

# Hongshan Guo

## List of Publications by Year in descending order

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16  
papers

3,902  
citations

567281

15  
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888059

17  
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17  
all docs

17  
docs citations

17  
times ranked

6210  
citing authors

#	ARTICLE	IF	CITATIONS
1	The DNA methylation landscape of human early embryos. <i>Nature</i> , 2014, 511, 606-610.	27.8	787
2	The Transcriptome and DNA Methylome Landscapes of Human Primordial Germ Cells. <i>Cell</i> , 2015, 161, 1437-1452.	28.9	500
3	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
4	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
5	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
6	Single-cell multiomics sequencing and analyses of human colorectal cancer. <i>Science</i> , 2018, 362, 1060-1063.	12.6	256
7	Single-cell DNA methylome sequencing of human preimplantation embryos. <i>Nature Genetics</i> , 2018, 50, 12-19.	21.4	248
8	Correction of a genetic disease by CRISPR-Cas9-mediated gene editing in mouse spermatogonial stem cells. <i>Cell Research</i> , 2015, 25, 67-79.	12.0	209
9	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
10	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
11	Single-Cell 5-Formylcytosine Landscapes of Mammalian Early Embryos and ESCs at Single-Base Resolution. <i>Cell Stem Cell</i> , 2017, 20, 720-731.e5.	11.1	135
12	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
13	DNA methylation and chromatin accessibility profiling of mouse and human fetal germ cells. <i>Cell Research</i> , 2017, 27, 165-183.	12.0	102
14	Bisulfite-Free, Nanoscale Analysis of 5-Hydroxymethylcytosine at Single Base Resolution. <i>Journal of the American Chemical Society</i> , 2018, 140, 13190-13194.	13.7	71
15	H3K4me3 epigenomic landscape derived from ChIP-Seq of 1 000 mouse early embryonic cells. <i>Cell Research</i> , 2015, 25, 143-147.	12.0	19
16	The methylome of a human polar body reflects that of its sibling oocyte and its aberrance may indicate poor embryo development. <i>Human Reproduction</i> , 2021, 36, 318-330.	0.9	8