

# Eileen E M Furlong

## 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.

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	scDALI: modeling allelic heterogeneity in single cells reveals context-specific genetic regulation.. <i>Genome Biology</i> , <b>2022</b> , 23, 8	18.3	0
80	Regulating specificity in enhancer-promoter communication.. <i>Current Opinion in Cell Biology</i> , <b>2022</b> , 75, 102065	9	1
79	The hourglass model of evolutionary conservation during embryogenesis extends to developmental enhancers with signatures of positive selection. <i>Genome Research</i> , <b>2021</b> , 31, 1573-1581	9.7	2
78	Extremely rapid and reversible optogenetic perturbation of nuclear proteins in living embryos. <i>Developmental Cell</i> , <b>2021</b> , 56, 2348-2363.e8	10.2	3
77	Chromatin accessibility profiling methods. <i>Nature Reviews Methods Primers</i> , <b>2021</b> , 1,		21
76	Lineage-Resolved Enhancer and Promoter Usage during a Time Course of Embryogenesis. <i>Developmental Cell</i> , <b>2020</b> , 55, 648-664.e9	10.2	14
75	Predictive features of gene expression variation reveal mechanistic link with differential expression. <i>Molecular Systems Biology</i> , <b>2020</b> , 16, e9539	12.2	12
74	The road ahead in genetics and genomics. <i>Nature Reviews Genetics</i> , <b>2020</b> , 21, 581-596	30.1	43
73	-acting variation is common across regulatory layers but is often buffered during embryonic development. <i>Genome Research</i> , <b>2020</b> ,	9.7	2
72	Accurate genome-wide predictions of spatio-temporal gene expression during embryonic development. <i>PLoS Genetics</i> , <b>2019</b> , 15, e1008382	6	4
71	The Role of Chromatin Accessibility in cis-Regulatory Evolution. <i>Genome Biology and Evolution</i> , <b>2019</b> , 11, 1813-1828	3.9	7
70	Expanding the mesodermal transcriptional network by genome-wide identification of Zinc finger homeodomain 1 (Zfh1) targets. <i>FEBS Letters</i> , <b>2019</b> , 593, 1698-1710	3.8	1
69	The role of transcription in shaping the spatial organization of the genome. <i>Nature Reviews Molecular Cell Biology</i> , <b>2019</b> , 20, 327-337	48.7	120
68	Highly rearranged chromosomes reveal uncoupling between genome topology and gene expression. <i>Nature Genetics</i> , <b>2019</b> , 51, 1272-1282	36.3	145
67	Characterization of Button Loci that Promote Homologous Chromosome Pairing and Cell-Type-Specific Interchromosomal Gene Regulation. <i>Developmental Cell</i> , <b>2019</b> , 51, 341-356.e7	10.2	16
66	Chromatin topology, condensates and gene regulation: shifting paradigms or just a phase?. <i>Development (Cambridge)</i> , <b>2019</b> , 146,	6.6	53
65	A Versatile, Low-Cost, Multiway Microfluidic Sorter for Droplets, Cells, and Embryos. <i>Analytical Chemistry</i> , <b>2018</b> , 90, 5982-5988	7.8	20

64	The degree of enhancer or promoter activity is reflected by the levels and directionality of eRNA transcription. <i>Genes and Development</i> , <b>2018</b> , 32, 42-57	12.6	125
63	The cis-regulatory dynamics of embryonic development at single-cell resolution. <i>Nature</i> , <b>2018</b> , 555, 538-544	56.4	199
62	The Insulator Protein CTCF Is Required for Correct Gene Expression, but Not for Embryonic Development in. <i>Genetics</i> , <b>2018</b> , 210, 129-136	4	32
61	A proteolytic fragment of histone deacetylase 4 protects the heart from failure by regulating the hexosamine biosynthetic pathway. <i>Nature Medicine</i> , <b>2018</b> , 24, 62-72	50.5	59
60	Developmental enhancers and chromosome topology. <i>Science</i> , <b>2018</b> , 361, 1341-1345	33.3	239
59	Non-coding RNA Expression, Function, and Variation during Drosophila Embryogenesis. <i>Current Biology</i> , <b>2018</b> , 28, 3547-3561.e9	6.3	26
58	Promoter shape varies across populations and affects promoter evolution and expression noise. <i>Nature Genetics</i> , <b>2017</b> , 49, 550-558	36.3	51
57	Correlation Does Not Imply Causation: Histone Methyltransferases, but Not Histone Methylation, SET the Stage for Enhancer Activation. <i>Molecular Cell</i> , <b>2017</b> , 66, 439-441	17.6	3
56	Dual functionality of -regulatory elements as developmental enhancers and Polycomb response elements. <i>Genes and Development</i> , <b>2017</b> , 31, 590-602	12.6	46
55	Genetic variants regulating expression levels and isoform diversity during embryogenesis. <i>Nature</i> , <b>2017</b> , 541, 402-406	50.4	39
54	Opbp is a new architectural/insulator protein required for ribosomal gene expression. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 12285-12300	20.1	18
53	Dynamix: dynamic visualization by automatic selection of informative tracks from hundreds of genomic datasets. <i>Bioinformatics</i> , <b>2017</b> , 33, 2194-2196	7.2	2
52	Uncoupling evolutionary changes in DNA sequence, transcription factor occupancy and enhancer activity. <i>ELife</i> , <b>2017</b> , 6,	8.9	24
51	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , <b>2016</b> , 167, 1145-1149	56.2	232
50	Next-generation sequencing-based detection of germline L1-mediated transductions. <i>BMC Genomics</i> , <b>2016</b> , 17, 342	4.5	7
49	Shadow Enhancers Are Pervasive Features of Developmental Regulatory Networks. <i>Current Biology</i> , <b>2016</b> , 26, 38-51	6.3	121
48	Qualitative Dynamical Modelling Can Formally Explain Mesoderm Specification and Predict Novel Developmental Phenotypes. <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1005073	5	8
47	Identification and in silico modeling of enhancers reveals new features of the cardiac differentiation network. <i>Development (Cambridge)</i> , <b>2016</b> , 143, 4533-4542	6.6	4

46	Chromatin Immunoprecipitation for Analyzing Transcription Factor Binding and Histone Modifications in <i>Drosophila</i> . <i>Methods in Molecular Biology</i> , <b>2016</b> , 1478, 263-277	1.4	8
45	Je, a versatile suite to handle multiplexed NGS libraries with unique molecular identifiers. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 419	3.6	73
44	FourCSeq: analysis of 4C sequencing data. <i>Bioinformatics</i> , <b>2015</b> , 31, 3085-91	7.2	74
43	Conservation of transcription factor binding specificities across 600 million years of bilateria evolution. <i>ELife</i> , <b>2015</b> , 4,	8.9	140
42	Author response: Conservation of transcription factor binding specificities across 600 million years of bilateria evolution <b>2015</b> ,		2
41	A conserved role for Snail as a potentiator of active transcription. <i>Genes and Development</i> , <b>2014</b> , 28, 167-181	8.16	57
40	Enhancer loops appear stable during development and are associated with paused polymerase. <i>Nature</i> , <b>2014</b> , 512, 96-100	50.4	332
39	Coordinated repression and activation of two transcriptional programs stabilizes cell fate during myogenesis. <i>Development (Cambridge)</i> , <b>2014</b> , 141, 2633-43	6.6	18
38	Subtle changes in motif positioning cause tissue-specific effects on robustness of an enhancer's activity. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004060	6	35
37	Logical modelling of <i>Drosophila</i> signalling pathways. <i>Molecular BioSystems</i> , <b>2013</b> , 9, 2248-58		17
36	Impact of genomic structural variation in <i>Drosophila melanogaster</i> based on population-scale sequencing. <i>Genome Research</i> , <b>2013</b> , 23, 568-79	9.7	53
35	Analysis of variation at transcription factor binding sites in <i>Drosophila</i> and humans. <i>Genome Biology</i> , <b>2012</b> , 13, R49	18.3	71
34	A transcription factor collective defines cardiac cell fate and reflects lineage history. <i>Cell</i> , <b>2012</b> , 148, 473-86	56.2	191
33	Cell type-specific chromatin immunoprecipitation from multicellular complex samples using BiTS-ChIP. <i>Nature Protocols</i> , <b>2012</b> , 7, 978-94	18.8	73
32	Fragmentation of DNA in a sub-microliter microfluidic sonication device. <i>Lab on A Chip</i> , <b>2012</b> , 12, 4677-87	7.2	21
31	Tissue-specific analysis of chromatin state identifies temporal signatures of enhancer activity during embryonic development. <i>Nature Genetics</i> , <b>2012</b> , 44, 148-56	36.3	370
30	Transcription factors: from enhancer binding to developmental control. <i>Nature Reviews Genetics</i> , <b>2012</b> , 13, 613-26	30.1	1156
29	Analyzing transcription factor occupancy during embryo development using ChIP-seq. <i>Methods in Molecular Biology</i> , <b>2012</b> , 786, 229-45	1.4	9

28	Predicting spatial and temporal gene expression using an integrative model of transcription factor occupancy and chromatin state. <i>PLoS Computational Biology</i> , <b>2012</b> , 8, e1002798	5	32
27	Challenges for modeling global gene regulatory networks during development: insights from <i>Drosophila</i> . <i>Developmental Biology</i> , <b>2010</b> , 340, 161-9	3.1	44
26	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> , <b>2010</b> , 107, 7793-8	11.5	67
25	Dynamic CRM occupancy reflects a temporal map of developmental progression. <i>Molecular Systems Biology</i> , <b>2010</b> , 6, 383	12.2	37
24	Combinatorial binding leads to diverse regulatory responses: Lmd is a tissue-specific modulator of Mef2 activity. <i>PLoS Genetics</i> , <b>2010</b> , 6, e1001014	6	27
23	Conservation and divergence in developmental networks: a view from <i>Drosophila</i> myogenesis. <i>Current Opinion in Cell Biology</i> , <b>2009</b> , 21, 754-60	9	26
22	Combinatorial binding predicts spatio-temporal cis-regulatory activity. <i>Nature</i> , <b>2009</b> , 462, 65-70	50.4	294
21	A systematic analysis of Tinman function reveals Eya and JAK-STAT signaling as essential regulators of muscle development. <i>Developmental Cell</i> , <b>2009</b> , 16, 280-91	10.2	71
20	Divergence in cis-regulatory networks: taking the SpeciesSout of cross-species analysis. <i>Genome Biology</i> , <b>2008</b> , 9, 240	18.3	8
19	cis-Regulatory networks during development: a view of <i>Drosophila</i> . <i>Current Opinion in Genetics and Development</i> , <b>2008</b> , 18, 513-20	4.9	47
18	Enhanced function annotations for <i>Drosophila</i> serine proteases: a case study for systematic annotation of multi-member gene families. <i>Gene</i> , <b>2008</b> , 407, 199-215	3.8	28
17	A topographical map of spatiotemporal patterns of gene expression. <i>Developmental Cell</i> , <b>2008</b> , 14, 639-40.2	10.2	2
16	Dynamic regulation by polycomb group protein complexes controls pattern formation and the cell cycle in <i>Drosophila</i> . <i>Developmental Cell</i> , <b>2008</b> , 15, 877-89	10.2	158
15	4DXpress: a database for cross-species expression pattern comparisons. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D847-53	20.1	31
14	Temporal CHIP-on-chip reveals Biniou as a universal regulator of the visceral muscle transcriptional network. <i>Genes and Development</i> , <b>2007</b> , 21, 2448-60	12.6	66
13	CoCo: a web application to display, store and curate CHIP-on-chip data integrated with diverse types of gene expression data. <i>Bioinformatics</i> , <b>2007</b> , 23, 771-3	7.2	
12	A core transcriptional network for early mesoderm development in <i>Drosophila melanogaster</i> . <i>Genes and Development</i> , <b>2007</b> , 21, 436-49	12.6	231
11	Identification of tightly regulated groups of genes during <i>Drosophila melanogaster</i> embryogenesis. <i>Molecular Systems Biology</i> , <b>2007</b> , 3, 72	12.2	62

10	Developmental control of nuclear size and shape by Kugelkern and Kurzkern. <i>Current Biology</i> , <b>2006</b> , 16, 543-52	6.3	90
9	Whole Genome Approaches to Studying Drosophila Muscle Development <b>2006</b> , 157-168		
8	A temporal map of transcription factor activity: mef2 directly regulates target genes at all stages of muscle development. <i>Developmental Cell</i> , <b>2006</b> , 10, 797-807	10.2	185
7	ChIP-on-chip protocol for genome-wide analysis of transcription factor binding in Drosophila melanogaster embryos. <i>Nature Protocols</i> , <b>2006</b> , 1, 2839-55	18.8	79
6	Myofilin, a protein in the thick filaments of insect muscle. <i>Journal of Cell Science</i> , <b>2005</b> , 118, 1527-36	5.3	43
5	A functional genomics approach to identify new regulators of Wnt signaling. <i>Developmental Cell</i> , <b>2005</b> , 8, 624-6	10.2	9
4	Integrating transcriptional and signalling networks during muscle development. <i>Current Opinion in Genetics and Development</i> , <b>2004</b> , 14, 343-50	4.9	33
3	Gene expression during the life cycle of Drosophila melanogaster. <i>Science</i> , <b>2002</b> , 297, 2270-5	33.3	74 <sup>o</sup>
2	The hourglass model of evolutionary conservation during embryogenesis extends to developmental enhancers with signatures of positive selection		1
1	scDALI: Modelling allelic heterogeneity of DNA accessibility in single-cells reveals context-specific genetic regulation		1