

# Lu Wen

## List of Publications by Year in descending order

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59  
papers

8,731  
citations

101543

36  
h-index

118850

62  
g-index

63  
all docs

63  
docs citations

63  
times ranked

12304  
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell RNA-Seq profiling of human preimplantation embryos and embryonic stem cells. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1131-1139.	8.2	1,416
2	The DNA methylation landscape of human early embryos. <i>Nature</i> , 2014, 511, 606-610.	27.8	787
3	The Transcriptome and DNA Methylome Landscapes of Human Primordial Germ Cells. <i>Cell</i> , 2015, 161, 1437-1452.	28.9	500
4	Single-cell triple omics sequencing reveals genetic, epigenetic, and transcriptomic heterogeneity in hepatocellular carcinomas. <i>Cell Research</i> , 2016, 26, 304-319.	12.0	492
5	Single-cell methylome landscapes of mouse embryonic stem cells and early embryos analyzed using reduced representation bisulfite sequencing. <i>Genome Research</i> , 2013, 23, 2126-2135.	5.5	439
6	Single-Cell RNA-Seq Analysis Maps Development of Human Germline Cells and Gonadal Niche Interactions. <i>Cell Stem Cell</i> , 2017, 20, 858-873.e4.	11.1	376
7	Single-Cell Transcriptome Analysis Maps the Developmental Track of the Human Heart. <i>Cell Reports</i> , 2019, 26, 1934-1950.e5.	6.4	355
8	Active and Passive Demethylation of Male and Female Pronuclear DNA in the Mammalian Zygote. <i>Cell Stem Cell</i> , 2014, 15, 447-459.	11.1	311
9	Tracing haematopoietic stem cell formation at single-cell resolution. <i>Nature</i> , 2016, 533, 487-492.	27.8	297
10	Single-cell multi-omics sequencing of mouse early embryos and embryonic stem cells. <i>Cell Research</i> , 2017, 27, 967-988.	12.0	281
11	Single-cell multiomics sequencing and analyses of human colorectal cancer. <i>Science</i> , 2018, 362, 1060-1063.	12.6	256
12	Single-cell DNA methylome sequencing of human preimplantation embryos. <i>Nature Genetics</i> , 2018, 50, 12-19.	21.4	248
13	Reconstituting the transcriptome and DNA methylome landscapes of human implantation. <i>Nature</i> , 2019, 572, 660-664.	27.8	207
14	Visualization of monoaminergic neurons and neurotoxicity of MPTP in live transgenic zebrafish. <i>Developmental Biology</i> , 2008, 314, 84-92.	2.0	160
15	Single-cell RNA-seq analysis unveils a prevalent epithelial/mesenchymal hybrid state during mouse organogenesis. <i>Genome Biology</i> , 2018, 19, 31.	8.8	153
16	Profiling DNA methylome landscapes of mammalian cells with single-cell reduced-representation bisulfite sequencing. <i>Nature Protocols</i> , 2015, 10, 645-659.	12.0	152
17	Single-Cell Multiomics Sequencing Reveals Prevalent Genomic Alterations in Tumor Stromal Cells of Human Colorectal Cancer. <i>Cancer Cell</i> , 2020, 38, 818-828.e5.	16.8	146
18	Single-cell sequencing in stem cell biology. <i>Genome Biology</i> , 2016, 17, 71.	8.8	144

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19	Single-cell multi-omics sequencing of human early embryos. <i>Nature Cell Biology</i> , 2018, 20, 847-858.	10.3	142
20	Tracing the expression of circular RNAs in human pre-implantation embryos. <i>Genome Biology</i> , 2016, 17, 130.	8.8	140
21	Tracing the temporal-spatial transcriptome landscapes of the human fetal digestive tract using single-cell RNA-sequencing. <i>Nature Cell Biology</i> , 2018, 20, 721-734.	10.3	125
22	Genome-scale detection of hypermethylated CpG islands in circulating cell-free DNA of hepatocellular carcinoma patients. <i>Cell Research</i> , 2015, 25, 1250-1264.	12.0	110
23	Dissecting the transcriptome landscape of the human fetal neural retina and retinal pigment epithelium by single-cell RNA-seq analysis. <i>PLoS Biology</i> , 2019, 17, e3000365.	5.6	108
24	DNA methylation and chromatin accessibility profiling of mouse and human fetal germ cells. <i>Cell Research</i> , 2017, 27, 165-183.	12.0	102
25	Dissecting the Global Dynamic Molecular Profiles of Human Fetal Kidney Development by Single-Cell RNA Sequencing. <i>Cell Reports</i> , 2018, 24, 3554-3567.e3.	6.4	91
26	Embryonic endothelial evolution towards first hematopoietic stem cells revealed by single-cell transcriptomic and functional analyses. <i>Cell Research</i> , 2020, 30, 376-392.	12.0	89
27	Single-cell transcriptome analysis reveals cell lineage specification in temporal-spatial patterns in human cortical development. <i>Science Advances</i> , 2020, 6, eaaz2978.	10.3	88
28	Genomic distribution and possible functions of DNA hydroxymethylation in the brain. <i>Genomics</i> , 2014, 104, 341-346.	2.9	84
29	Single-cell transcriptomics identifies divergent developmental lineage trajectories during human pituitary development. <i>Nature Communications</i> , 2020, 11, 5275.	12.8	79
30	Heterogeneity of glial progenitor cells during the neurogenesis-to-gliogenesis switch in the developing human cerebral cortex. <i>Cell Reports</i> , 2021, 34, 108788.	6.4	55
31	Tcf7l2 Is Required for Left-Right Asymmetric Differentiation of Habenular Neurons. <i>Current Biology</i> , 2014, 24, 2217-2227.	3.9	52
32	Human Germline Cell Development: from the Perspective of Single-Cell Sequencing. <i>Molecular Cell</i> , 2019, 76, 320-328.	9.7	48
33	Comprehensive DNA methylation analysis of tissue of origin of plasma cell-free DNA by methylated CpG tandem amplification and sequencing (MCTA-Seq). <i>Clinical Epigenetics</i> , 2019, 11, 93.	4.1	47
34	Single-cell RNA-seq analysis of mouse preimplantation embryos by third-generation sequencing. <i>PLoS Biology</i> , 2020, 18, e3001017.	5.6	46
35	Epigenomic Landscape of Human Fetal Brain, Heart, and Liver. <i>Journal of Biological Chemistry</i> , 2016, 291, 4386-4398.	3.4	45
36	Recent advances in single-cell sequencing technologies. <i>Precision Clinical Medicine</i> , 2022, 5, .	3.3	44

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37	Boosting the power of single-cell analysis. <i>Nature Biotechnology</i> , 2018, 36, 408-409.	17.5	43
38	SMOOTH-seq: single-cell genome sequencing of human cells on a third-generation sequencing platform. <i>Genome Biology</i> , 2021, 22, 195.	8.8	43
39	Genomic and transcriptomic profiling of carcinogenesis in patients with familial adenomatous polyposis. <i>Gut</i> , 2020, 69, 1283-1293.	12.1	36
40	Single cell epigenome sequencing technologies. <i>Molecular Aspects of Medicine</i> , 2018, 59, 62-69.	6.4	30
41	Heterogeneity in endothelial cells and widespread venous arterialization during early vascular development in mammals. <i>Cell Research</i> , 2022, 32, 333-348.	12.0	30
42	Single-cell transcriptome and genome analyses of pituitary neuroendocrine tumors. <i>Neuro-Oncology</i> , 2021, 23, 1859-1871.	1.2	29
43	Systematic evaluation of colorectal cancer organoid system by single-cell RNA-Seq analysis. <i>Genome Biology</i> , 2022, 23, 106.	8.8	29
44	Dissecting the epigenomic dynamics of human fetal germ cell development at single-cell resolution. <i>Cell Research</i> , 2021, 31, 463-477.	12.0	28
45	Detection of Colorectal Cancer in Circulating Cell-Free DNA by Methylated CpG Tandem Amplification and Sequencing. <i>Clinical Chemistry</i> , 2019, 65, 916-926.	3.2	25
46	DNA methylome reveals cellular origin of cell-free DNA in spent medium of human preimplantation embryos. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	25
47	Recent advances in mammalian reproductive biology. <i>Science China Life Sciences</i> , 2020, 63, 18-58.	4.9	23
48	Integrated single-cell multiomics analysis reveals novel candidate markers for prognosis in human pancreatic ductal adenocarcinoma. <i>Cell Discovery</i> , 2022, 8, 13.	6.7	23
49	Genome-Scale Methylation Analysis of Circulating Cell-Free DNA in Gastric Cancer Patients. <i>Clinical Chemistry</i> , 2022, 68, 354-364.	3.2	18
50	Reconstructing Complex Tissues from Single-Cell Analyses. <i>Cell</i> , 2014, 157, 771-773.	28.9	16
51	<i>De novo</i> assembly of human genome at single-cell levels. <i>Nucleic Acids Research</i> , 2022, 50, 7479-7492.	14.5	13
52	How to catch rare cell types. <i>Nature</i> , 2015, 525, 197-198.	27.8	9
53	Dissecting Human Gonadal Cell Lineage Specification and Sex Determination Using A Single-cell RNA-seq Approach. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 223-245.	6.9	9
54	MR-seq: measuring a single cell's transcriptome repeatedly by RNA-seq. <i>Science Bulletin</i> , 2017, 62, 391-398.	9.0	8

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55	5-Formylcytosine landscapes of human preimplantation embryos at single-cell resolution. PLoS Biology, 2020, 18, e3000799.	5.6	8
56	Heart-specific DNA methylation analysis in plasma for the investigation of myocardial damage. Journal of Translational Medicine, 2022, 20, 36.	4.4	7
57	Integrated transcriptomics and epigenomics reveal chamber-specific and species-specific characteristics of human and mouse hearts. PLoS Biology, 2021, 19, e3001229.	5.6	5
58	Integrating single-cell datasets with ambiguous batch information by incorporating molecular network features. Briefings in Bioinformatics, 2022, 23, .	6.5	5
59	Charting a Map through the Cellular Reprogramming Landscape. Cell Stem Cell, 2015, 16, 215-216.	11.1	3