

Daofeng Li

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.

62

papers

7,436

citations

32

h-index

73

g-index

73

ext. papers

9,865

ext. citations

15

avg, IF

5.07

L-index

#	Paper	IF	Citations
62	The Human Pangenome Project: a global resource to map genomic diversity.. <i>Nature</i> , 2022 , 604, 437-446	50.4	7
61	WashU Epigenome Browser update 2022.. <i>Nucleic Acids Research</i> , 2022 ,	20.1	3
60	Epigenetic dynamics shaping melanophore and iridophore cell fate in zebrafish. <i>Genome Biology</i> , 2021 , 22, 282	18.3	4
59	Human placental cytotrophoblast epigenome dynamics over gestation and alterations in placental disease. <i>Developmental Cell</i> , 2021 , 56, 1238-1252.e5	10.2	7
58	The qBED track: a novel genome browser visualization for point processes. <i>Bioinformatics</i> , 2021 , 37, 1168-1170	2	2
57	AIAP: A Quality Control and Integrative Analysis Package to Improve ATAC-seq Data Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , 2021 ,	6.5	6
56	DeepH&M: Estimating single-CpG hydroxymethylation and methylation levels from enrichment and restriction enzyme sequencing methods. <i>Science Advances</i> , 2020 , 6,	14.3	2
55	A map of cis-regulatory elements and 3D genome structures in zebrafish. <i>Nature</i> , 2020 , 588, 337-343	50.4	18
54	Exploring the coronavirus pandemic with the WashU Virus Genome Browser. <i>Nature Genetics</i> , 2020 , 52, 986-991	36.3	8
53	Epigenomic differences in the human and chimpanzee genomes are associated with structural variation. <i>Genome Research</i> , 2020 ,	9.7	3
52	WashU Epigenome Browser update 2019. <i>Nucleic Acids Research</i> , 2019 , 47, W158-W165	20.1	107
51	Transposable elements drive widespread expression of oncogenes in human cancers. <i>Nature Genetics</i> , 2019 , 51, 611-617	36.3	112
50	A non-randomized procedure for large-scale heterogeneous multiple discrete testing based on randomized tests. <i>Biometrics</i> , 2019 , 75, 638-649	1.8	1
49	The NIEHS TaRGET II Consortium and environmental epigenomics. <i>Nature Biotechnology</i> , 2018 , 36, 225-227	27.5	44
48	Maternal high-fat diet associated with altered gene expression, DNA methylation, and obesity risk in mouse offspring. <i>PLoS ONE</i> , 2018 , 13, e0192606	3.7	66
47	Comprehensive Whole DNA Methylome Analysis by Integrating MeDIP-seq and MRE-seq. <i>Methods in Molecular Biology</i> , 2018 , 1708, 209-246	1.4	14
46	Characterization of a Mouse Model of Björnsen-Forssman-Lehmann Syndrome. <i>Cell Reports</i> , 2018 , 25, 1404-1414.e6	10.6	11

45	A high-fat diet alters genome-wide DNA methylation and gene expression in SM/J mice. <i>BMC Genomics</i> , 2018 , 19, 888	4.5	20
44	The 3D Genome Browser: a web-based browser for visualizing 3D genome organization and long-range chromatin interactions. <i>Genome Biology</i> , 2018 , 19, 151	18.3	226
43	Soluble inflammatory mediators induce transcriptional re-organization that is independent of dna methylation changes in cultured human chorionic villous trophoblasts. <i>Journal of Reproductive Immunology</i> , 2018 , 128, 2-8	4.2	2
42	Whole-Genome DNA Methylation Profiling Identifies Epigenetic Signatures of Uterine Carcinosarcoma. <i>Neoplasia</i> , 2017 , 19, 100-111	6.4	18
41	ETV2/ER71 regulates hematopoietic regeneration by promoting hematopoietic stem cell proliferation. <i>Journal of Experimental Medicine</i> , 2017 , 214, 1643-1653	16.6	13
40	DNMT and HDAC inhibitors induce cryptic transcription start sites encoded in long terminal repeats. <i>Nature Genetics</i> , 2017 , 49, 1052-1060	36.3	157
39	The 4D nucleome project. <i>Nature</i> , 2017 , 549, 219-226	50.4	332
38	MicroRNAs Induce a Permissive Chromatin Environment that Enables Neuronal Subtype-Specific Reprogramming of Adult Human Fibroblasts. <i>Cell Stem Cell</i> , 2017 , 21, 332-348.e9	18	76
37	Tissue-specific DNA methylation is conserved across human, mouse, and rat, and driven by primary sequence conservation. <i>BMC Genomics</i> , 2017 , 18, 724	4.5	35
36	DNA methyltransferase 3b regulates articular cartilage homeostasis by altering metabolism. <i>JCI Insight</i> , 2017 , 2,	9.9	35
35	Mapping of Variable DNA Methylation Across Multiple Cell Types Defines a Dynamic Regulatory Landscape of the Human Genome. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 973-86	3.2	34
34	Epigenetic Drug Treatment Globally Induces Cryptic Transcription Start Sites Encoded in Long Terminal Repeats. <i>Blood</i> , 2016 , 128, 3931-3931	2.2	
33	Developmental enhancers revealed by extensive DNA methylome maps of zebrafish early embryos. <i>Nature Communications</i> , 2015 , 6, 6315	17.4	62
32	Induction of hematopoietic and endothelial cell program orchestrated by ETS transcription factor ER71/ETV2. <i>EMBO Reports</i> , 2015 , 16, 654-69	6.5	65
31	Combining MeDIP-seq and MRE-seq to investigate genome-wide CpG methylation. <i>Methods</i> , 2015 , 72, 29-40	4.6	73
30	De novo transcriptome analysis of <i>Medicago falcata</i> reveals novel insights about the mechanisms underlying abiotic stress-responsive pathway. <i>BMC Genomics</i> , 2015 , 16, 818	4.5	36
29	Potato virus Y HC-Pro Reduces the ATPase Activity of NtMinD, Which Results in Enlarged Chloroplasts in HC-Pro Transgenic Tobacco. <i>PLoS ONE</i> , 2015 , 10, e0136210	3.7	3
28	Perinatal deiodinase 2 expression in hepatocytes defines epigenetic susceptibility to liver steatosis and obesity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 14018-23	11.5	27

27	Intermediate DNA methylation is a conserved signature of genome regulation. <i>Nature Communications</i> , 2015 , 6, 6363	17.4	67
26	Epigenomic annotation of genetic variants using the Roadmap Epigenome Browser. <i>Nature Biotechnology</i> , 2015 , 33, 345-6	44.5	66
25	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015 , 518, 317-30	50.4	3849
24	Monoacylglycerol lipase (MGLL) polymorphism rs604300 interacts with childhood adversity to predict cannabis dependence symptoms and amygdala habituation: Evidence from an endocannabinoid system-level analysis. <i>Journal of Abnormal Psychology</i> , 2015 , 124, 860-77	7	26
23	methyLC Track: visual integration of single-base resolution DNA methylation data on the WashU EpiGenome Browser. <i>Bioinformatics</i> , 2014 , 30, 2206-7	7.2	19
22	Widespread contribution of transposable elements to the innovation of gene regulatory networks. <i>Genome Research</i> , 2014 , 24, 1963-76	9.7	251
21	Recurrent epimutations activate gene body promoters in primary glioblastoma. <i>Genome Research</i> , 2014 , 24, 761-74	9.7	35
20	Regulatory network decoded from epigenomes of surface ectoderm-derived cell types. <i>Nature Communications</i> , 2014 , 5, 5442	17.4	22
19	DNA unmethylome profiling by covalent capture of CpG sites. <i>Nature Communications</i> , 2013 , 4, 2190	17.4	41
18	Estimating absolute methylation levels at single-CpG resolution from methylation enrichment and restriction enzyme sequencing methods. <i>Genome Research</i> , 2013 , 23, 1541-53	9.7	114
17	Exploring long-range genome interactions using the WashU Epigenome Browser. <i>Nature Methods</i> , 2013 , 10, 375-6	21.6	167
16	DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. <i>Nature Genetics</i> , 2013 , 45, 836-41	36.3	154
15	Functional DNA methylation differences between tissues, cell types, and across individuals discovered using the M&M algorithm. <i>Genome Research</i> , 2013 , 23, 1522-40	9.7	119
14	Medicago truncatula transporter database: a comprehensive database resource for M. truncatula transporters. <i>BMC Genomics</i> , 2012 , 13, 60	4.5	8
13	Transcriptional profiling of Medicago truncatula under salt stress identified a novel CBF transcription factor MtCBF4 that plays an important role in abiotic stress responses. <i>BMC Plant Biology</i> , 2011 , 11, 109	5.3	89
12	The Human Epigenome Browser at Washington University. <i>Nature Methods</i> , 2011 , 8, 989-90	21.6	240
11	PMRD: plant microRNA database. <i>Nucleic Acids Research</i> , 2010 , 38, D806-13	20.1	272
10	Cloning and characterization of a functional flavanone-3-hydroxylase gene from Medicago truncatula. <i>Molecular Biology Reports</i> , 2010 , 37, 3283-9	2.8	13

9	An expression database for roots of the model legume <i>Medicago truncatula</i> under salt stress. <i>BMC Genomics</i> , 2009 , 10, 517	4.5	56
8	Identification and characterization of MtMTP1, a Zn transporter of CDF family, in the <i>Medicago truncatula</i> . <i>Plant Physiology and Biochemistry</i> , 2009 , 47, 1089-94	5.4	17
7	HC-Pro protein of Potato virus Y can interact with three Arabidopsis 20S proteasome subunits in planta. <i>Journal of Virology</i> , 2007 , 81, 12881-8	6.6	62
6	The HC-pro protein of potato virus Y interacts with NtMinD of tobacco. <i>Molecular Plant-Microbe Interactions</i> , 2007 , 20, 1505-11	3.6	68
5	The Human Epigenome Browser at Washington University		1
4	The 3D Genome Browser: a web-based browser for visualizing 3D genome organization and long-range chromatin interactions		32
3	Exploring the coronavirus epidemic using the new WashU Virus Genome Browser		3
2	Improving ATAC-seq Data Analysis with AIAP, a Quality Control and Integrative Analysis Package		8
1	Automated assembly of high-quality diploid human reference genomes		3