Xinglong Wu

List of Publications by Year
in descending order

25 papers	6,280 citations	394421 19 h-index	552781 26 g-index
28 all docs	28 docs citations	28 times ranked	9924 citing authors

#	Article	IF	Citations
1	Integrated single-cell multiomics analysis reveals novel candidate markers for prognosis in human pancreatic ductal adenocarcinoma. Cell Discovery, 2022, 8, 13.	6.7	23
2	Dissecting the epigenomic dynamics of human fetal germ cell development at single-cell resolution. Cell Research, 2021, 31, 463-477.	12.0	28
3	Heterogeneity of glial progenitor cells during the neurogenesis-to-gliogenesis switch in the developing human cerebral cortex. Cell Reports, 2021, 34, 108788.	6.4	55
4	Genomic and transcriptomic profiling of carcinogenesis in patients with familial adenomatous polyposis. Gut, 2020, 69, 1283-1293.	12.1	36
5	5-Formylcytosine landscapes of human preimplantation embryos at single-cell resolution. PLoS Biology, 2020, 18, e3000799.	5.6	8
6	Surveying brain tumor heterogeneity by single-cell RNA-sequencing of multi-sector biopsies. National Science Review, 2020, 7, 1306-1318.	9.5	84
7	Effects of Intrauterine Air Bubbles on Embryonic Development in Mice. Journal of the American Association for Laboratory Animal Science, 2019, 58, 7-15.	1.2	0
8	Single-Cell Transcriptome Analysis Maps the Developmental Track of the Human Heart. Cell Reports, 2019, 26, 1934-1950.e5.	6.4	355
9	Single-cell RNA-seq analysis unveils a prevalent epithelial/mesenchymal hybrid state during mouse organogenesis. Genome Biology, 2018, 19, 31.	8.8	153
10	Tracing the temporal-spatial transcriptome landscapes of the human fetal digestive tract using single-cell RNA-sequencing. Nature Cell Biology, 2018, 20, 721-734.	10.3	125
11	MR-seq: measuring a single cellâ€™s transcriptome repeatedly by RNA-seq. Science Bulletin, 2017, 62, 391-398.	9.0	8
12	Single-Cell RNA-Seq Analysis Maps Development of Human Germline Cells and Gonadal Niche Interactions. Cell Stem Cell, 2017, 20, 858-873.e4.	11.1	376
13	Single-cell multi-omics sequencing of mouse early embryos and embryonic stem cells. Cell Research, 2017, 27, 967-988.	12.0	281
14	Single-Cell 5-Formylcytosine Landscapes of Mammalian Early Embryos and ESCs at Single-Base Resolution. Cell Stem Cell, 2017, 20, 720-731.e5.	11.1	135
15	Single-cell triple omics sequencing reveals genetic, epigenetic, and transcriptomic heterogeneity in hepatocellular carcinomas. Cell Research, 2016, 26, 304-319.	12.0	492
16	H3K4me3 epigenomic landscape derived from ChIP-Seq of 1 000 mouse early embryonic cells. Cell Research, 2015, 25, 143-147.	12.0	19
17	Single-cell RNA-seq transcriptome analysis of linear and circular RNAs in mouse preimplantation embryos. Genome Biology, 2015, 16, 148.	9.6	369
18	Profiling DNA methylome landscapes of mammalian cells with single-cell reduced-representation bisulfite sequencing. Nature Protocols, 2015, 10, 645-659.	12.0	152

#	Article	IF	Citations
19	Whole-genome analysis of 5-hydroxymethylcytosine and 5-methylcytosine at base resolution in the human brain. Genome Biology, 2014, 15, R49.	9.6	232
20	The DNA methylation landscape of human early embryos. Nature, 2014, 511, 606-610.	27.8	787
21	Active and Passive Demethylation of Male and Female Pronuclear DNA in the Mammalian Zygote. Cell Stem Cell, 2014, 15, 447-459.	11.1	311
22	Microfluidic single-cell whole-transcriptome sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7048-7053.	7.1	259
23	Single-cell RNA-Seq profiling of human preimplantation embryos and embryonic stem cells. Nature Structural and Molecular Biology, 2013, 20, 1131-1139.	8.2	1,416
24	Single-cell methylome landscapes of mouse embryonic stem cells and early embryos analyzed using reduced representation bisulfite sequencing. Genome Research, 2013, 23, 2126-2135.	5.5	439
25	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.	1.5	22