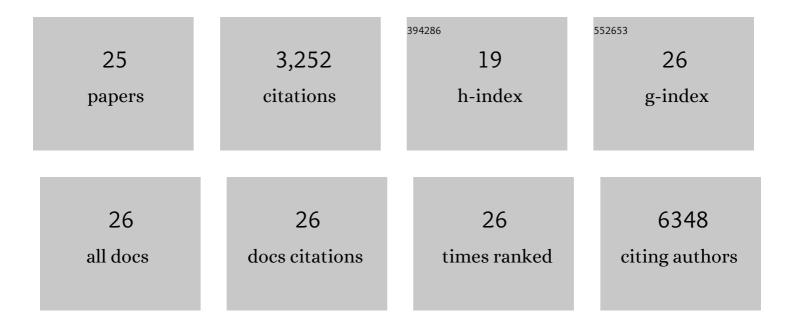
Ji Dong

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A single-cell RNA-seq survey of the developmental landscape of the human prefrontal cortex. Nature, 2018, 555, 524-528.	13.7	551
2	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
3	Single-Cell Transcriptome Analysis Maps the Developmental Track of the Human Heart. Cell Reports, 2019, 26, 1934-1950.e5.	2.9	355
4	Single-Cell RNA Sequencing Analysis Reveals Sequential Cell Fate Transition during Human Spermatogenesis. Cell Stem Cell, 2018, 23, 599-614.e4.	5.2	309
5	Single-cell multiomics sequencing and analyses of human colorectal cancer. Science, 2018, 362, 1060-1063.	6.0	256
6	Single-cell DNA methylome sequencing of human preimplantation embryos. Nature Genetics, 2018, 50, 12-19.	9.4	248
7	Spatial transcriptomic survey of human embryonic cerebral cortex by single-cell RNA-seq analysis. Cell Research, 2018, 28, 730-745.	5.7	179
8	Single-cell RNA-seq analysis unveils a prevalent epithelial/mesenchymal hybrid state during mouse organogenesis. Genome Biology, 2018, 19, 31.	3.8	153
9	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.	2.6	108
10	DNA methylation and chromatin accessibility profiling of mouse and human fetal germ cells. Cell Research, 2017, 27, 165-183.	5.7	102
11	Embryonic endothelial evolution towards first hematopoietic stem cells revealed by single-cell transcriptomic and functional analyses. Cell Research, 2020, 30, 376-392.	5.7	89
12	Single-cell transcriptome analysis reveals cell lineage specification in temporal-spatial patterns in human cortical development. Science Advances, 2020, 6, eaaz2978.	4.7	88
13	In vitro differentiation of human embryonic stem cells into ovarian follicle-like cells. Nature Communications, 2017, 8, 15680.	5.8	82
14	Differentiation of transplanted haematopoietic stem cells tracked by single-cell transcriptomic analysis. Nature Cell Biology, 2020, 22, 630-639.	4.6	65
15	TGF-β1 Negatively Regulates the Number and Function of Hematopoietic Stem Cells. Stem Cell Reports, 2018, 11, 274-287.	2.3	39
16	Circulating re-entrant waves promote maturation of hiPSC-derived cardiomyocytes in self-organized tissue ring. Communications Biology, 2020, 3, 122.	2.0	32
17	Cell-fate transition and determination analysis of mouse male germ cells throughout development. Nature Communications, 2021, 12, 6839.	5.8	31
18	Heterogeneity in endothelial cells and widespread venous arterialization during early vascular development in mammals. Cell Research, 2022, 32, 333-348.	5.7	30

Ji Dong

#	Article	IF	CITATIONS
19	Distinct enhancer signatures in the mouse gastrula delineate progressive cell fate continuum during embryo development. Cell Research, 2019, 29, 911-926.	5.7	16
20	Heteroplasmy and Ancient Translocation of Mitochondrial DNA to the Nucleus in the Chinese Horseshoe Bat (Rhinolophus sinicus) Complex. PLoS ONE, 2014, 9, e98035.	1.1	9
21	Single-cell analyses identify distinct and intermediate states of zebrafish pancreatic islet development. Journal of Molecular Cell Biology, 2019, 11, 435-447.	1.5	9
22	Repetitive transpositions of mitochondrial DNA sequences to the nucleus during the radiation of horseshoe bats (Rhinolophus, Chiroptera). Gene, 2016, 581, 161-169.	1.0	8
23	Integrating single-cell datasets with ambiguous batch information by incorporating molecular network features. Briefings in Bioinformatics, 2022, 23, .	3.2	5
24	Introgression of mitochondrial DNA promoted by natural selection in the Japanese pipistrelle bat (Pipistrellus abramus). Genetica, 2014, 142, 483-494.	0.5	4
25	The complete mitochondrial genome of a Chinese rufous horseshoe bat subspecies, Rhinolophus sinicus sinicus (Chiroptera: Rhinolophidae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3301-3302.	0.7	4