Daofeng Li

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1193294/publications.pdf

Version: 2024-02-01

61 papers	11,272 citations	109137 35 h-index	128067 60 g-index
73 all docs	73 docs citations	73 times ranked	24381 citing authors

#	Article	IF	Citations
1	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	13.7	5,653
2	The 4D nucleome project. Nature, 2017, 549, 219-226.	13.7	579
3	Widespread contribution of transposable elements to the innovation of gene regulatory networks. Genome Research, 2014, 24, 1963-1976.	2.4	408
4	The 3D Genome Browser: a web-based browser for visualizing 3D genome organization and long-range chromatin interactions. Genome Biology, 2018, 19, 151.	3.8	393
5	PMRD: plant microRNA database. Nucleic Acids Research, 2010, 38, D806-D813.	6.5	326
6	The Human Epigenome Browser at Washington University. Nature Methods, 2011, 8, 989-990.	9.0	302
7	Transposable elements drive widespread expression of oncogenes in human cancers. Nature Genetics, 2019, 51, 611-617.	9.4	253
8	DNMT and HDAC inhibitors induce cryptic transcription start sites encoded in long terminal repeats. Nature Genetics, 2017, 49, 1052-1060.	9.4	235
9	WashU Epigenome Browser update 2019. Nucleic Acids Research, 2019, 47, W158-W165.	6.5	223
10	DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. Nature Genetics, 2013, 45, 836-841.	9.4	207
11	Exploring long-range genome interactions using the WashU Epigenome Browser. Nature Methods, 2013, 10, 375-376.	9.0	199
12	The Human Pangenome Project: a global resource to map genomic diversity. Nature, 2022, 604, 437-446.	13.7	192
13	Functional DNA methylation differences between tissues, cell types, and across individuals discovered using the M&M algorithm. Genome Research, 2013, 23, 1522-1540.	2.4	162
14	Estimating absolute methylation levels at single-CpG resolution from methylation enrichment and restriction enzyme sequencing methods. Genome Research, 2013, 23, 1541-1553.	2.4	138
15	MicroRNAs Induce a Permissive Chromatin Environment that Enables Neuronal Subtype-Specific Reprogramming of Adult Human Fibroblasts. Cell Stem Cell, 2017, 21, 332-348.e9.	5.2	112
16	Transcriptional profiling of Medicago truncatula under salt stress identified a novel CBF transcription factor MtCBF4 that plays an important role in abiotic stress responses. BMC Plant Biology, 2011, 11, 109.	1.6	111
17	Induction of hematopoietic and endothelial cell program orchestrated by <scp>ETS</scp> transcription factor <scp>ER</scp> 71/ <scp>ETV</scp> 2. EMBO Reports, 2015, 16, 654-669.	2.0	95
18	Maternal high-fat diet associated with altered gene expression, DNA methylation, and obesity risk in mouse offspring. PLoS ONE, 2018, 13, e0192606.	1.1	95

#	Article	IF	Citations
19	Combining MeDIP-seq and MRE-seq to investigate genome-wide CpG methylation. Methods, 2015, 72, 29-40.	1.9	93
20	Intermediate DNA methylation is a conserved signature of genome regulation. Nature Communications, 2015, 6, 6363.	5.8	91
21	Epigenomic annotation of genetic variants using the Roadmap Epigenome Browser. Nature Biotechnology, 2015, 33, 345-346.	9.4	83
22	A map of cis-regulatory elements and 3D genome structures in zebrafish. Nature, 2020, 588, 337-343.	13.7	80
23	The NIEHS TaRGET II Consortium and environmental epigenomics. Nature Biotechnology, 2018, 36, 225-227.	9.4	79
24	The HC-Pro Protein of <i>Potato Virus Y</i> Interacts with NtMinD of Tobacco. Molecular Plant-Microbe Interactions, 2007, 20, 1505-1511.	1.4	73
25	Developmental enhancers revealed by extensive DNA methylome maps of zebrafish early embryos. Nature Communications, 2015, 6, 6315.	5.8	73
26	Tissue-specific DNA methylation is conserved across human, mouse, and rat, and driven by primary sequence conservation. BMC Genomics, 2017, 18, 724.	1.2	71
27	HC-Pro Protein of <i>Potato Virus Y</i> Can Interact with Three <i>Arabidopsis</i> 20S Proteasome Subunits In Planta. Journal of Virology, 2007, 81, 12881-12888.	1.5	70
28	An expression database for roots of the model legume Medicago truncatula under salt stress. BMC Genomics, 2009, 10, 517.	1.2	65
29	WashU Epigenome Browser update 2022. Nucleic Acids Research, 2022, 50, W774-W781.	6.5	62
30	DNA methyltransferase 3b regulates articular cartilage homeostasis by altering metabolism. JCI Insight, 2017, 2, .	2.3	55
31	DNA unmethylome profiling by covalent capture of CpG sites. Nature Communications, 2013, 4, 2190.	5.8	53
32	De novo transcriptome analysis of Medicago falcata reveals novel insights about the mechanisms underlying abiotic stress-responsive pathway. BMC Genomics, 2015, 16, 818.	1.2	48
33	Mapping of Variable DNA Methylation Across Multiple Cell Types Defines a Dynamic Regulatory Landscape of the Human Genome. G3: Genes, Genomes, Genetics, 2016, 6, 973-986.	0.8	41
34	Recurrent epimutations activate gene body promoters in primary glioblastoma. Genome Research, 2014, 24, 761-774.	2.4	39
35	Monoacylglycerol lipase (MGLL) polymorphism rs604300 interacts with childhood adversity to predict cannabis dependence symptoms and amygdala habituation: Evidence from an endocannabinoid system-level analysis.. Journal of Abnormal Psychology, 2015, 124, 860-877.	2.0	39
36	Perinatal deiodinase 2 expression in hepatocytes defines epigenetic susceptibility to liver steatosis and obesity. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14018-14023.	3.3	34

#	Article	IF	Citations
37	A high-fat diet alters genome-wide DNA methylation and gene expression in SM/J mice. BMC Genomics, 2018, 19, 888.	1.2	34
38	Human placental cytotrophoblast epigenome dynamics over gestation and alterations in placental disease. Developmental Cell, 2021, 56, 1238-1252.e5.	3.1	29
39	Whole-Genome DNA Methylation Profiling Identifies Epigenetic Signatures of Uterine Carcinosarcoma. Neoplasia, 2017, 19, 100-111.	2.3	27
40	methylC Track: visual integration of single-base resolution DNA methylation data on the WashU EpiGenome Browser. Bioinformatics, 2014, 30, 2206-2207.	1.8	26
41	Regulatory network decoded from epigenomes of surface ectoderm-derived cell types. Nature Communications, 2014, 5, 5442.	5.8	25
42	Identification and characterization of MtMTP1, a Zn transporter of CDF family, in the Medicago truncatula. Plant Physiology and Biochemistry, 2009, 47, 1089-1094.	2.8	22
43	ETV2/ER71 regulates hematopoietic regeneration by promoting hematopoietic stem cell proliferation. Journal of Experimental Medicine, 2017, 214, 1643-1653.	4.2	22
44	Cloning and characterization of a functional flavanone-3ÃŸ-hydroxylase gene from Medicago truncatula. Molecular Biology Reports, 2010, 37, 3283-3289.	1.0	20
45	Comprehensive Whole DNA Methylome Analysis by Integrating MeDIP-seq and MRE-seq. Methods in Molecular Biology, 2018, 1708, 209-246.	0.4	20
46	Characterization of a Mouse Model of BÃ¶rjeson-Forssman-Lehmann Syndrome. Cell Reports, 2018, 25, 1404-1414.e6.	2.9	19
47	AIAP: A Quality Control and Integrative Analysis Package to Improve ATAC-seq Data Analysis. Genomics, Proteomics and Bioinformatics, 2021, 19, 641-651.	3.0	19
48	Whole-genome profiling of DNA methylation and hydroxymethylation identifies distinct regulatory programs among innate lymphocytes. Nature Immunology, 2022, 23, 619-631.	7.0	14
49	Exploring the coronavirus pandemic with the WashU Virus Genome Browser. Nature Genetics, 2020, 52, 986-991.	9.4	13
50	Single-cell transcriptional regulation and genetic evolution of neuroendocrine prostate cancer. IScience, 2022, 25, 104576.	1.9	13
51	Medicago truncatula transporter database: a comprehensive database resource for M. truncatula transporters. BMC Genomics, 2012, 13, 60.	1.2	9
52	DeepH&M: Estimating single-CpG hydroxymethylation and methylation levels from enrichment and restriction enzyme sequencing methods. Science Advances, 2020, 6, .	4.7	8
53	Epigenetic dynamics shaping melanophore and iridophore cell fate in zebrafish. Genome Biology, 2021, 22, 282.	3.8	8
54	Epigenomic differences in the human and chimpanzee genomes are associated with structural variation. Genome Research, 2021, 31, 279-290.	2.4	7

#	ARTICLE	IF	CITATIONS
55	Potato virus Y HC-Pro Reduces the ATPase Activity of NtMinD, Which Results in Enlarged Chloroplasts in HC-Pro Transgenic Tobacco. PLoS ONE, 2015, 10, e0136210.	1.1	4
56	The qBED track: a novel genome browser visualization for point processes. Bioinformatics, 2021, 37, 1168-1170.	1.8	4
57	Soluble inflammatory mediators induce transcriptional re-organization that is independent of dna methylation changes in cultured human chorionic villous trophoblasts. Journal of Reproductive Immunology, 2018, 128, 2-8.	0.8	3
58	A Non-Randomized Procedure for Large-Scale Heterogeneous Multiple Discrete Testing Based on Randomized Tests. Biometrics, 2019, 75, 638-649.	0.8	3
59	The Human Epigenome Browser at Washington University. , 0, .		1
60	Abstract 2225: Transposable elements are an abundant and pan-cancer source of shared tumor-specific antigens and membrane targets. , 2021, , .		0
61	Epigenetic Drug Treatment Globally Induces Cryptic Transcription Start Sites Encoded in Long Terminal Repeats. Blood, 2016, 128, 3931-3931.	0.6	0