

Hongbo Liu

List of Publications by Year in descending order

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Version: 2024-02-01

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	Epigenomic and transcriptomic analyses define core cell types, genes and targetable mechanisms for kidney disease. <i>Nature Genetics</i> , 2022, 54, 950-962.	21.4	71
2	Genome-wide meta-analysis and omics integration identifies novel genes associated with diabetic kidney disease. <i>Diabetologia</i> , 2022, 65, 1495-1509.	6.3	16
3	The Nuclear Receptor ESRRRA Protects from Kidney Disease by Coupling Metabolism and Differentiation. <i>Cell Metabolism</i> , 2021, 33, 379-394.e8.	16.2	93
4	Urinary Single-Cell Profiling Captures the Cellular Diversity of the Kidney. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 614-627.	6.1	64
5	Single cell regulatory landscape of the mouse kidney highlights cellular differentiation programs and disease targets. <i>Nature Communications</i> , 2021, 12, 2277.	12.8	122
6	Transcriptome-wide association analysis identifies DACH1 as a kidney disease risk gene that contributes to fibrosis. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	49
7	A single genetic locus controls both expression of DPEP1/CHMP1A and kidney disease development via ferroptosis. <i>Nature Communications</i> , 2021, 12, 5078.	12.8	45
8	Renal Histologic Analysis Provides Complementary Information to Kidney Function Measurement for Patients with Early Diabetic or Hypertensive Disease. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 2863-2876.	6.1	18
9	Mapping the genetic architecture of human traits to cell types in the kidney identifies mechanisms of disease and potential treatments. <i>Nature Genetics</i> , 2021, 53, 1322-1333.	21.4	87
10	Genome-wide association studies identify the role of caspase-9 in kidney disease. <i>Science Advances</i> , 2021, 7, eabi8051.	10.3	14
11	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. <i>Nature Communications</i> , 2021, 12, 7173.	12.8	8
12	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021, 12, 7174.	12.8	30
13	Dnmt3a and Dnmt3b-Decommissioned Fetal Enhancers are Linked to Kidney Disease. <i>Journal of the American Society of Nephrology: JASN</i> , 2020, 31, 765-782.	6.1	13
14	Systematic integrated analysis of genetic and epigenetic variation in diabetic kidney disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 29013-29024.	7.1	46
15	IL1RN mediates the suppressive effect of methionine deprivation on glioma proliferation. <i>Cancer Letters</i> , 2019, 454, 146-157.	7.2	7
16	Long-Range Chromatin Interactions in the Kidney. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 367-369.	6.1	2
17	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. <i>Cell Death and Disease</i> , 2019, 10, 920.	6.3	11
18	Specific breast cancer prognosis subtype distinctions based on DNA methylation patterns. <i>Molecular Oncology</i> , 2018, 12, 1047-1060.	4.6	68

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19	Cell subpopulation deconvolution reveals breast cancer heterogeneity based on DNA methylation signature. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw028.	6.5	18
20	DiseaseMeth version 2.0: a major expansion and update of the human disease methylation database. <i>Nucleic Acids Research</i> , 2017, 45, D888-D895.	14.5	126
21	Survival differences of CIMP subtypes integrated with CNA information in human breast cancer. <i>Oncotarget</i> , 2017, 8, 48807-48819.	1.8	3
22	Identification and functional analysis of long intergenic noncoding RNA genes in porcine pre-implantation embryonic development. <i>Scientific Reports</i> , 2016, 6, 38333.	3.3	24
23	DNA methylation, the charm of dynamics. <i>Briefings in Functional Genomics</i> , 2016, 15, 397-398.	2.7	12
24	DNA methylation dynamics: identification and functional annotation. <i>Briefings in Functional Genomics</i> , 2016, 15, elw029.	2.7	13
25	Computational identification of putative lincRNAs in mouse embryonic stem cell. <i>Scientific Reports</i> , 2016, 6, 34892.	3.3	3
26	The identification of age-associated cancer markers by an integrative analysis of dynamic DNA methylation changes. <i>Scientific Reports</i> , 2016, 6, 22722.	3.3	31
27	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. <i>Nucleic Acids Research</i> , 2016, 44, 75-94.	14.5	83
28	Folic Acid Alters Methylation Profile of JAK-STAT and Long-Term Depression Signaling Pathways in Alzheimer's Disease Models. <i>Molecular Neurobiology</i> , 2016, 53, 6548-6556.	4.0	27
29	SEA: a super-enhancer archive. <i>Nucleic Acids Research</i> , 2016, 44, D172-D179.	14.5	88
30	CellMethy: Identification of a focal concordantly methylated pattern of CpGs revealed wide differences between normal and cancer tissues. <i>Scientific Reports</i> , 2015, 5, 18037.	3.3	5
31	Identification of 4438 novel lincRNAs involved in mouse pre-implantation embryonic development. <i>Molecular Genetics and Genomics</i> , 2015, 290, 685-697.	2.1	24
32	Chromatin modifications and genomic contexts linked to dynamic DNA methylation patterns across human cell types. <i>Scientific Reports</i> , 2015, 5, 8410.	3.3	11
33	The Identification of Specific Methylation Patterns across Different Cancers. <i>PLoS ONE</i> , 2015, 10, e0120361.	2.5	48
34	DNA Methylation Patterns Can Estimate Nonequivalent Outcomes of Breast Cancer with the Same Receptor Subtypes. <i>PLoS ONE</i> , 2015, 10, e0142279.	2.5	17
35	Revealing the architecture of genetic and epigenetic regulation: a maximum likelihood model. <i>Briefings in Bioinformatics</i> , 2014, 15, 1028-1043.	6.5	9
36	DevMouse, the mouse developmental methylome database and analysis tools. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bat084-bat084.	3.0	10

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37	MetalPrint: an information repository of mammalian imprinted genes. <i>Development (Cambridge)</i> , 2014, 141, 2516-2523.	2.5	68
38	Rice protein regulates HDL metabolism-related gene expression and enzyme activity in adult rats. <i>Food Bioscience</i> , 2014, 8, 1-7.	4.4	6
39	Identification and characterization of long intergenic non-coding RNAs related to mouse liver development. <i>Molecular Genetics and Genomics</i> , 2014, 289, 1225-1235.	2.1	28
40	Detection of type 2 diabetes related modules and genes based on epigenetic networks. <i>BMC Systems Biology</i> , 2014, 8, S5.	3.0	7
41	Identification of the differential DNA methylation markers among cancers. , 2013, , .		0
42	Genome-wide identification of Polycomb target genes in human embryonic stem cells. <i>Gene</i> , 2013, 518, 425-430.	2.2	3
43	Z curve theory-based analysis of the dynamic nature of nucleosome positioning in <i>Saccharomyces cerevisiae</i> . <i>Gene</i> , 2013, 530, 8-18.	2.2	6
44	Quantitative epigenetic co-variation in CpG islands and co-regulation of developmental genes. <i>Scientific Reports</i> , 2013, 3, 2576.	3.3	20
45	Long non-coding RNA identification over mouse brain development by integrative modeling of chromatin and genomic features. <i>Nucleic Acids Research</i> , 2013, 41, 10044-10061.	14.5	65
46	CpG_MPs: identification of CpG methylation patterns of genomic regions from high-throughput bisulfite sequencing data. <i>Nucleic Acids Research</i> , 2013, 41, e4-e4.	14.5	48
47	Long intergenic non-coding RNA detection benefited from integrative modeling of (Epi)genomic data. , 2013, , .		0
48	Identification and Characterization of Long Non-Coding RNAs Related to Mouse Embryonic Brain Development from Available Transcriptomic Data. <i>PLoS ONE</i> , 2013, 8, e71152.	2.5	55
49	DiseaseMeth: a human disease methylation database. <i>Nucleic Acids Research</i> , 2012, 40, D1030-D1035.	14.5	81
50	Genome-wide dynamic changes of DNA methylation of repetitive elements in human embryonic stem cells and fetal fibroblasts. <i>Genomics</i> , 2012, 99, 10-17.	2.9	45
51	Revealing epigenetic patterns in gene regulation through integrative analysis of epigenetic interaction network. <i>Molecular Biology Reports</i> , 2012, 39, 1701-1712.	2.3	9
52	Advances in Bioinformatics Tools for High-Throughput Sequencing Data of DNA Methylation. <i>Hereditary Genetics: Current Research</i> , 2012, 01, .	0.1	2
53	QDMR: a quantitative method for identification of differentially methylated regions by entropy. <i>Nucleic Acids Research</i> , 2011, 39, e58-e58.	14.5	105
54	Prioritizing cancer-related genes with aberrant methylation based on a weighted protein-protein interaction network. <i>BMC Systems Biology</i> , 2011, 5, 158.	3.0	20

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55	Rice Protein Extracted by Different Methods Affects Cholesterol Metabolism in Rats Due to Its Lower Digestibility. <i>International Journal of Molecular Sciences</i> , 2011, 12, 7594-7608.	4.1	26
56	Detecting novel hypermethylated genes in Breast cancer benefiting from feature selection. <i>Computers in Biology and Medicine</i> , 2010, 40, 159-167.	7.0	10
57	CpG_MI: a novel approach for identifying functional CpG islands in mammalian genomes. <i>Nucleic Acids Research</i> , 2010, 38, e6-e6.	14.5	40
58	HHMD: the human histone modification database. <i>Nucleic Acids Research</i> , 2010, 38, D149-D154.	14.5	79
59	Discovering Cooperative Relationships of Chromatin Modifications in Human T Cells Based on a Proposed Closeness Measure. <i>PLoS ONE</i> , 2010, 5, e14219.	2.5	8
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	Heterogeneity in Breast cancer. <i>Cancer Genetics and Epigenetics</i> , 0, , .	0.0	1
63	High-Throughput Computational Approaches to Analyzing Histone Modification Next-Generation Sequencing Data. <i>Computational Molecular Biology</i> , 0, , .	0.0	0
64	Identification of the <i>Bona fide</i> Differentially Methylated Gene Markers among Cancers. <i>Computational Molecular Biology</i> , 0, , .	0.0	0
65	Predicting Long Non-coding RNAs Based on Genomic Sequence Information. <i>Computational Molecular Biology</i> , 0, , .	0.0	0
66	Detection of candidate melanoma blood biomarkers by RNA-Sequencing. <i>Cancer Genetics and Epigenetics</i> , 0, , .	0.0	0
67	Genetics and epigenetics in human cancer. <i>Cancer Genetics and Epigenetics</i> , 0, , .	0.0	0
68	Long Non-coding RNAs: key players in brain and central nervous system development. <i>Computational Molecular Biology</i> , 0, , .	0.0	0
69	Genomic and functional characterization of histone H3 lysine 4 methylation co-localized marks. <i>Computational Molecular Biology</i> , 0, , .	0.0	1
70	Signaling pathways in endometrial carcinoma. <i>Cancer Genetics and Epigenetics</i> , 0, , .	0.0	0
71	Epigenetic of Somatic Cells Reprogramming. <i>Cancer Genetics and Epigenetics</i> , 0, , .	0.0	0
72	QBioDiff: a web-based tool for quantification and interpretation of biological differences among multiple samples. <i>Cancer Genetics and Epigenetics</i> , 0, , .	0.0	0