## Xinglong Wu

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9275454/publications.pdf

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25 papers

6,280 citations

393982 19 h-index 26 g-index

28 all docs 28 docs citations

times ranked

28

9924 citing authors

#	Article	IF	CITATIONS
1	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
2	The DNA methylation landscape of human early embryos. Nature, 2014, 511, 606-610.	13.7	787
3	Single-cell triple omics sequencing reveals genetic, epigenetic, and transcriptomic heterogeneity in hepatocellular carcinomas. Cell Research, 2016, 26, 304-319.	5.7	492
4	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
5	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
6	Single-cell RNA-seq transcriptome analysis of linear and circular RNAs in mouse preimplantation embryos. Genome Biology, 2015, 16, 148.	13.9	369
7	Single-Cell Transcriptome Analysis Maps the Developmental Track of the Human Heart. Cell Reports, 2019, 26, 1934-1950.e5.	2.9	355
8	Active and Passive Demethylation of Male and Female Pronuclear DNA in the Mammalian Zygote. Cell Stem Cell, 2014, 15, 447-459.	5.2	311
9	Single-cell multi-omics sequencing of mouse early embryos and embryonic stem cells. Cell Research, 2017, 27, 967-988.	5.7	281
10	Microfluidic single-cell whole-transcriptome sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7048-7053.	3.3	259
11	Whole-genome analysis of 5-hydroxymethylcytosine and 5-methylcytosine at base resolution in the human brain. Genome Biology, 2014, 15, R49.	13.9	232
12	Single-cell RNA-seq analysis unveils a prevalent epithelial/mesenchymal hybrid state during mouse organogenesis. Genome Biology, 2018, 19, 31.	3.8	153
13	Profiling DNA methylome landscapes of mammalian cells with single-cell reduced-representation bisulfite sequencing. Nature Protocols, 2015, 10, 645-659.	5.5	152
14	Single-Cell 5-Formylcytosine Landscapes of Mammalian Early Embryos and ESCs at Single-Base Resolution. Cell Stem Cell, 2017, 20, 720-731.e5.	5.2	135
15	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
16	Surveying brain tumor heterogeneity by single-cell RNA-sequencing of multi-sector biopsies. National Science Review, 2020, 7, 1306-1318.	4.6	84
17	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
18	Genomic and transcriptomic profiling of carcinogenesis in patients with familial adenomatous polyposis. Gut, 2020, 69, 1283-1293.	6.1	36

#	Article	IF	CITATION
19	Dissecting the epigenomic dynamics of human fetal germ cell development at single-cell resolution. Cell Research, 2021, 31, 463-477.	5 <b>.</b> 7	28
20	Integrated single-cell multiomics analysis reveals novel candidate markers for prognosis in human pancreatic ductal adenocarcinoma. Cell Discovery, 2022, 8, 13.	3.1	23
21	Rho kinase inhibitor Y-27632 and Accutase dramatically increase mouse embryonic stem cell derivation. In Vitro Cellular and Developmental Biology - Animal, 2012, 48, 30-36.	0.7	22
22	H3K4me3 epigenomic landscape derived from ChIP-Seq of 1 000 mouse early embryonic cells. Cell Research, 2015, 25, 143-147.	5.7	19
23	MR-seq: measuring a single cell's transcriptome repeatedly by RNA-seq. Science Bulletin, 2017, 62, 391-398.	4.3	8
24	5-Formylcytosine landscapes of human preimplantation embryos at single-cell resolution. PLoS Biology, 2020, 18, e3000799.	2.6	8
25	Effects of Intrauterine Air Bubbles on Embryonic Development in Mice. Journal of the American Association for Laboratory Animal Science, 2019, 58, 7-15.	0.6	0