Lu Wen

List of Publications by Year
in descending order

59 papers	8,731 citations	101496 36 h-index	118793 62 g-index
63 all docs	63 docs citations	63 times ranked	12304 citing authors

#	Article	IF	Citations
1	Integrating single-cell datasets with ambiguous batch information by incorporating molecular network features. Briefings in Bioinformatics, 2022, 23, .	3.2	5
2	Genome-Scale Methylation Analysis of Circulating Cell-Free DNA in Gastric Cancer Patients. Clinical Chemistry, 2022, 68, 354-364.	1.5	18
3	Heterogeneity in endothelial cells and widespread venous arterialization during early vascular development in mammals. Cell Research, 2022, 32, 333-348.	5.7	30
4	Recent advances in single-cell sequencing technologies. Precision Clinical Medicine, 2022, 5, .	1.3	44
5	Heart-specific DNA methylation analysis in plasma for the investigation of myocardial damage. Journal of Translational Medicine, 2022, 20, 36.	1.8	7
6	Integrated single-cell multiomics analysis reveals novel candidate markers for prognosis in human pancreatic ductal adenocarcinoma. Cell Discovery, 2022, 8, 13.	3.1	23
7	Systematic evaluation of colorectal cancer organoid system by single-cell RNA-Seq analysis. Genome Biology, 2022, 23, 106.	3.8	29
8	Dissecting Human Gonadal Cell Lineage Specification and Sex Determination Using A Single-cell RNA-seq Approach. Genomics, Proteomics and Bioinformatics, 2022, 20, 223-245.	3.0	9
9	De novoassembly of human genome at single-cell levels. Nucleic Acids Research, 2022, 50, 7479-7492.	6.5	13
10	Dissecting the epigenomic dynamics of human fetal germ cell development at single-cell resolution. Cell Research, 2021, 31, 463-477.	5.7	28
11	Heterogeneity of glial progenitor cells during the neurogenesis-to-gliogenesis switch in the developing human cerebral cortex. Cell Reports, 2021, 34, 108788.	2.9	55
12	Single-cell transcriptome and genome analyses of pituitary neuroendocrine tumors. Neuro-Oncology, 2021, 23, 1859-1871.	0.6	29
13	Integrated transcriptomics and epigenomics reveal chamber-specific and species-specific characteristics of human and mouse hearts. PLoS Biology, 2021, 19, e3001229.	2.6	5
14	SMOOTH-seq: single-cell genome sequencing of human cells on a third-generation sequencing platform. Genome Biology, 2021, 22, 195.	3.8	43
15	DNA methylome reveals cellular origin of cell-free DNA in spent medium of human preimplantation embryos. Journal of Clinical Investigation, 2021, 131, .	3.9	25
16	Recent advances in mammalian reproductive biology. Science China Life Sciences, 2020, 63, 18-58.	2.3	23
17	Genomic and transcriptomic profiling of carcinogenesis in patients with familial adenomatous polyposis. Gut, 2020, 69, 1283-1293.	6.1	36
18	Single-cell transcriptomics identifies divergent developmental lineage trajectories during human pituitary development. Nature Communications, 2020, 11, 5275.	5.8	79

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19	5-Formylcytosine landscapes of human preimplantation embryos at single-cell resolution. PLoS Biology, 2020, 18, e3000799.	2.6	8
20	Single-Cell Multiomics Sequencing Reveals Prevalent Genomic Alterations in Tumor Stromal Cells of Human Colorectal Cancer. Cancer Cell, 2020, 38, 818-828.e5.	7.7	146
21	Single-cell transcriptome analysis reveals cell lineage specification in temporal-spatial patterns in human cortical development. Science Advances, 2020, 6, eaaz2978.	4.7	88
22	Embryonic endothelial evolution towards first hematopoietic stem cells revealed by single-cell transcriptomic and functional analyses. Cell Research, 2020, 30, 376-392.	5.7	89
23	Single-cell RNA-seq analysis of mouse preimplantation embryos by third-generation sequencing. PLoS Biology, 2020, 18, e3001017.	2.6	46
24	Reconstituting the transcriptome and DNA methylome landscapes of human implantation. Nature, 2019, 572, 660-664.	13.7	207
25	Comprehensive DNA methylation analysis of tissue of origin of plasma cell-free DNA by methylated CpG tandem amplification and sequencing (MCTA-Seq). Clinical Epigenetics, 2019, 11, 93.	1.8	47
26	Dissecting the transcriptome landscape of the human fetal neural retina and retinal pigment epithelium by single-cell RNA-seq analysis. PLoS Biology, 2019, 17, e3000365.	2.6	108
27	Human Germline Cell Development: from the Perspective of Single-Cell Sequencing. Molecular Cell, 2019, 76, 320-328.	4.5	48
28	Detection of Colorectal Cancer in Circulating Cell-Free DNA by Methylated CpG Tandem Amplification and Sequencing. Clinical Chemistry, 2019, 65, 916-926.	1.5	25
29	Single-Cell Transcriptome Analysis Maps the Developmental Track of the Human Heart. Cell Reports, 2019, 26, 1934-1950.e5.	2.9	355
30	Single-cell RNA-seq analysis unveils a prevalent epithelial/mesenchymal hybrid state during mouse organogenesis. Genome Biology, 2018, 19, 31.	3.8	153
31	Single-cell DNA methylome sequencing of human preimplantation embryos. Nature Genetics, 2018, 50, 12-19.	9.4	248
32	Single cell epigenome sequencing technologies. Molecular Aspects of Medicine, 2018, 59, 62-69.	2.7	30
33	Single-cell multiomics sequencing and analyses of human colorectal cancer. Science, 2018, 362, 1060-1063.	6.0	256
34	Dissecting the Global Dynamic Molecular Profiles of Human Fetal Kidney Development by Single-Cell RNA Sequencing. Cell Reports, 2018, 24, 3554-3567.e3.	2.9	91
35	Tracing the temporal-spatial transcriptome landscapes of the human fetal digestive tract using single-cell RNA-sequencing. Nature Cell Biology, 2018, 20, 721-734.	4.6	125
36	Boosting the power of single-cell analysis. Nature Biotechnology, 2018, 36, 408-409.	9.4	43

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37	Single-cell multi-omics sequencing of human early embryos. Nature Cell Biology, 2018, 20, 847-858.	4.6	142
38	MR-seq: measuring a single cellâ€™s transcriptome repeatedly by RNA-seq. Science Bulletin, 2017, 62, 391-398.	4.3	8
39	Single-Cell RNA-Seq Analysis Maps Development of Human Germline Cells and Gonadal Niche Interactions. Cell Stem Cell, 2017, 20, 858-873.e4.	5.2	376
40	Single-cell multi-omics sequencing of mouse early embryos and embryonic stem cells. Cell Research, 2017, 27, 967-988.	5.7	281
41	DNA methylation and chromatin accessibility profiling of mouse and human fetal germ cells. Cell Research, 2017, 27, 165-183.	5.7	102
42	Tracing haematopoietic stem cell formation at single-cell resolution. Nature, 2016, 533, 487-492.	13.7	297
43	Single-cell sequencing in stem cell biology. Genome Biology, 2016, 17, 71.	3.8	144
44	Tracing the expression of circular RNAs in human pre-implantation embryos. Genome Biology, 2016, 17, 130.	3.8	140
45	Single-cell triple omics sequencing reveals genetic, epigenetic, and transcriptomic heterogeneity in hepatocellular carcinomas. Cell Research, 2016, 26, 304-319.	5.7	492
46	Epigenomic Landscape of Human Fetal Brain, Heart, and Liver. Journal of Biological Chemistry, 2016, 291, 4386-4398.	1.6	45
47	The Transcriptome and DNA Methylome Landscapes of Human Primordial Germ Cells. Cell, 2015, 161, 1437-1452.	13.5	500
48	Charting a Map through the Cellular Reprogramming Landscape. Cell Stem Cell, 2015, 16, 215-216.	5.2	3
49	Profiling DNA methylome landscapes of mammalian cells with single-cell reduced-representation bisulfite sequencing. Nature Protocols, 2015, 10, 645-659.	5.5	152
50	Genome-scale detection of hypermethylated CpG islands in circulating cell-free DNA of hepatocellular carcinoma patients. Cell Research, 2015, 25, 1250-1264.	5.7	110
51	How to catch rare cell types. Nature, 2015, 525, 197-198.	13.7	9
52	Tcf7l2 Is Required for Left-Right Asymmetric Differentiation of Habenular Neurons. Current Biology, 2014, 24, 2217-2227.	1.8	52
53	Reconstructing Complex Tissues from Single-Cell Analyses. Cell, 2014, 157, 771-773.	13.5	16
54	Genomic distribution and possible functions of DNA hydroxymethylation in the brain. Genomics, 2014, 104, 341-346.	1.3	84

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55	The DNA methylation landscape of human early embryos. Nature, 2014, 511, 606-610.	13.7	787
56	Active and Passive Demethylation of Male and Female Pronuclear DNA in the Mammalian Zygote. Cell Stem Cell, 2014, 15, 447-459.	5.2	311
57	Single-cell RNA-Seq profiling of human preimplantation embryos and embryonic stem cells. Nature Structural and Molecular Biology, 2013, 20, 1131-1139.	3.6	1,416
58	Single-cell methylome landscapes of mouse embryonic stem cells and early embryos analyzed using reduced representation bisulfite sequencing. Genome Research, 2013, 23, 2126-2135.	2.4	439
59	Visualization of monoaminergic neurons and neurotoxicity of MPTP in live transgenic zebrafish. Developmental Biology, 2008, 314, 84-92.	0.9	160