Hongbo Liu

List of Publications by Year
in descending order

72 papers	2,058 citations	236925 25 h-index	265206 42 g-index
77 all docs	77 docs citations	77 times ranked	2941 citing authors

#	Article	IF	Citations
1	DiseaseMeth version 2.0: a major expansion and update of the human disease methylation database. Nucleic Acids Research, 2017, 45, D888-D895.	14.5	126
2	Single cell regulatory landscape of the mouse kidney highlights cellular differentiation programs and disease targets. Nature Communications, 2021, 12, 2277.	12.8	122
3	QDMR: a quantitative method for identification of differentially methylated regions by entropy. Nucleic Acids Research, 2011, 39, e58-e58.	14.5	105
4	The Nuclear Receptor ESRRA Protects from Kidney Disease by Coupling Metabolism and Differentiation. Cell Metabolism, 2021, 33, 379-394.e8.	16.2	93
5	SEA: a super-enhancer archive. Nucleic Acids Research, 2016, 44, D172-D179.	14.5	88
6	Mapping the genetic architecture of human traits to cell types in the kidney identifies mechanisms of disease and potential treatments. Nature Genetics, 2021, 53, 1322-1333.	21.4	87
7	Systematic identification and annotation of human methylation marks based on bisulfite sequencing methylomes reveals distinct roles of cell type-specific hypomethylation in the regulation of cell identity genes. Nucleic Acids Research, 2016, 44, 75-94.	14.5	83
8	DiseaseMeth: a human disease methylation database. Nucleic Acids Research, 2012, 40, D1030-D1035.	14.5	81
9	HHMD: the human histone modification database. Nucleic Acids Research, 2010, 38, D149-D154.	14.5	79
10	Epigenomic and transcriptomic analyses define core cell types, genes and targetable mechanisms for kidney disease. Nature Genetics, 2022, 54, 950-962.	21.4	71
11	MetaImprint: an information repository of mammalian imprinted genes. Development (Cambridge), 2014, 141, 2516-2523.	2.5	68
12	Specific breast cancer prognosisâ€subtype distinctions based on <scp>DNA</scp> methylation patterns. Molecular Oncology, 2018, 12, 1047-1060.	4.6	68
13	Long non-coding RNA identification over mouse brain development by integrative modeling of chromatin and genomic features. Nucleic Acids Research, 2013, 41, 10044-10061.	14.5	65
14	Urinary Single-Cell Profiling Captures the Cellular Diversity of the Kidney. Journal of the American Society of Nephrology: JASN, 2021, 32, 614-627.	6.1	64
15	Identification and Characterization of Long Non-Coding RNAs Related to Mouse Embryonic Brain Development from Available Transcriptomic Data. PLoS ONE, 2013, 8, e71152.	2.5	55
16	Transcriptome-wide association analysis identifies DACH1 as a kidney disease risk gene that contributes to fibrosis. Journal of Clinical Investigation, 2021, 131, .	8.2	49
17	CpG_MPs: identification of CpG methylation patterns of genomic regions from high-throughput bisulfite sequencing data. Nucleic Acids Research, 2013, 41, e4-e4.	14.5	48
18	The Identification of Specific Methylation Patterns across Different Cancers. PLoS ONE, 2015, 10, e0120361.	2.5	48

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19	Systematic integrated analysis of genetic and epigenetic variation in diabetic kidney disease. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 29013-29024.	7.1	46
20	Genome-wide dynamic changes of DNA methylation of repetitive elements in human embryonic stem cells and fetal fibroblasts. Genomics, 2012, 99, 10-17.	2.9	45
21	A single genetic locus controls both expression of DPEP1/CHMP1A and kidney disease development via ferroptosis. Nature Communications, 2021, 12, 5078.	12.8	45
22	CpG_MI: a novel approach for identifying functional CpG islands in mammalian genomes. Nucleic Acids Research, 2010, 38, e6-e6.	14.5	40
23	The identification of age-associated cancer markers by an integrative analysis of dynamic DNA methylation changes. Scientific Reports, 2016, 6, 22722.	3.3	31
24	Meta-analyses identify DNA methylation associated with kidney function and damage. Nature Communications, 2021, 12, 7174.	12.8	30
25	Identification and characterization of long intergenic non-coding RNAs related to mouse liver development. Molecular Genetics and Genomics, 2014, 289, 1225-1235.	2.1	28
26	Folic Acid Alters Methylation Profile of JAK-STAT and Long-Term Depression Signaling Pathways in Alzheimer's Disease Models. Molecular Neurobiology, 2016, 53, 6548-6556.	4.0	27
27	Rice Protein Extracted by Different Methods Affects Cholesterol Metabolism in Rats Due to Its Lower Digestibility. International Journal of Molecular Sciences, 2011, 12, 7594-7608.	4.1	26
28	Identification of 4438 novel lincRNAs involved in mouse pre-implantation embryonic development. Molecular Genetics and Genomics, 2015, 290, 685-697.	2.1	24
29	Identification and functional analysis of long intergenic noncoding RNA genes in porcine pre-implantation embryonic development. Scientific Reports, 2016, 6, 38333.	3.3	24
30	Prioritizing cancer-related genes with aberrant methylation based on a weighted protein-protein interaction network. BMC Systems Biology, 2011, 5, 158.	3.0	20
31	Quantitative epigenetic co-variation in CpG islands and co-regulation of developmental genes. Scientific Reports, 2013, 3, 2576.	3.3	20
32	Cell subpopulation deconvolution reveals breast cancer heterogeneity based on DNA methylation signature. Briefings in Bioinformatics, 2017, 18, bbw028.	6.5	18
33	Renal Histologic Analysis Provides Complementary Information to Kidney Function Measurement for Patients with Early Diabetic or Hypertensive Disease. Journal of the American Society of Nephrology: JASN, 2021, 32, 2863-2876.	6.1	18
34	DNA Methylation Patterns Can Estimate Nonequivalent Outcomes of Breast Cancer with the Same Receptor Subtypes. PLoS ONE, 2015, 10, e0142279.	2.5	17
35	Genome-wide meta-analysis and omics integration identifies novel genes associated with diabetic kidney disease. Diabetologia, 2022, 65, 1495-1509.	6.3	16
36	Genome-wide association studies identify the role of caspase-9 in kidney disease. Science Advances, 2021, 7, eabi8051.	10.3	14

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37	DNA methylation dynamics: identification and functional annotation. Briefings in Functional Genomics, 2016, 15, elw029.	2.7	13
38	Dnmt3a and Dnmt3b-Decommissioned Fetal Enhancers are Linked to Kidney Disease. Journal of the American Society of Nephrology: JASN, 2020, 31, 765-782.	6.1	13
39	DNA methylation, the charm of dynamics. Briefings in Functional Genomics, 2016, 15, 397-398.	2.7	12
40	Chromatin modifications and genomic contexts linked to dynamic DNA methylation patterns across human cell types. Scientific Reports, 2015, 5, 8410.	3.3	11
41	The MS-lincRNA landscape reveals a novel lincRNA BCLIN25 that contributes to tumorigenesis by upregulating ERBB2 expression via epigenetic modification and RNA–RNA interactions in breast cancer. Cell Death and Disease, 2019, 10, 920.	6.3	11
42	Detecting novel hypermethylated genes in Breast cancer benefiting from feature selection. Computers in Biology and Medicine, 2010, 40, 159-167.	7.0	10
43	DevMouse, the mouse developmental methylome database and analysis tools. Database: the Journal of Biological Databases and Curation, 2014, 2014, bat084-bat084.	3.0	10
44	Revealing epigenetic patterns in gene regulation through integrative analysis of epigenetic interaction network. Molecular Biology Reports, 2012, 39, 1701-1712.	2.3	9
45	Revealing the architecture of genetic and epigenetic regulation: a maximum likelihood model. Briefings in Bioinformatics, 2014, 15, 1028-1043.	6.5	9
46	Discovering Cooperative Relationships of Chromatin Modifications in Human T Cells Based on a Proposed Closeness Measure. PLoS ONE, 2010, 5, e14219.	2.5	8
47	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. Nature Communications, 2021, 12, 7173.	12.8	8
48	Detection of type 2 diabetes related modules and genes based on epigenetic networks. BMC Systems Biology, 2014, 8, S5.	3.0	7
49	IL1RN mediates the suppressive effect of methionine deprivation on glioma proliferation. Cancer Letters, 2019, 454, 146-157.	7.2	7
50	Z curve theory-based analysis of the dynamic nature of nucleosome positioning in Saccharomyces cerevisiae. Gene, 2013, 530, 8-18.	2.2	6
51	Rice protein regulates HDL metabolism-related gene expression and enzyme activity in adult rats. Food Bioscience, 2014, 8, 1-7.	4.4	6
52	CellMethy: Identification of a focal concordantly methylated pattern of CpGs revealed wide differences between normal and cancer tissues. Scientific Reports, 2015, 5, 18037.	3.3	5
53	Genome-wide identification of Polycomb target genes in human embryonic stem cells. Gene, 2013, 518, 425-430.	2.2	3
54	Computational identification of putative lincRNAs in mouse embryonic stem cell. Scientific Reports, 2016, 6, 34892.	3.3	3

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55	Survival differences of CIMP subtypes integrated with CNA information in human breast cancer. Oncotarget, 2017, 8, 48807-48819.	1.8	3
56	Long-Range Chromatin Interactions in the Kidney. Journal of the American Society of Nephrology: JASN, 2019, 30, 367-369.	6.1	2
57	Advances in Bioinformatics Tools for High-Throughput Sequencing Data of DNA Methylation. Hereditary Genetics: Current Research, 2012, 01, .	0.1	2
58	Heterogeneity in Breast cancer. Cancer Genetics and Epigenetics, 0, , .	0.0	1
59	Genomic and functional characterization of histone H3 lysine 4 methylation co-localized marks. Computational Molecular Biology, 0, , .	0.0	1
60	ChIP-seq Data Plays an Important Role in a Cytosine-Based DNA Methylation Prediction Model. , 2009, , .		0
61	Deducing Causal Relationships among Different Histone Modifications, DNA Methylation and Gene Expression. , 2009, , .		0
62	Identification of the differential DNA methylation markers among cancers. , 2013, , .		0
63	Long intergenic non-coding RNA detection benefited from integrative modeling of (Epi)genomic data. , 2013, , .		0
64	High-Throughput Computational Approaches to Analyzing Histone Modification Next-Generation Sequencing Data. Computational Molecular Biology, 0, , .	0.0	0
65	Identification of the <i>Bona fide</i> Differentially Methylated Gene Markers among Cancers. Computational Molecular Biology, 0, , .	0.0	0
66	Predicting Long Non-coding RNAs Based on Genomic Sequence Information. Computational Molecular Biology, 0, , .	0.0	0
67	Detection of candidate melanoma blood biomarkers by RNA-Sequencing. Cancer Genetics and Epigenetics, 0, , .	0.0	0
68	Genetics and epigenetics in human cancer. Cancer Genetics and Epigenetics, 0, , .	0.0	0
69	Long Non-coding RNAs: key players in brain and central nervous system development. Computational Molecular Biology, 0, , .	0.0	0
70	Signaling pathways in endometrial carcinoma. Cancer Genetics and Epigenetics, 0, , .	0.0	0
71	Epigenetic of Somatic Cells Reprogramming. Cancer Genetics and Epigenetics, 0, , .	0.0	0
72	QBioDiff: a web-based tool for quantification and interpretation of biological dif-ferences among multiple samples. Cancer Genetics and Epigenetics, 0, , .	0.0	0