biology</i> , 2016 , 26, 38-51	6.3	121
65	The role of transcription in shaping the spatial organization of the genome. <i>Nature Reviews Molecular Cell Biology</i> , 2019 , 20, 327-337	48.7	120

64	Developmental control of nuclear size and shape by Kugelkern and Kurzkern. <i>Current Biology</i> , 2006 , 16, 543-52	6.3	90
63	ChIP-on-chip protocol for genome-wide analysis of transcription factor binding in <i>Drosophila melanogaster</i> embryos. <i>Nature Protocols</i> , 2006 , 1, 2839-55	18.8	79
62	FourCSeq: analysis of 4C sequencing data. <i>Bioinformatics</i> , 2015 , 31, 3085-91	7.2	74
61	Cell type-specific chromatin immunoprecipitation from multicellular complex samples using BITS-ChIP. <i>Nature Protocols</i> , 2012 , 7, 978-94	18.8	73
60	Je, a versatile suite to handle multiplexed NGS libraries with unique molecular identifiers. <i>BMC Bioinformatics</i> , 2016 , 17, 419	3.6	73
59	Analysis of variation at transcription factor binding sites in <i>Drosophila</i> and humans. <i>Genome Biology</i> , 2012 , 13, R49	18.3	71
58	A systematic analysis of Tinman function reveals Eya and JAK-STAT signaling as essential regulators of muscle development. <i>Developmental Cell</i> , 2009 , 16, 280-91	10.2	71
57	Model-based method for transcription factor target identification with limited data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 7793-8	11.5	67
56	Temporal ChIP-on-chip reveals Biniou as a universal regulator of the visceral muscle transcriptional network. <i>Genes and Development</i> , 2007 , 21, 2448-60	12.6	66
55	Identification of tightly regulated groups of genes during <i>Drosophila melanogaster</i> embryogenesis. <i>Molecular Systems Biology</i> , 2007 , 3, 72	12.2	62
54	A proteolytic fragment of histone deacetylase 4 protects the heart from failure by regulating the hexosamine biosynthetic pathway. <i>Nature Medicine</i> , 2018 , 24, 62-72	50.5	59
53	A conserved role for Snail as a potentiator of active transcription. <i>Genes and Development</i> , 2014 , 28, 167-181	16	57
52	Chromatin topology, condensates and gene regulation: shifting paradigms or just a phase?. <i>Development (Cambridge)</i> , 2019 , 146,	6.6	53
51	Impact of genomic structural variation in <i>Drosophila melanogaster</i> based on population-scale sequencing. <i>Genome Research</i> , 2013 , 23, 568-79	9.7	53
50	Promoter shape varies across populations and affects promoter evolution and expression noise. <i>Nature Genetics</i> , 2017 , 49, 550-558	36.3	51
49	cis-Regulatory networks during development: a view of <i>Drosophila</i> . <i>Current Opinion in Genetics and Development</i> , 2008 , 18, 513-20	4.9	47
48	Dual functionality of -regulatory elements as developmental enhancers and Polycomb response elements. <i>Genes and Development</i> , 2017 , 31, 590-602	12.6	46
47	Challenges for modeling global gene regulatory networks during development: insights from <i>Drosophila</i> . <i>Developmental Biology</i> , 2010 , 340, 161-9	3.1	44

46	Myofilin, a protein in the thick filaments of insect muscle. <i>Journal of Cell Science</i> , 2005 , 118, 1527-36	5.3	43
45	The road ahead in genetics and genomics. <i>Nature Reviews Genetics</i> , 2020 , 21, 581-596	30.1	43
44	Genetic variants regulating expression levels and isoform diversity during embryogenesis. <i>Nature</i> , 2017 , 541, 402-406	50.4	39
43	Dynamic CRM occupancy reflects a temporal map of developmental progression. <i>Molecular Systems Biology</i> , 2010 , 6, 383	12.2	37
42	Subtle changes in motif positioning cause tissue-specific effects on robustness of an enhancer's activity. <i>PLoS Genetics</i> , 2014 , 10, e1004060	6	35
41	Integrating transcriptional and signalling networks during muscle development. <i>Current Opinion in Genetics and Development</i> , 2004 , 14, 343-50	4.9	33
40	The Insulator Protein CTCF Is Required for Correct Gene Expression, but Not for Embryonic Development in. <i>Genetics</i> , 2018 , 210, 129-136	4	32
39	Predicting spatial and temporal gene expression using an integrative model of transcription factor occupancy and chromatin state. <i>PLoS Computational Biology</i> , 2012 , 8, e1002798	5	32
38	4DXpress: a database for cross-species expression pattern comparisons. <i>Nucleic Acids Research</i> , 2008 , 36, D847-53	20.1	31
37	Enhanced function annotations for Drosophila serine proteases: a case study for systematic annotation of multi-member gene families. <i>Gene</i> , 2008 , 407, 199-215	3.8	28
36	Combinatorial binding leads to diverse regulatory responses: Lmd is a tissue-specific modulator of Mef2 activity. <i>PLoS Genetics</i> , 2010 , 6, e1001014	6	27
35	Conservation and divergence in developmental networks: a view from Drosophila myogenesis. <i>Current Opinion in Cell Biology</i> , 2009 , 21, 754-60	9	26
34	Non-coding RNA Expression, Function, and Variation during Drosophila Embryogenesis. <i>Current Biology</i> , 2018 , 28, 3547-3561.e9	6.3	26
33	Uncoupling evolutionary changes in DNA sequence, transcription factor occupancy and enhancer activity. <i>ELife</i> , 2017 , 6,	8.9	24
32	Fragmentation of DNA in a sub-microliter microfluidic sonication device. <i>Lab on A Chip</i> , 2012 , 12, 4677-87.2	7.2	21
31	Chromatin accessibility profiling methods. <i>Nature Reviews Methods Primers</i> , 2021 , 1,		21
30	A Versatile, Low-Cost, Multiway Microfluidic Sorter for Droplets, Cells, and Embryos. <i>Analytical Chemistry</i> , 2018 , 90, 5982-5988	7.8	20
29	Opbp is a new architectural/insulator protein required for ribosomal gene expression. <i>Nucleic Acids Research</i> , 2017 , 45, 12285-12300	20.1	18

28	Coordinated repression and activation of two transcriptional programs stabilizes cell fate during myogenesis. <i>Development (Cambridge)</i> , 2014 , 141, 2633-43	6.6	18
27	Logical modelling of Drosophila signalling pathways. <i>Molecular BioSystems</i> , 2013 , 9, 2248-58		17
26	Characterization of Button Loci that Promote Homologous Chromosome Pairing and Cell-Type-Specific Interchromosomal Gene Regulation. <i>Developmental Cell</i> , 2019 , 51, 341-356.e7	10.2	16
25	Lineage-Resolved Enhancer and Promoter Usage during a Time Course of Embryogenesis. <i>Developmental Cell</i> , 2020 , 55, 648-664.e9	10.2	14
24	Predictive features of gene expression variation reveal mechanistic link with differential expression. <i>Molecular Systems Biology</i> , 2020 , 16, e9539	12.2	12
23	Analyzing transcription factor occupancy during embryo development using ChIP-seq. <i>Methods in Molecular Biology</i> , 2012 , 786, 229-45	1.4	9
22	A functional genomics approach to identify new regulators of Wnt signaling. <i>Developmental Cell</i> , 2005 , 8, 624-6	10.2	9
21	Divergence in cis-regulatory networks: taking the SpeciesSout of cross-species analysis. <i>Genome Biology</i> , 2008 , 9, 240	18.3	8
20	Qualitative Dynamical Modelling Can Formally Explain Mesoderm Specification and Predict Novel Developmental Phenotypes. <i>PLoS Computational Biology</i> , 2016 , 12, e1005073	5	8
19	Chromatin Immunoprecipitation for Analyzing Transcription Factor Binding and Histone Modifications in Drosophila. <i>Methods in Molecular Biology</i> , 2016 , 1478, 263-277	1.4	8
18	The Role of Chromatin Accessibility in cis-Regulatory Evolution. <i>Genome Biology and Evolution</i> , 2019 , 11, 1813-1828	3.9	7
17	Next-generation sequencing-based detection of germline L1-mediated transductions. <i>BMC Genomics</i> , 2016 , 17, 342	4.5	7
16	Accurate genome-wide predictions of spatio-temporal gene expression during embryonic development. <i>PLoS Genetics</i> , 2019 , 15, e1008382	6	4
15	Identification and in silico modeling of enhancers reveals new features of the cardiac differentiation network. <i>Development (Cambridge)</i> , 2016 , 143, 4533-4542	6.6	4
14	Correlation Does Not Imply Causation: Histone Methyltransferases, but Not Histone Methylation, SET the Stage for Enhancer Activation. <i>Molecular Cell</i> , 2017 , 66, 439-441	17.6	3
13	Extremely rapid and reversible optogenetic perturbation of nuclear proteins in living embryos. <i>Developmental Cell</i> , 2021 , 56, 2348-2363.e8	10.2	3
12	Dynamix: dynamic visualization by automatic selection of informative tracks from hundreds of genomic datasets. <i>Bioinformatics</i> , 2017 , 33, 2194-2196	7.2	2
11	A topographical map of spatiotemporal patterns of gene expression. <i>Developmental Cell</i> , 2008 , 14, 639-40.2	40.2	2

10	Author response: Conservation of transcription factor binding specificities across 600 million years of bilateria evolution 2015 ,		2
9	-acting variation is common across regulatory layers but is often buffered during embryonic development. <i>Genome Research</i> , 2020 ,	9.7	2
8	The hourglass model of evolutionary conservation during embryogenesis extends to developmental enhancers with signatures of positive selection. <i>Genome Research</i> , 2021 , 31, 1573-1581	9.7	2
7	Expanding the mesodermal transcriptional network by genome-wide identification of Zinc finger homeodomain 1 (Zfh1) targets. <i>FEBS Letters</i> , 2019 , 593, 1698-1710	3.8	1
6	The hourglass model of evolutionary conservation during embryogenesis extends to developmental enhancers with signatures of positive selection		1
5	scDALI: Modelling allelic heterogeneity of DNA accessibility in single-cells reveals context-specific genetic regulation		1
4	Regulating specificity in enhancer-promoter communication.. <i>Current Opinion in Cell Biology</i> , 2022 , 75, 102065	9	1
3	scDALI: modeling allelic heterogeneity in single cells reveals context-specific genetic regulation.. <i>Genome Biology</i> , 2022 , 23, 8	18.3	0
2	Whole Genome Approaches to Studying Drosophila Muscle Development 2006 , 157-168		
1	CoCo: a web application to display, store and curate ChIP-on-chip data integrated with diverse types of gene expression data. <i>Bioinformatics</i> , 2007 , 23, 771-3	7.2	