Mingyao Li

List of Publications by Year
in descending order

97 papers	9,345 citations	71102 41 h-index	48315 88 g-index
98 all docs	98 docs citations	98 times ranked	16612 citing authors

#	Article	IF	Citations
1	A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. Nature Genetics, 2016, 48, 134-143.	21.4	1,167
2	Single-cell transcriptomics of the mouse kidney reveals potential cellular targets of kidney disease. Science, 2018, 360, 758-763.	12.6	797
3	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	27.8	581
4	SAVER: gene expression recovery for single-cell RNA sequencing. Nature Methods, 2018, 15, 539-542.	19.0	574
5	Bulk tissue cell type deconvolution with multi-subject single-cell expression reference. Nature Communications, 2019, 10, 380.	12.8	526
6	Widespread RNA and DNA Sequence Differences in the Human Transcriptome. Science, 2011, 333, 53-58.	12.6	414
7	Common variation in KITLG and at 5q31.3 predisposes to testicular germ cell cancer. Nature Genetics, 2009, 41, 811-815.	21.4	319
8	SpaGCN: Integrating gene expression, spatial location and histology to identify spatial domains and spatially variable genes by graph convolutional network. Nature Methods, 2021, 18, 1342-1351.	19.0	291
9	Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. American Journal of Human Genetics, 2014, 94, 223-232.	6.2	287
10	RNA-Seq identifies novel myocardial gene expression signatures of heart failure. Genomics, 2015, 105, 83-89.	2.9	220
11	Single cell transcriptomics identifies a unique adipose lineage cell population that regulates bone marrow environment. ELife, 2020, 9, .	6.0	191
12	Deep learning enables accurate clustering with batch effect removal in single-cell RNA-seq analysis. Nature Communications, 2020, 11, 2338.	12.8	180
13	Single-cell dissection of intratumoral heterogeneity and lineage diversity in metastatic gastric adenocarcinoma. Nature Medicine, 2021, 27, 141-151.	30.7	134
14	Adeno-Associated Virus-Induced Dorsal Root Ganglion Pathology. Human Gene Therapy, 2020, 31, 808-818.	2.7	129
15	A second independent locus within DMRT1 is associated with testicular germ cell tumor susceptibility. Human Molecular Genetics, 2011, 20, 3109-3117.	2.9	124
16	Single cell regulatory landscape of the mouse kidney highlights cellular differentiation programs and disease targets. Nature Communications, 2021, 12, 2277.	12.8	122
17	Functional Analysis and Transcriptomic Profiling of iPSC-Derived Macrophages and Their Application in Modeling Mendelian Disease. Circulation Research, 2015, 117, 17-28.	4.5	120
18	Î²-Hydroxybutyrate suppresses colorectal cancer. Nature, 2022, 605, 160-165.	27.8	120

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19	APOE and TREM2 regulate amyloid-responsive microglia in Alzheimerâ€™s disease. Acta Neuropathologica, 2020, 140, 477-493.	7.7	117
20	Secretory Phospholipase A2-IIA and Cardiovascular Disease. Journal of the American College of Cardiology, 2013, 62, 1966-1976.	2.8	115
21	Genetics of age-related macular degeneration (AMD). Human Molecular Genetics, 2017, 26, R45-R50.	2.9	109
22	Efficient Study Designs for Test of Genetic Association Using Sibship Data and Unrelated Cases and Controls. American Journal of Human Genetics, 2006, 78, 778-792.	6.2	107
23	Evaluation of coverage variation of SNP chips for genome-wide association studies. European Journal of Human Genetics, 2008, 16, 635-643.	2.8	106
24	Response to Comments on â€œWidespread RNA and DNA Sequence Differences in the Human Transcriptomeâ€. Science, 2012, 335, 1302-1302.	12.6	98
25	MicroRNA-mediated inhibition of transgene expression reduces dorsal root ganglion toxicity by AAV vectors in primates. Science Translational Medicine, 2020, 12, .	12.4	96
26	Meganuclease targeting of PCSK9 in macaque liver leads to stable reduction in serum cholesterol. Nature Biotechnology, 2018, 36, 717-725.	17.5	95
27	Gene expression distribution deconvolution in single-cell RNA sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6437-E6446.	7.1	93
28	The Nuclear Receptor ESRRA Protects from Kidney Disease by Coupling Metabolism and Differentiation. Cell Metabolism, 2021, 33, 379-394.e8.	16.2	93
29	Single-Cell RNA Sequencing to Dissect the Immunological Network of Autoimmune Myocarditis. Circulation, 2020, 142, 384-400.	1.6	90
30	SCALE: modeling allele-specific gene expression by single-cell RNA sequencing. Genome Biology, 2017, 18, 74.	8.8	89
31	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
32	Iterative transfer learning with neural network for clustering and cell type classification in single-cell RNA-seq analysis. Nature Machine Intelligence, 2020, 2, 607-618.	16.0	83
33	Cell-Type-Specific Complement Expression in the Healthy and Diseased Retina. Cell Reports, 2019, 29, 2835-2848.e4.	6.4	81
34	Accounting for technical noise in differential expression analysis of single-cell RNA sequencing data. Nucleic Acids Research, 2017, 45, 10978-10988.	14.5	73
35	Transcriptome of the human retina, retinal pigmented epithelium and choroid. Genomics, 2015, 105, 253-264.	2.9	71
36	The long noncoding RNA landscape in hypoxic and inflammatory renal epithelial injury. American Journal of Physiology - Renal Physiology, 2015, 309, F901-F913.	2.7	70

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37	Group Lasso Regularized Deep Learning for Cancer Prognosis from Multi-Omics and Clinical Features. Genes, 2019, 10, 240.	2.4	59
38	CRISPR/Cas9-mediated in vivo gene targeting corrects hemostasis in newborn and adult factor IXâ€“knockout mice. Blood, 2019, 133, 2745-2752.	1.4	57
39	Assessing departure from Hardyâ€Weinberg equilibrium in the presence of disease association. Genetic Epidemiology, 2008, 32, 589-599.	1.3	53
40	Statistical and machine learning methods for spatially resolved transcriptomics with histology. Computational and Structural Biotechnology Journal, 2021, 19, 3829-3841.	4.1	52
41	LIQA: long-read isoform quantification and analysis. Genome Biology, 2021, 22, 182.	8.8	49
42	Rare copy number variants in over 100,000 European ancestry subjects reveal multiple disease associations. Nature Communications, 2020, 11, 255.	12.8	48
43	ATOM: a powerful gene-based association test by combining optimally weighted markers. Bioinformatics, 2009, 25, 497-503.	4.1	45
44	Childhood retinol-binding protein 4 (RBP4) levels predicting the 10-year risk of insulin resistance and metabolic syndrome: the BCAMS study. Cardiovascular Diabetology, 2018, 17, 69.	6.8	44
45	A mutation-independent CRISPR-Cas9â€“mediated gene targeting approach to treat a murine model of ornithine transcarbamylase deficiency. Science Advances, 2020, 6, eaax5701.	10.3	44
46	Interrogation of nonconserved human adipose lincRNAs identifies a regulatory role of linc-ADAL in adipocyte metabolism. Science Translational Medicine, 2018, 10, .	12.4	42
47	ASEP: Gene-based detection of allele-specific expression across individuals in a population by RNA sequencing. PLoS Genetics, 2020, 16, e1008786.	3.5	42
48	Long-term stable reduction of low-density lipoprotein in nonhuman primates following inÂvivo genome editing of PCSK9. Molecular Therapy, 2021, 29, 2019-2029.	8.2	42
49	Assessment of Probable Opioid Use Disorder Using Electronic Health Record Documentation. JAMA Network Open, 2020, 3, e2015909.	5.9	41
50	Runs of Homozygosity: Association with Coronary Artery Disease and Gene Expression in Monocytes and Macrophages. American Journal of Human Genetics, 2015, 97, 228-237.	6.2	37
51	Deep RNA Sequencing Uncovers a Repertoire of Human Macrophage Long Intergenic Noncoding RNAs Modulated by Macrophage Activation and Associated With Cardiometabolic Diseases. Journal of the American Heart Association, 2017, 6, .	3.7	36
52	A joint deep learning model enables simultaneous batch effect correction, denoising, and clustering in single-cell transcriptomics. Genome Research, 2021, 31, 1753-1766.	5.5	36
53	Thymic stromal lymphopoietin induces adipose loss through sebum hypersecretion. Science, 2021, 373, .	12.6	36
54	Transcriptome-Wide Analysis Reveals Modulation of Human Macrophage Inflammatory Phenotype Through Alternative Splicing. Arteriosclerosis, Thrombosis, and Vascular Biology, 2016, 36, 1434-1447.	2.4	35

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55	Correcting population stratification in genetic association studies using a phylogenetic approach. Bioinformatics, 2010, 26, 798-806.	4.1	32
56	Adipose tissue RNASeq reveals novel geneâ€“nutrient interactions following n-3 PUFA supplementation and evoked inflammation in humans. Journal of Nutritional Biochemistry, 2016, 30, 126-132.	4.2	30
57	Genome-wide interrogation reveals hundreds of long intergenic noncoding RNAs that associate with cardiometabolic traits. Human Molecular Genetics, 2016, 25, ddw154.	2.9	30
58	Childhood sleep duration modifies the polygenic risk for obesity in youth through leptin pathway: the Beijing Child and Adolescent Metabolic Syndrome cohort study. International Journal of Obesity, 2019, 43, 1556-1567.	3.4	29
59	Vitamin D modifies the associations between circulating betatrophin and cardiometabolic risk factors among youths at risk for metabolic syndrome. Cardiovascular Diabetology, 2016, 15, 142.	6.8	28
60	Quantitative Trait Linkage Analysis Using Gaussian Copulas. Genetics, 2006, 173, 2317-2327.	2.9	27
61	Identification of 22 susceptibility loci associated with testicular germ cell tumors. Nature Communications, 2021, 12, 4487.	12.8	27
62	Sleep Duration and Cardiometabolic Risk Among Chinese School-aged Children: Do Adipokines Play a Mediating Role?. Sleep, 2017, 40, .	1.1	26
63	Expression of Calgranulin Genes S100A8, S100A9 and S100A12 Is Modulated by n-3 PUFA during Inflammation in Adipose Tissue and Mononuclear Cells. PLoS ONE, 2017, 12, e0169614.	2.5	24
64	LinkedSV for detection of mosaic structural variants from linked-read exome and genome sequencing data. Nature Communications, 2019, 10, 5585.	12.8	24
65	Pathologic gene network rewiring implicates PPP1R3A as a central regulator in pressure overload heart failure. Nature Communications, 2019, 10, 2760.	12.8	22
66	Detecting differential alternative splicing events in scRNA-seq with or without Unique Molecular Identifiers. PLoS Computational Biology, 2020, 16, e1007925.	3.2	20
67	Implication of specific retinal cell-type involvement and gene expression changes in AMD progression using integrative analysis of single-cell and bulk RNA-seq profiling. Scientific Reports, 2021, 11, 15612.	3.3	20
68	DISSCO: direct imputation of summary statistics allowing covariates. Bioinformatics, 2015, 31, 2434-2442.	4.1	18
69	Intrathecal Viral Vector Delivery of Trastuzumab Prevents or Inhibits Tumor Growth of Human HER2-Positive Xenografts in Mice. Cancer Research, 2018, 78, 6171-6182.	0.9	15
70	PennDiff: detecting differential alternative splicing and transcription by RNA sequencing. Bioinformatics, 2018, 34, 2384-2391.	4.1	14
71	Detecting cell-type-specific allelic expression imbalance by integrative analysis of bulk and single-cell RNA sequencing data. PLoS Genetics, 2021, 17, e1009080.	3.5	14
72	Copula Regression Analysis of Simultaneously Recorded Frontal Eye Field and Inferotemporal Spiking Activity during Object-Based Working Memory. Journal of Neuroscience, 2015, 35, 8745-8757.	3.6	13

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73	Sequence and Expression of Complement Factor H Gene Cluster Variants and Their Roles in Age-Related Macular Degeneration Risk. , 2016, 57, 2763.		13
74	Applications of single-cell genomics and computational strategies to study common disease and population-level variation. Genome Research, 2021, 31, 1728-1741.	5.5	11
75	The role of established East Asian obesity-related loci on pediatric leptin levels highlights a neuronal influence on body weight regulation in Chinese children and adolescents: the BCAMS study. Oncotarget, 2017, 8, 93593-93607.	1.8	11
76	RNA expression in human retina. Human Molecular Genetics, 2017, 26, R68-R74.	2.9	10
77	MetaDiff: differential isoform expression analysis using random-effects meta-regression. BMC Bioinformatics, 2015, 16, 208.	2.6	9
78	Joint analysis of spikes and local field potentials using copula. NeuroImage, 2016, 133, 457-467.	4.2	9
79	De novo RNA sequence assembly during in vivo inflammatory stress reveals hundreds of unannotated lincRNAs in human blood CD14+ monocytes and in adipose tissue. Physiological Genomics, 2017, 49, 287-305.	2.3	9
80	Role of adipokines FGF21, leptin and adiponectin in self-concept of youths with obesity. European Neuropsychopharmacology, 2018, 28, 892-902.	0.7	9
81	Classes of ITD Predict Outcomes in AML Patients Treated with FLT3 Inhibitors. Clinical Cancer Research, 2019, 25, 573-583.	7.0	8
82	Mapping Splicing Quantitative Trait Loci in RNA-Seq. Cancer Informatics, 2015, 14s1, CIN.S24832.	1.9	7
83	Loss of Cardio-Protective Effects at the CDH13 Locus Due to Gene-Sleep Interaction: The BCAMS Study. EBioMedicine, 2018, 32, 164-171.	6.1	7
84	Mapping Splicing Quantitative Trait Loci in RNA-Seq. Cancer Informatics, 2014, 13s4, CIN.S13971.	1.9	6
85	Accurate and Rapid Sequence Analysis of Adeno-Associated Virus Plasmids by Illumina Next-Generation Sequencing. Human Gene Therapy Methods, 2018, 29, 201-211.	2.1	6
86	First Giant Steps Toward a Cell Atlas of Atherosclerosis. Circulation Research, 2018, 122, 1632-1634.	4.5	6
87	Adeno-associated virus-mediated expression of human butyrylcholinesterase to treat organophosphate poisoning. PLoS ONE, 2019, 14, e0225188.	2.5	5
88	Tissue-Specific Differential Expression of Novel Genes and Long Intergenic Noncoding RNAs in Humans With Extreme Response to Evoked Endotoxemia. Circulation Genomic and Precision Medicine, 2018, 11, e001907.	3.6	4
89	MultiGeMS: detection of SNVs from multiple samples using model selection on high-throughput sequencing data. Bioinformatics, 2016, 32, 1486-1492.	4.1	3
90	Cognitive Abilities of Dogs with Mucopolysaccharidosis I: Learning and Memory. Animals, 2020, 10, 397.	2.3	3

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91	Rejoinder to â€œJoint Regression Analysis for Discrete Longitudinal Dataâ€•by Madsen and Fang. Biometrics, 2011, 67, 1175-1176.	1.4	1
92	Data on copula modeling of mixed discrete and continuous neural time series. Data in Brief, 2016, 7, 1364-1369.	1.0	1
93	Longitudinal Large-Scale Semiquantitative Proteomic Data Stability Across Multiple Instrument Platforms. Journal of Proteome Research, 2021, 20, 5203-5211.	3.7	1
94	93137 Interrogating cardio-protective MTSS1 variants in human populations. Journal of Clinical and Translational Science, 2021, 5, 124-125.	0.6	0
95	Discussion of â€œExponential-Family Embedding With Application to Cell Developmental Trajectories for Single-Cell RNA-Seq Dataâ€• Journal of the American Statistical Association, 2021, 116, 475-477.	3.1	0
96	Glycogenome signatures in complex cardiometabolic disease (789.4). FASEB Journal, 2014, 28, 789.4.	0.5	0
97	Single-cell transcriptomics of the kidney reveals unexpected cellular targets of kidney diseases. Proceedings for Annual Meeting of the Japanese Pharmacological Society, 2018, WCP2018, SY10-2.	0.0	0