

Fuchou Tang

List of Publications by Year in descending order

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Version: 2024-02-01

167
papers

25,491
citations

10070

75
h-index

9118

149
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186
all docs

186
docs citations

186
times ranked

32468
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrating single-cell datasets with ambiguous batch information by incorporating molecular network features. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	5
2	Genome-Scale Methylation Analysis of Circulating Cell-Free DNA in Gastric Cancer Patients. <i>Clinical Chemistry</i> , 2022, 68, 354-364.	1.5	18
3	Somatic cell-derived BMPs induce premature meiosis in male germ cells during the embryonic stage by upregulating <i>Dazl</i> expression. <i>FASEB Journal</i> , 2022, 36, e22131.	0.2	1
4	Heterogeneity in endothelial cells and widespread venous arterialization during early vascular development in mammals. <i>Cell Research</i> , 2022, 32, 333-348.	5.7	30
5	Recent advances in single-cell sequencing technologies. <i>Precision Clinical Medicine</i> , 2022, 5, .	1.3	44
6	Heart-specific DNA methylation analysis in plasma for the investigation of myocardial damage. <i>Journal of Translational Medicine</i> , 2022, 20, 36.	1.8	7
7	Integrated single-cell multiomics analysis reveals novel candidate markers for prognosis in human pancreatic ductal adenocarcinoma. <i>Cell Discovery</i> , 2022, 8, 13.	3.1	23
8	Systematic evaluation of colorectal cancer organoid system by single-cell RNA-Seq analysis. <i>Genome Biology</i> , 2022, 23, 106.	3.8	29
9	Transcriptome profiling in swine macrophages infected with African swine fever virus at single-cell resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2201288119.	3.3	39
10	Dissecting Human Gonadal Cell Lineage Specification and Sex Determination Using A Single-cell RNA-seq Approach. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 223-245.	3.0	9
11	<i>De novo</i> assembly of human genome at single-cell levels. <i>Nucleic Acids Research</i> , 2022, 50, 7479-7492.	6.5	13
12	Deciphering primate retinal aging at single-cell resolution. <i>Protein and Cell</i> , 2021, 12, 889-898.	4.8	26
13	A single-cell transcriptomic atlas of primate pancreatic islet aging. <i>National Science Review</i> , 2021, 8, nwaa127.	4.6	37
14	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.	0.4	8
15	Dissecting the epigenomic dynamics of human fetal germ cell development at single-cell resolution. <i>Cell Research</i> , 2021, 31, 463-477.	5.7	28
16	Pathway-based classification of glioblastoma uncovers a mitochondrial subtype with therapeutic vulnerabilities. <i>Nature Cancer</i> , 2021, 2, 141-156.	5.7	163
17	Heterogeneity of glial progenitor cells during the neurogenesis-to-gliogenesis switch in the developing human cerebral cortex. <i>Cell Reports</i> , 2021, 34, 108788.	2.9	55
18	DNMTs Play an Important Role in Maintaining the Pluripotency of Leukemia Inhibitory Factor-Dependent Embryonic Stem Cells. <i>Stem Cell Reports</i> , 2021, 16, 582-596.	2.3	12

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19	Establishment of bovine expanded potential stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	36
20	Single-cell transcriptome and genome analyses of pituitary neuroendocrine tumors. Neuro-Oncology, 2021, 23, 1859-1871.	0.6	29
21	Integrated transcriptomics and epigenomics reveal chamber-specific and species-specific characteristics of human and mouse hearts. PLoS Biology, 2021, 19, e3001229.	2.6	5
22	SMOOTH-seq: single-cell genome sequencing of human cells on a third-generation sequencing platform. Genome Biology, 2021, 22, 195.	3.8	43
23	Single-cell transcriptomic profiling of non-hematopoietic circulating cells in mid-gestational mouse embryos. Journal of Genetics and Genomics, 2021, 48, 508-511.	1.7	0
24	Single-cell analysis of ploidy and the transcriptome reveals functional and spatial divergency in murine megakaryopoiesis. Blood, 2021, 138, 1211-1224.	0.6	59
25	Human embryo research, stem cell-derived embryo models and inÂvitro gametogenesis: Considerations leading to the revised ISSCR guidelines. Stem Cell Reports, 2021, 16, 1416-1424.	2.3	59
26	ISSCR Guidelines for Stem Cell Research and Clinical Translation: The 2021 update. Stem Cell Reports, 2021, 16, 1398-1408.	2.3	134
27	DNA methylome reveals cellular origin of cell-free DNA in spent medium of human preimplantation embryos. Journal of Clinical Investigation, 2021, 131, .	3.9	25
28	The comprehensive DNA methylation landscape of hematopoietic stem cell development. Cell Discovery, 2021, 7, 86.	3.1	6
29	A genome-wide CRISPR-based screen identifies <i>KAT7</i> as a driver of cellular senescence. Science Translational Medicine, 2021, 13, .	5.8	79
30	Cell-fate transition and determination analysis of mouse male germ cells throughout development. Nature Communications, 2021, 12, 6839.	5.8	31
31	OUP accepted manuscript. Molecular Human Reproduction, 2021, , .	1.3	3
32	Advanced Single-cell Omics Technologies and Informatics Tools for Genomics, Proteomics, and Bioinformatics Analysis. Genomics, Proteomics and Bioinformatics, 2021, 19, 343-345.	3.0	8
33	In vitro expansion of human sperm through nuclear transfer. Cell Research, 2020, 30, 356-359.	5.7	16
34	Recent advances in mammalian reproductive biology. Science China Life Sciences, 2020, 63, 18-58.	2.3	23
35	Genomic and transcriptomic profiling of carcinogenesis in patients with familial adenomatous polyposis. Gut, 2020, 69, 1283-1293.	6.1	36
36	Single-cell transcriptomics identifies divergent developmental lineage trajectories during human pituitary development. Nature Communications, 2020, 11, 5275.	5.8	79

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37	5-Formylcytosine landscapes of human preimplantation embryos at single-cell resolution. <i>PLoS Biology</i> , 2020, 18, e3000799.	2.6	8
38	Single-Cell Multiomics Sequencing Reveals Prevalent Genomic Alterations in Tumor Stromal Cells of Human Colorectal Cancer. <i>Cancer Cell</i> , 2020, 38, 818-828.e5.	7.7	146
39	Single-cell transcriptome analysis reveals cell lineage specification in temporal-spatial patterns in human cortical development. <i>Science Advances</i> , 2020, 6, eaaz2978.	4.7	88
40	A map of tumor-host interactions in glioma at single-cell resolution. <i>GigaScience</i> , 2020, 9, .	3.3	32
41	Differentiation of transplanted haematopoietic stem cells tracked by single-cell transcriptomic analysis. <i>Nature Cell Biology</i> , 2020, 22, 630-639.	4.6	65
42	A single-cell transcriptomic landscape of primate arterial aging. <i>Nature Communications</i> , 2020, 11, 2202.	5.8	95
43	Surveying brain tumor heterogeneity by single-cell RNA-sequencing of multi-sector biopsies. <i>National Science Review</i> , 2020, 7, 1306-1318.	4.6	84
44	Embryonic endothelial evolution towards first hematopoietic stem cells revealed by single-cell transcriptomic and functional analyses. <i>Cell Research</i> , 2020, 30, 376-392.	5.7	89
45	Circulating re-entrant waves promote maturation of hiPSC-derived cardiomyocytes in self-organized tissue ring. <i>Communications Biology</i> , 2020, 3, 122.	2.0	32
46	Meningeal lymphatic vessels regulate brain tumor drainage and immunity. <i>Cell Research</i> , 2020, 30, 229-243.	5.7	209
47	Activin A and BMP4 Signaling Expands Potency of Mouse Embryonic Stem Cells in Serum-Free Media. <i>Stem Cell Reports</i> , 2020, 14, 241-255.	2.3	13
48	Refined spatial temporal epigenomic profiling reveals intrinsic connection between PRDM9-mediated H3K4me3 and the fate of double-stranded breaks. <i>Cell Research</i> , 2020, 30, 256-268.	5.7	37
49	Decoding the development of the human hippocampus. <i>Nature</i> , 2020, 577, 531-536.	13.7	141
50	Single-Cell Transcriptomic Atlas of Primate Ovarian Aging. <i>Cell</i> , 2020, 180, 585-600.e19.	13.5	306
51	Nuclear actin regulates inducible transcription by enhancing RNA polymerase II clustering. <i>Science Advances</i> , 2020, 6, eaay6515.	4.7	81
52	Single-Cell Transcriptomics Reveal Immune Mechanisms of the Onset and Progression of IgA Nephropathy. <i>Cell Reports</i> , 2020, 33, 108525.	2.9	49
53	Single-cell RNA-seq analysis of mouse preimplantation embryos by third-generation sequencing. <i>PLoS Biology</i> , 2020, 18, e3001017.	2.6	46
54	Single-cell RNA-seq analysis reveals the progression of human osteoarthritis. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 100-110.	0.5	237

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55	Single-cell RNA-seq identifies a reversible mesodermal activation in abnormally specified epithelia of p63 EEC syndrome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17361-17370.	3.3	19
56	Reconstituting the transcriptome and DNA methylome landscapes of human implantation. <i>Nature</i> , 2019, 572, 660-664.	13.7	207
57	Comprehensive DNA methylation analysis of tissue of origin of plasma cell-free DNA by methylated CpG tandem amplification and sequencing (MCTA-Seq). <i>Clinical Epigenetics</i> , 2019, 11, 93.	1.8	47
58	Dissecting the transcriptome landscape of the human fetal neural retina and retinal pigment epithelium by single-cell RNA-seq analysis. <i>PLoS Biology</i> , 2019, 17, e3000365.	2.6	108
59	The lncRNA <i>Hand2os1</i> / <i>Uph</i> locus orchestrates heart development through regulation of precise expression of <i>Hand2</i> . <i>Development (Cambridge)</i> , 2019, 146, .	1.2	48
60	Human Germline Cell Development: from the Perspective of Single-Cell Sequencing. <i>Molecular Cell</i> , 2019, 76, 320-328.	4.5	48
61	Distinct enhancer signatures in the mouse gastrula delineate progressive cell fate continuum during embryo development. <i>Cell Research</i> , 2019, 29, 911-926.	5.7	16
62	Effects of Intrauterine Air Bubbles on Embryonic Development in Mice. <i>Journal of the American Association for Laboratory Animal Science</i> , 2019, 58, 7-15.	0.6	0
63	Detection of Colorectal Cancer in Circulating Cell-Free DNA by Methylated CpG Tandem Amplification and Sequencing. <i>Clinical Chemistry</i> , 2019, 65, 916-926.	1.5	25
64	Single-Cell 5fC Sequencing. <i>Methods in Molecular Biology</i> , 2019, 1979, 251-267.	0.4	2
65	Maintenance of Nucleolar Homeostasis by CBX4 Alleviates Senescence and Osteoarthritis. <i>Cell Reports</i> , 2019, 26, 3643-3656.e7.	2.9	81
66	Epigenetic Regulation and Risk Factors During the Development of Human Gametes and Early Embryos. <i>Annual Review of Genomics and Human Genetics</i> , 2019, 20, 21-40.	2.5	29
67	Up-regulation of FOXD1 by YAP alleviates senescence and osteoarthritis. <i>PLoS Biology</i> , 2019, 17, e3000201.	2.6	104
68	Single-Cell Transcriptome Analysis Maps the Developmental Track of the Human Heart. <i>Cell Reports</i> , 2019, 26, 1934-1950.e5.	2.9	355
69	FOXO3-Engineered Human ESC-Derived Vascular Cells Promote Vascular Protection and Regeneration. <i>Cell Stem Cell</i> , 2019, 24, 447-461.e8.	5.2	78
70	Combined Single-Cell Profiling of lncRNAs and Functional Screening Reveals that H19 Is Pivotal for Embryonic Hematopoietic Stem Cell Development. <i>Cell Stem Cell</i> , 2019, 24, 285-298.e5.	5.2	96
71	<i>Xist</i> Intron 1 Repression by Transcriptional-Activator-Like Effectors Designer Transcriptional Factor Improves Somatic Cell Reprogramming in Mice. <i>Stem Cells</i> , 2019, 37, 599-608.	1.4	7
72	Transcriptional and Spatial Heterogeneity of Mouse Megakaryocytes at Single-Cell Resolution. <i>Blood</i> , 2019, 134, 275-275.	0.6	4

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73	Silencing of developmental genes by H3K27me3 and DNA methylation reflects the discrepant plasticity of embryonic and extraembryonic lineages. <i>Cell Research</i> , 2018, 28, 593-596.	5.7	26
74	Single-cell RNA-seq analysis unveils a prevalent epithelial/mesenchymal hybrid state during mouse organogenesis. <i>Genome Biology</i> , 2018, 19, 31.	3.8	153
75	Single-cell DNA methylome sequencing of human preimplantation embryos. <i>Nature Genetics</i> , 2018, 50, 12-19.	9.4	248
76	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells. <i>Cell Discovery</i> , 2018, 4, 2.	3.1	49
77	A single-cell RNA-seq survey of the developmental landscape of the human prefrontal cortex. <i>Nature</i> , 2018, 555, 524-528.	13.7	551
78	Derivation of hypermethylated pluripotent embryonic stem cells with high potency. <i>Cell Research</i> , 2018, 28, 22-34.	5.7	43
79	Single cell epigenome sequencing technologies. <i>Molecular Aspects of Medicine</i> , 2018, 59, 62-69.	2.7	30
80	Single-cell multiomics sequencing and analyses of human colorectal cancer. <i>Science</i> , 2018, 362, 1060-1063.	6.0	256
81	Dissecting the Global Dynamic Molecular Profiles of Human Fetal Kidney Development by Single-Cell RNA Sequencing. <i>Cell Reports</i> , 2018, 24, 3554-3567.e3.	2.9	91
82	Single-Cell RNA Sequencing Analysis Reveals Sequential Cell Fate Transition during Human Spermatogenesis. <i>Cell Stem Cell</i> , 2018, 23, 599-614.e4.	5.2	309
83	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.	4.6	125
84	TGF- β 1 Negatively Regulates the Number and Function of Hematopoietic Stem Cells. <i>Stem Cell Reports</i> , 2018, 11, 274-287.	2.3	39
85	Low Cell-Matrix Adhesion Reveals Two Subtypes of Human Pluripotent Stem Cells. <i>Stem Cell Reports</i> , 2018, 11, 142-156.	2.3	37
86	Single-cell RNA-seq uncovers dynamic processes and critical regulators in mouse spermatogenesis. <i>Cell Research</i> , 2018, 28, 879-896.	5.7	253
87	Boosting the power of single-cell analysis. <i>Nature Biotechnology</i> , 2018, 36, 408-409.	9.4	43
88	Spatial transcriptomic survey of human embryonic cerebral cortex by single-cell RNA-seq analysis. <i>Cell Research</i> , 2018, 28, 730-745.	5.7	179
89	Single-cell multi-omics sequencing of human early embryos. <i>Nature Cell Biology</i> , 2018, 20, 847-858.	4.6	142
90	MAPK cascade couples maternal mRNA translation and degradation to meiotic cell cycle progression in mouse oocyte. <i>Development (Cambridge)</i> , 2017, 144, 452-463.	1.2	78

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91	MR-seq: measuring a single cell's transcriptome repeatedly by RNA-seq. <i>Science Bulletin</i> , 2017, 62, 391-398.	4.3	8
92	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.	5.2	376
93	Clonal analysis reveals remarkable functional heterogeneity during hematopoietic stem cell emergence. <i>Cell Research</i> , 2017, 27, 1065-1068.	5.7	13
94	Single-cell multi-omics sequencing of mouse early embryos and embryonic stem cells. <i>Cell Research</i> , 2017, 27, 967-988.	5.7	281
95	Comprehensive Analysis of the Discordance of EGFR Mutation Status between Tumor Tissues and Matched Circulating Tumor DNA in Advanced Non-Small Cell Lung Cancer. <i>Journal of Thoracic Oncology</i> , 2017, 12, 1376-1387.	0.5	39
96	In vitro differentiation of human embryonic stem cells into ovarian follicle-like cells. <i>Nature Communications</i> , 2017, 8, 15680.	5.8	82
97	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.	5.2	135
98	The Primate-Specific Gene TMEM14B Marks Outer Radial Glia Cells and Promotes Cortical Expansion and Folding. <i>Cell Stem Cell</i> , 2017, 21, 635-649.e8.	5.2	102
99	β -Catenin directs the transformation of testis Sertoli cells to ovarian granulosa-like cells by inducing Foxl2 expression. <i>Journal of Biological Chemistry</i> , 2017, 292, 17577-17586.	1.6	33
100	CFP1 Regulates Histone H3K4 Trimethylation and Developmental Potential in Mouse Oocytes. <i>Cell Reports</i> , 2017, 20, 1161-1172.	2.9	89
101	Genetic enhancement in cultured human adult stem cells conferred by a single nucleotide recoding. <i>Cell Research</i> , 2017, 27, 1178-1181.	5.7	40
102	DNA methylation and chromatin accessibility profiling of mouse and human fetal germ cells. <i>Cell Research</i> , 2017, 27, 165-183.	5.7	102
103	The sequence preference of DNA methylation variation in mammals. <i>PLoS ONE</i> , 2017, 12, e0186559.	1.1	8
104	Histone Acetyltransferase GCN5 Regulates Osteogenic Differentiation of Mesenchymal Stem Cells by Inhibiting NF- κ B. <i>Journal of Bone and Mineral Research</i> , 2016, 31, 391-402.	3.1	48
105	Tracing haematopoietic stem cell formation at single-cell resolution. <i>Nature</i> , 2016, 533, 487-492.	13.7	297
106	Single-cell sequencing in stem cell biology. <i>Genome Biology</i> , 2016, 17, 71.	3.8	144
107	BTG4 is a meiotic cell cycle-coupled maternal-zygotic-transition licensing factor in oocytes. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 387-394.	3.6	209
108	TET-mediated DNA demethylation controls gastrulation by regulating Lefty-Nodal signalling. <i>Nature</i> , 2016, 538, 528-532.	13.7	163

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109	Tracing the expression of circular RNAs in human pre-implantation embryos. <i>Genome Biology</i> , 2016, 17, 130.	3.8	140
110	Embryonic hematopoiesis in vertebrate somites gives rise to definitive hematopoietic stem cells. <i>Journal of Molecular Cell Biology</i> , 2016, 8, 288-301.	1.5	16
111	SIRT6 safeguards human mesenchymal stem cells from oxidative stress by coactivating NRF2. <i>Cell Research</i> , 2016, 26, 190-205.	5.7	261
112	Divergent lncRNAs Regulate Gene Expression and Lineage Differentiation in Pluripotent Cells. <i>Cell Stem Cell</i> , 2016, 18, 637-652.	5.2	358
113	Oocyte-expressed yes-associated protein is a key activator of the early zygotic genome in mouse. <i>Cell Research</i> , 2016, 26, 275-287.	5.7	108
114	Single-cell triple omics sequencing reveals genetic, epigenetic, and transcriptomic heterogeneity in hepatocellular carcinomas. <i>Cell Research</i> , 2016, 26, 304-319.	5.7	492
115	Epigenomic Landscape of Human Fetal Brain, Heart, and Liver. <i>Journal of Biological Chemistry</i> , 2016, 291, 4386-4398.	1.6	45
116	Tracing the Formation of Haematopoietic Stem Cells in Mouse Embryos By Single-Cell Functional and RNA-Seq Analyses. <i>Blood</i> , 2016, 128, 5046-5046.	0.6	1
117	The Transcriptome and DNA Methylome Landscapes of Human Primordial Germ Cells. <i>Cell</i> , 2015, 161, 1437-1452.	13.5	500
118	PTEN deficiency reprogrammes human neural stem cells towards a glioblastoma stem cell-like phenotype. <i>Nature Communications</i> , 2015, 6, 10068.	5.8	122
119	Live births after simultaneous avoidance of monogenic diseases and chromosome abnormality by next-generation sequencing with linkage analyses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15964-15969.	3.3	115
120	H3K4me3 epigenomic landscape derived from ChIP-Seq of 1 000 mouse early embryonic cells. <i>Cell Research</i> , 2015, 25, 143-147.	5.7	19
121	Charting a Map through the Cellular Reprogramming Landscape. <i>Cell Stem Cell</i> , 2015, 16, 215-216.	5.2	3
122	Gadd45a promotes DNA demethylation through TDG. <i>Nucleic Acids Research</i> , 2015, 43, 3986-3997.	6.5	77
123	Single-cell RNA-seq transcriptome analysis of linear and circular RNAs in mouse preimplantation embryos. <i>Genome Biology</i> , 2015, 16, 148.	13.9	369
124	A Werner syndrome stem cell model unveils heterochromatin alterations as a driver of human aging. <i>Science</i> , 2015, 348, 1160-1163.	6.0	429
125	Single Cell Transcriptome Amplification with MALBAC. <i>PLoS ONE</i> , 2015, 10, e0120889.	1.1	44
126	Profiling DNA methylome landscapes of mammalian cells with single-cell reduced-representation bisulfite sequencing. <i>Nature Protocols</i> , 2015, 10, 645-659.	5.5	152

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127	Dynamic transcriptional symmetry-breaking in pre-implantation mammalian embryo development revealed by single-cell RNA-seq. <i>Development (Cambridge)</i> , 2015, 142, 3468-77.	1.2	75
128	Genome-scale detection of hypermethylated CpG islands in circulating cell-free DNA of hepatocellular carcinoma patients. <i>Cell Research</i> , 2015, 25, 1250-1264.	5.7	110
129	How to catch rare cell types. <i>Nature</i> , 2015, 525, 197-198.	13.7	9
130	Uniform and accurate single-cell sequencing based on emulsion whole-genome amplification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11923-11928.	3.3	191
131	Correction of a genetic disease by CRISPR-Cas9-mediated gene editing in mouse spermatogonial stem cells. <i>Cell Research</i> , 2015, 25, 67-79.	5.7	209
132	Whole-genome analysis of 5-hydroxymethylcytosine and 5-methylcytosine at base resolution in the human brain. <i>Genome Biology</i> , 2014, 15, R49.	13.9	232
133	Tet and TDG Mediate DNA Demethylation Essential for Mesenchymal-to-Epithelial Transition in Somatic Cell Reprogramming. <i>Cell Stem Cell</i> , 2014, 14, 512-522.	5.2	290
134	Reconstructing Complex Tissues from Single-Cell Analyses. <i>Cell</i> , 2014, 157, 771-773.	13.5	16
135	Programming and Inheritance of Parental DNA Methylomes in Mammals. <i>Cell</i> , 2014, 157, 979-991.	13.5	451
136	Genomic distribution and possible functions of DNA hydroxymethylation in the brain. <i>Genomics</i> , 2014, 104, 341-346.	1.3	84
137	Validation of multiple annealing and looping-based amplification cycle sequencing for 24-chromosome aneuploidy screening of cleavage-stage embryos. <i>Fertility and Sterility</i> , 2014, 102, 1685-1691.	0.5	31
138	The DNA methylation landscape of human early embryos. <i>Nature</i> , 2014, 511, 606-610.	13.7	787
139	Active and Passive Demethylation of Male and Female Pronuclear DNA in the Mammalian Zygote. <i>Cell Stem Cell</i> , 2014, 15, 447-459.	5.2	311
140	Microfluidic single-cell whole-transcriptome sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7048-7053.	3.3	259
141	A tripartite transcription factor network regulates primordial germ cell specification in mice. <i>Nature Cell Biology</i> , 2013, 15, 905-915.	4.6	240
142	Single-cell RNA-Seq profiling of human preimplantation embryos and embryonic stem cells. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1131-1139.	3.6	1,416
143	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.	2.4	439
144	Genome Analyses of Single Human Oocytes. <i>Cell</i> , 2013, 155, 1492-1506.	13.5	279

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145	Dynamics of 5-hydroxymethylcytosine during mouse spermatogenesis. Nature Communications, 2013, 4, 1995.	5.8	171
146	Tet1 Regulates Adult Hippocampal Neurogenesis and Cognition. Cell Stem Cell, 2013, 13, 237-245.	5.2	309
147	<i>Prdm14</i> promotes germline fate and naive pluripotency by repressing FGF signalling and DNA methylation. EMBO Reports, 2013, 14, 629-637.	2.0	145
148	Microfluidics Facilitated Genome Sequencing for Limited Number of Cells. , 2013, , .		0
149	Microfluidics Facilitated Genome Sequencing for Limited Number of Cells. , 2013, , .		0
150	Probing Meiotic Recombination and Aneuploidy of Single Sperm Cells by Whole-Genome Sequencing. Science, 2012, 338, 1627-1630.	6.0	273
151	The Germ Cell Determinant Blimp1 Is Not Required for Derivation of Pluripotent Stem Cells. Cell Stem Cell, 2012, 11, 110-117.	5.2	23
152	Deterministic and Stochastic Allele Specific Gene Expression in Single Mouse Blastomeres. PLoS ONE, 2011, 6, e21208.	1.1	134
153	Development and applications of single-cell transcriptome analysis. Nature Methods, 2011, 8, S6-S11.	9.0	280
154	RNA-Seq analysis to capture the transcriptome landscape of a single cell. Nature Protocols, 2010, 5, 516-535.	5.5	450
155	Tracing the Derivation of Embryonic Stem Cells from the Inner Cell Mass by Single-Cell RNA-Seq Analysis. Cell Stem Cell, 2010, 6, 468-478.	5.2	479
156	Essential role for Argonaute2 protein in mouse oogenesis. Epigenetics and Chromatin, 2009, 2, 9.	1.8	95
157	Epigenetic reversion of post-implantation epiblast to pluripotent embryonic stem cells. Nature, 2009, 461, 1292-1295.	13.7	357
158	mRNA-Seq whole-transcriptome analysis of a single cell. Nature Methods, 2009, 6, 377-382.	9.0	2,736
159	Dynamic Equilibrium and Heterogeneity of Mouse Pluripotent Stem Cells with Distinct Functional and Epigenetic States. Cell Stem Cell, 2008, 3, 391-401.	5.2	596
160	A sensitive multiplex assay for piRNA expression. Biochemical and Biophysical Research Communications, 2008, 369, 1190-1194.	1.0	17
161	MicroRNAs are tightly associated with RNA-induced gene silencing complexes in vivo. Biochemical and Biophysical Research Communications, 2008, 372, 24-29.	1.0	26
162	Reprogramming Primordial Germ Cells into Pluripotent Stem Cells. PLoS ONE, 2008, 3, e3531.	1.1	140

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163	MicroRNA Biogenesis Is Required for Mouse Primordial Germ Cell Development and Spermatogenesis. PLoS ONE, 2008, 3, e1738.	1.1	442
164	Maternal microRNAs are essential for mouse zygotic development. Genes and Development, 2007, 21, 644-648.	2.7	496
165	220-plex microRNA expression profile of a single cell. Nature Protocols, 2006, 1, 1154-1159.	5.5	97
166	MicroRNA expression profiling of single whole embryonic stem cells. Nucleic Acids Research, 2006, 34, e9-e9.	6.5	306
167	Generation of single cell microRNA expression profile. , 0, , 489-496.		0