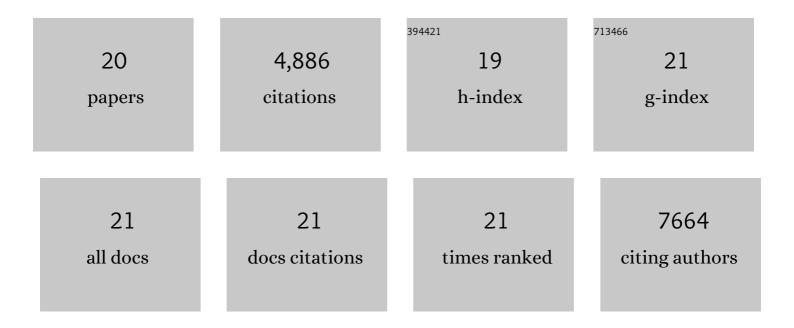
## **Boqiang Hu**

List of Publications by Year in descending order

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| #  | Article   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | The DNA methylation landscape of human early embryos. Nature, 2014, 511, 606-610.   | 27.8 | 787       |
| 2  | The Transcriptome and DNA Methylome Landscapes of Human Primordial Germ Cells. Cell, 2015, 161, 1437-1452.  | 28.9 | 500       |
| 3  | Single-cell triple omics sequencing reveals genetic, epigenetic, and transcriptomic heterogeneity in hepatocellular carcinomas. Cell Research, 2016, 26, 304-319.         | 12.0 | 492       |
| 4  | Single-Cell RNA-Seq Analysis Maps Development of Human Germline Cells and Gonadal Niche<br>Interactions. Cell Stem Cell, 2017, 20, 858-873.e4.                            | 11.1 | 376       |
| 5  | Active and Passive Demethylation of Male and Female Pronuclear DNA in the Mammalian Zygote. Cell<br>Stem Cell, 2014, 15, 447-459.   | 11.1 | 311       |
| 6  | Single-Cell RNA Sequencing Analysis Reveals Sequential Cell Fate Transition during Human<br>Spermatogenesis. Cell Stem Cell, 2018, 23, 599-614.e4.                        | 11.1 | 309       |
| 7  | Tet and TDG Mediate DNA Demethylation Essential for Mesenchymal-to-Epithelial Transition in Somatic<br>Cell Reprogramming. Cell Stem Cell, 2014, 14, 512-522.             | 11.1 | 290       |
| 8  | Single-cell multi-omics sequencing of mouse early embryos and embryonic stem cells. Cell Research, 2017, 27, 967-988.   | 12.0 | 281       |
| 9  | Single-cell multiomics sequencing and analyses of human colorectal cancer. Science, 2018, 362, 1060-1063.   | 12.6 | 256       |
| 10 | Single-cell DNA methylome sequencing of human preimplantation embryos. Nature Genetics, 2018, 50, 12-19.  | 21.4 | 248       |
| 11 | BTG4 is a meiotic cell cycle–coupled maternal-zygotic-transition licensing factor in oocytes. Nature<br>Structural and Molecular Biology, 2016, 23, 387-394.              | 8.2  | 209       |
| 12 | Single-cell RNA-seq analysis unveils a prevalent epithelial/mesenchymal hybrid state during mouse organogenesis. Genome Biology, 2018, 19, 31.                            | 8.8  | 153       |
| 13 | Single-cell multi-omics sequencing of human early embryos. Nature Cell Biology, 2018, 20, 847-858.  | 10.3 | 142       |
| 14 | Tracing the expression of circular RNAs in human pre-implantation embryos. Genome Biology, 2016, 17, 130.   | 8.8  | 140       |
| 15 | 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       |
| 16 | DNA methylation and chromatin accessibility profiling of mouse and human fetal germ cells. Cell<br>Research, 2017, 27, 165-183.   | 12.0 | 102       |
| 17 | Maintenance of Nucleolar Homeostasis by CBX4 Alleviates Senescence and Osteoarthritis. Cell<br>Reports, 2019, 26, 3643-3656.e7.   | 6.4  | 81        |
| 18 | ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells. Cell<br>Discovery, 2018, 4, 2.  | 6.7  | 49        |

| #  | Article   | IF   | CITATIONS |
|----|---|------|-----------|
| 19 | 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        |
| 20 | Distinct enhancer signatures in the mouse gastrula delineate progressive cell fate continuum during<br>embryo development. Cell Research, 2019, 29, 911-926.                    | 12.0 | 16        |