## **Boqiang Hu**

List of Publications by Year in descending order

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ROOMNIC HU

#	Article	IF	CITATIONS
1	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.	5.6	108
2	Distinct enhancer signatures in the mouse gastrula delineate progressive cell fate continuum during embryo development. Cell Research, 2019, 29, 911-926.	12.0	16
3	Maintenance of Nucleolar Homeostasis by CBX4 Alleviates Senescence and Osteoarthritis. Cell Reports, 2019, 26, 3643-3656.e7.	6.4	81
4	Silencing of developmental genes by H3K27me3 and DNA methylation reflects the discrepant plasticity of embryonic and extraembryonic lineages. Cell Research, 2018, 28, 593-596.	12.0	26
5	Single-cell RNA-seq analysis unveils a prevalent epithelial/mesenchymal hybrid state during mouse organogenesis. Genome Biology, 2018, 19, 31.	8.8	153
6	Single-cell DNA methylome sequencing of human preimplantation embryos. Nature Genetics, 2018, 50, 12-19.	21.4	248
7	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells. Cell Discovery, 2018, 4, 2.	6.7	49
8	Single-cell multiomics sequencing and analyses of human colorectal cancer. Science, 2018, 362, 1060-1063.	12.6	256
9	Single-Cell RNA Sequencing Analysis Reveals Sequential Cell Fate Transition during Human Spermatogenesis. Cell Stem Cell, 2018, 23, 599-614.e4.	11.1	309
10	Single-cell multi-omics sequencing of human early embryos. Nature Cell Biology, 2018, 20, 847-858.	10.3	142
11	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
12	Single-cell multi-omics sequencing of mouse early embryos and embryonic stem cells. Cell Research, 2017, 27, 967-988.	12.0	281
13	DNA methylation and chromatin accessibility profiling of mouse and human fetal germ cells. Cell Research, 2017, 27, 165-183.	12.0	102
14	BTG4 is a meiotic cell cycle–coupled maternal-zygotic-transition licensing factor in oocytes. Nature Structural and Molecular Biology, 2016, 23, 387-394.	8.2	209
15	Tracing the expression of circular RNAs in human pre-implantation embryos. Genome Biology, 2016, 17, 130.	8.8	140
16	Single-cell triple omics sequencing reveals genetic, epigenetic, and transcriptomic heterogeneity in hepatocellular carcinomas. Cell Research, 2016, 26, 304-319.	12.0	492
17	The Transcriptome and DNA Methylome Landscapes of Human Primordial Germ Cells. Cell, 2015, 161, 1437-1452.	28.9	500
18	Tet and TDG Mediate DNA Demethylation Essential for Mesenchymal-to-Epithelial Transition in Somatic Cell Reprogramming. Cell Stem Cell, 2014, 14, 512-522.	11.1	290

#	Article	IF	CITATIONS
19	The DNA methylation landscape of human early embryos. Nature, 2014, 511, 606-610.	27.8	787
20	Active and Passive Demethylation of Male and Female Pronuclear DNA in the Mammalian Zygote. Cell Stem Cell, 2014, 15, 447-459.	11.1	311