

Daofeng Li

List of Publications by Citations

Source: <https://exaly.com/author-pdf/1193294/daofeng-li-publications-by-citations.pdf>

Version: 2024-04-19

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015 , 518, 317-30	50.4	3849
61	The 4D nucleome project. <i>Nature</i> , 2017 , 549, 219-226	50.4	332
60	PMRD: plant microRNA database. <i>Nucleic Acids Research</i> , 2010 , 38, D806-13	20.1	272
59	Widespread contribution of transposable elements to the innovation of gene regulatory networks. <i>Genome Research</i> , 2014 , 24, 1963-76	9.7	251
58	The Human Epigenome Browser at Washington University. <i>Nature Methods</i> , 2011 , 8, 989-90	21.6	240
57	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
56	Exploring long-range genome interactions using the WashU Epigenome Browser. <i>Nature Methods</i> , 2013 , 10, 375-6	21.6	167
55	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
54	DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. <i>Nature Genetics</i> , 2013 , 45, 836-41	36.3	154
53	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
52	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
51	Transposable elements drive widespread expression of oncogenes in human cancers. <i>Nature Genetics</i> , 2019 , 51, 611-617	36.3	112
50	WashU Epigenome Browser update 2019. <i>Nucleic Acids Research</i> , 2019 , 47, W158-W165	20.1	107
49	Transcriptional profiling of <i>Medicago truncatula</i> 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
48	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
47	Combining MeDIP-seq and MRE-seq to investigate genome-wide CpG methylation. <i>Methods</i> , 2015 , 72, 29-40	4.6	73
46	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

45	Intermediate DNA methylation is a conserved signature of genome regulation. <i>Nature Communications</i> , 2015 , 6, 6363	17.4	67
44	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
43	Epigenomic annotation of genetic variants using the Roadmap Epigenome Browser. <i>Nature Biotechnology</i> , 2015 , 33, 345-6	44.5	66
42	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
41	Developmental enhancers revealed by extensive DNA methylome maps of zebrafish early embryos. <i>Nature Communications</i> , 2015 , 6, 6315	17.4	62
40	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
39	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
38	The NIEHS TaRGET II Consortium and environmental epigenomics. <i>Nature Biotechnology</i> , 2018 , 36, 225-227	44.5	44
37	DNA unmethylome profiling by covalent capture of CpG sites. <i>Nature Communications</i> , 2013 , 4, 2190	17.4	41
36	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
35	Recurrent epimutations activate gene body promoters in primary glioblastoma. <i>Genome Research</i> , 2014 , 24, 761-74	9.7	35
34	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
33	DNA methyltransferase 3b regulates articular cartilage homeostasis by altering metabolism. <i>JCI Insight</i> , 2017 , 2,	9.9	35
32	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
31	The 3D Genome Browser: a web-based browser for visualizing 3D genome organization and long-range chromatin interactions		32
30	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
29	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
28	Regulatory network decoded from epigenomes of surface ectoderm-derived cell types. <i>Nature Communications</i> , 2014 , 5, 5442	17.4	22

27	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
26	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
25	Whole-Genome DNA Methylation Profiling Identifies Epigenetic Signatures of Uterine Carcinosarcoma. <i>Neoplasia</i> , 2017 , 19, 100-111	6.4	18
24	A map of cis-regulatory elements and 3D genome structures in zebrafish. <i>Nature</i> , 2020 , 588, 337-343	50.4	18
23	Identification and characterization of MtMTP1, a Zn transporter of CDF family, in the Medicago truncatula. <i>Plant Physiology and Biochemistry</i> , 2009 , 47, 1089-94	5.4	17
22	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
21	ETV2/ER71 regulates hematopoietic regeneration by promoting hematopoietic stem cell proliferation. <i>Journal of Experimental Medicine</i> , 2017 , 214, 1643-1653	16.6	13
20	Cloning and characterization of a functional flavanone-3 β hydroxylase gene from Medicago truncatula. <i>Molecular Biology Reports</i> , 2010 , 37, 3283-9	2.8	13
19	Characterization of a Mouse Model of B β eson-Forsman-Lehmann Syndrome. <i>Cell Reports</i> , 2018 , 25, 1404-1414.e6	10.6	11
18	Medicago truncatula transporter database: a comprehensive database resource for M. truncatula transporters. <i>BMC Genomics</i> , 2012 , 13, 60	4.5	8
17	Improving ATAC-seq Data Analysis with AIAP, a Quality Control and Integrative Analysis Package		8
16	Exploring the coronavirus pandemic with the WashU Virus Genome Browser. <i>Nature Genetics</i> , 2020 , 52, 986-991	36.3	8
15	Human placental cytotrophoblast epigenome dynamics over gestation and alterations in placental disease. <i>Developmental Cell</i> , 2021 , 56, 1238-1252.e5	10.2	7
14	The Human Pangenome Project: a global resource to map genomic diversity.. <i>Nature</i> , 2022 , 604, 437-446	50.4	7
13	AIAP: A Quality Control and Integrative Analysis Package to Improve ATAC-seq Data Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , 2021 ,	6.5	6
12	Epigenetic dynamics shaping melanophore and iridophore cell fate in zebrafish. <i>Genome Biology</i> , 2021 , 22, 282	18.3	4
11	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
10	Exploring the coronavirus epidemic using the new WashU Virus Genome Browser		3

9	Epigenomic differences in the human and chimpanzee genomes are associated with structural variation. <i>Genome Research</i> , 2020 ,	9.7	3
8	Automated assembly of high-quality diploid human reference genomes		3
7	WashU Epigenome Browser update 2022.. <i>Nucleic Acids Research</i> , 2022 ,	20.1	3
6	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
5	The qBED track: a novel genome browser visualization for point processes. <i>Bioinformatics</i> , 2021 , 37, 1168-1170		2
4	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
3	The Human Epigenome Browser at Washington University		1
2	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
1	Epigenetic Drug Treatment Globally Induces Cryptic Transcription Start Sites Encoded in Long Terminal Repeats. <i>Blood</i> , 2016 , 128, 3931-3931	2.2	