

Integrating single-cell transcriptomic data across different species

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Granatum: a graphical single-cell RNA-Seq analysis pipeline for genomics scientists. <i>Genome Medicine</i> , 2017, 9, 108.	3.6	63
2	Developmental diversification of cortical inhibitory interneurons. <i>Nature</i> , 2018, 555, 457-462.	13.7	393
3	Observation weights unlock bulk RNA-seq tools for zero inflation and single-cell applications. <i>Genome Biology</i> , 2018, 19, 24.	3.8	180
4	Sorting apples from oranges in single-cell expression comparisons. <i>Nature Methods</i> , 2018, 15, 321-322.	9.0	0
5	Single-Cell Deconvolution of Fibroblast Heterogeneity in Mouse Pulmonary Fibrosis. <i>Cell Reports</i> , 2018, 22, 3625-3640.	2.9	392
6	The impact of single-cell RNA sequencing on understanding the functional organization of the immune system. <i>Briefings in Functional Genomics</i> , 2018, 17, 265-272.	1.3	30
7	Asymmetric Integration of Single-Cell Transcriptomic Data using Latent Dirichlet Allocation and Procrustes Analysis. , 2018, , .		1
8	Comparison of clustering tools in R for medium-sized 10x Genomics single-cell RNA-sequencing data. <i>F1000Research</i> , 2018, 7, 1297.	0.8	131
9	Expression reflects population structure. <i>PLoS Genetics</i> , 2018, 14, e1007841.	1.5	27
10	Human bone marrow assessment by single-cell RNA sequencing, mass cytometry, and flow cytometry. <i>JCI Insight</i> , 2018, 3, .	2.3	135
11	Single-cell transcriptional analysis reveals ILC-like cells in zebrafish. <i>Science Immunology</i> , 2018, 3, .	5.6	103
12	Identification of novel circadian transcripts in the zebrafish retina. <i>Journal of Experimental Biology</i> , 2019, 222, .	0.8	3
13	Machine learning based classification of cells into chronological stages using single-cell transcriptomics. <i>Scientific Reports</i> , 2018, 8, 17156.	1.6	17
14	Inflammatory Cytokine TNF α Promotes the Long-Term Expansion of Primary Hepatocytes in 3D Culture. <i>Cell</i> , 2018, 175, 1607-1619.e15.	13.5	211
15	A web server for comparative analysis of single-cell RNA-seq data. <i>Nature Communications</i> , 2018, 9, 4768.	5.8	48
16	Single-cell RNA-sequencing reveals transcriptional dynamics of estrogen-induced dysplasia in the ovarian surface epithelium. <i>PLoS Genetics</i> , 2018, 14, e1007788.	1.5	16
17	Single-cell reconstruction of the early maternal-fetal interface in humans. <i>Nature</i> , 2018, 563, 347-353.	13.7	1,547
18	Genome-wide CRISPR Screens in Primary Human T Cells Reveal Key Regulators of Immune Function. <i>Cell</i> , 2018, 175, 1958-1971.e15.	13.5	378

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19	Comparative Analysis and Refinement of Human PSC-Derived Kidney Organoid Differentiation with Single-Cell Transcriptomics. <i>Cell Stem Cell</i> , 2018, 23, 869-881.e8.	5.2	419
20	Single-Cell Analysis Identifies Thymic Maturation Delay in Growth-Restricted Neonatal Mice. <i>Frontiers in Immunology</i> , 2018, 9, 2523.	2.2	4
21	Human retinoic acid α -regulated CD161+ regulatory T cells support wound repair in intestinal mucosa. <i>Nature Immunology</i> , 2018, 19, 1403-1414.	7.0	86
22	The Mammalian Spermatogenesis Single-Cell Transcriptome, from Spermatogonial Stem Cells to Spermatids. <i>Cell Reports</i> , 2018, 25, 1650-1667.e8.	2.9	384
23	Identity Noise and Adipogenic Traits Characterize Dermal Fibroblast Aging. <i>Cell</i> , 2018, 175, 1575-1590.e22.	13.5	168
24	ddSeeker: a tool for processing Bio-Rad ddSEQ single cell RNA-seq data. <i>BMC Genomics</i> , 2018, 19, 960.	1.2	22
25	An integrative approach for building personalized gene regulatory networks for precision medicine. <i>Genome Medicine</i> , 2018, 10, 96.	3.6	49
26	Arg1 expression defines immunosuppressive subsets of tumor-associated macrophages. <i>Theranostics</i> , 2018, 8, 5842-5854.	4.6	203
27	A Cellular Anatomy of the Normal Adult Human Prostate and Prostatic Urethra. <i>Cell Reports</i> , 2018, 25, 3530-3542.e5.	2.9	204
28	Single-Cell Transcriptome Profiling of Mouse and hESC-Derived Pancreatic Progenitors. <i>Stem Cell Reports</i> , 2018, 11, 1551-1564.	2.3	94
29	Murine hematopoietic stem cell activity is derived from pre-circulation embryos but not yolk sacs. <i>Nature Communications</i> , 2018, 9, 5405.	5.8	19
30	Identification of cancer subtypes from single-cell RNA-seq data using a consensus clustering method. <i>BMC Medical Genomics</i> , 2018, 11, 117.	0.7	33
31	Cell Hashing with barcoded antibodies enables multiplexing and doublet detection for single cell genomics. <i>Genome Biology</i> , 2018, 19, 224.	3.8	674
32	Transcriptome and epigenome landscape of human cortical development modeled in organoids. <i>Science</i> , 2018, 362, .	6.0	220
33	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. <i>Science</i> , 2018, 362, .	6.0	516
34	Spatiotemporal transcriptomic divergence across human and macaque brain development. <i>Science</i> , 2018, 362, .	6.0	279
35	Visualizing and Interpreting Single-Cell Gene Expression Datasets with Similarity Weighted Nonnegative Embedding. <i>Cell Systems</i> , 2018, 7, 656-666.e4.	2.9	63
36	Single cell dissection of plasma cell heterogeneity in symptomatic and asymptomatic myeloma. <i>Nature Medicine</i> , 2018, 24, 1867-1876.	15.2	179

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37	Transcriptomic landscape of the blastema niche in regenerating adult axolotl limbs at single-cell resolution. <i>Nature Communications</i> , 2018, 9, 5153.	5.8	133
38	Single-Cell RNA-Seq of Mouse Olfactory Bulb Reveals Cellular Heterogeneity and Activity-Dependent Molecular Census of Adult-Born Neurons. <i>Cell Reports</i> , 2018, 25, 2689-2703.e3.	2.9	109
39	Lineage tracking reveals dynamic relationships of T cells in colorectal cancer. <i>Nature</i> , 2018, 564, 268-272.	13.7	742
40	Single-cell mapping of lineage and identity in direct reprogramming. <i>Nature</i> , 2018, 564, 219-224.	13.7	255
41	Understanding tumor ecosystems by single-cell sequencing: promises and limitations. <i>Genome Biology</i> , 2018, 19, 211.	3.8	161
42	PDGFR β Cells Rapidly Relay Inflammatory Signal from the Circulatory System to Neurons via Chemokine CCL2. <i>Neuron</i> , 2018, 100, 183-200.e8.	3.8	134
43	Lineage dynamics of murine pancreatic development at single-cell resolution. <i>Nature Communications</i> , 2018, 9, 3922.	5.8	137
44	Muscle Satellite Cell Cross-Talk with a Vascular Niche Maintains Quiescence via VEGF and Notch Signaling. <i>Cell Stem Cell</i> , 2018, 23, 530-543.e9.	5.2	223
45	Acquired cancer resistance to combination immunotherapy from transcriptional loss of class I HLA. <i>Nature Communications</i> , 2018, 9, 3868.	5.8	211
46	Neonatally imprinted stromal cell subsets induce tolerogenic dendritic cells in mesenteric lymph nodes. <i>Nature Communications</i> , 2018, 9, 3903.	5.8	69
47	Single-Cell RNA-Seq Uncovers a Robust Transcriptional Response to Morphine by Glia. <i>Cell Reports</i> , 2018, 24, 3619-3629.e4.	2.9	109
48	Disease-relevant transcriptional signatures identified in individual smooth muscle cells from healthy mouse vessels. <i>Nature Communications</i> , 2018, 9, 4567.	5.8	219
49	Large-scale reconstruction of cell lineages using single-cell readout of transcriptomes and CRISPR-Cas9 barcodes by scGESTALT. <i>Nature Protocols</i> , 2018, 13, 2685-2713.	5.5	55
50	Comparison of clustering tools in R for medium-sized 10x Genomics single-cell RNA-sequencing data. <i>F1000Research</i> , 2018, 7, 1297.	0.8	157
51	A Population of Navigator Neurons Is Essential for Olfactory Map Formation during the Critical Period. <i>Neuron</i> , 2018, 100, 1066-1082.e6.	3.8	28
52	High-Dimensional Analysis Delineates Myeloid and Lymphoid Compartment Remodeling during Successful Immune-Checkpoint Cancer Therapy. <i>Cell</i> , 2018, 175, 1014-1030.e19.	13.5	292
53	A Cancer Cell Program Promotes T Cell Exclusion and Resistance to Checkpoint Blockade. <i>Cell</i> , 2018, 175, 984-997.e24.	13.5	892
54	A single-cell survey of the human first-trimester placenta and decidua. <i>Science Advances</i> , 2018, 4, eaau4788.	4.7	282

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55	Quantitative assessment of cell population diversity in single-cell landscapes. <i>PLoS Biology</i> , 2018, 16, e2006687.	2.6	40
56	Paired-cell sequencing enables spatial gene expression mapping of liver endothelial cells. <i>Nature Biotechnology</i> , 2018, 36, 962-970.	9.4	262
57	Rapid CLIP dissociation from MHC II promotes an unusual antigen presentation pathway in autoimmunity. <i>Journal of Experimental Medicine</i> , 2018, 215, 2617-2635.	4.2	20
58	Single-cell analysis of progenitor cell dynamics and lineage specification in the human fetal kidney. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	130
59	clusterExperiment and RSEC: A Bioconductor package and framework for clustering of single-cell and other large gene expression datasets. <i>PLoS Computational Biology</i> , 2018, 14, e1006378.	1.5	48
60	Regulatory cocktail for dopaminergic neurons in a protovertebrate identified by whole-embryo single-cell transcriptomics. <i>Genes and Development</i> , 2018, 32, 1297-1302.	2.7	34
61	Single Cell and Open Chromatin Analysis Reveals Molecular Origin of Epidermal Cells of the Skin. <i>Developmental Cell</i> , 2018, 47, 21-37.e5.	3.1	56
62	Quantitative single-cell transcriptomics. <i>Briefings in Functional Genomics</i> , 2018, 17, 220-232.	1.3	50
63	Power in Numbers: Single-Cell RNA-Seq Strategies to Dissect Complex Tissues. <i>Annual Review of Genetics</i> , 2018, 52, 203-221.	3.2	94
64	Long-term pain relief in canine osteoarthritis by a single intra-articular injection of resiniferatoxin, a potent TRPV1 agonist. <i>Pain</i> , 2018, 159, 2105-2114.	2.0	52
65	Transcription Factor PROX1 Suppresses Notch Pathway Activation via the Nucleosome Remodeling and Deacetylase Complex in Colorectal Cancer Stemâ€like Cells. <i>Cancer Research</i> , 2018, 78, 5820-5832.	0.4	20
66	Experimental Considerations for Single-Cell RNA Sequencing Approaches. <i>Frontiers in Cell and Developmental Biology</i> , 2018, 6, 108.	1.8	152
67	Single-cell genomics to guide human stem cell and tissue engineering. <i>Nature Methods</i> , 2018, 15, 661-667.	9.0	52
68	Exploring the single-cell RNA-seq analysis landscape with the scRNA-tools database. <i>PLoS Computational Biology</i> , 2018, 14, e1006245.	1.5	222
69	Comparative transcriptomic analysis of hematopoietic system between human and mouse by Microwell-seq. <i>Cell Discovery</i> , 2018, 4, 34.	3.1	16
70	Single-cell RNA-seq reveals hidden transcriptional variation in malaria parasites. <i>ELife</i> , 2018, 7, .	2.8	171
71	Toward mapping the human body at a cellular resolution. <i>Molecular Biology of the Cell</i> , 2018, 29, 1779-1785.	0.9	11
72	Elucidating T Cell Activation-Dependent Mechanisms for Bifurcation of Regulatory and Effector T Cell Differentiation by Multidimensional and Single-Cell Analysis. <i>Frontiers in Immunology</i> , 2018, 9, 1444.	2.2	12

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73	Sensory Neuron Diversity in the Inner Ear Is Shaped by Activity. <i>Cell</i> , 2018, 174, 1229-1246.e17.	13.5	309
74	Hair Cell Mechanotransduction Regulates Spontaneous Activity and Spiral Ganglion Subtype Specification in the Auditory System. <i>Cell</i> , 2018, 174, 1247-1263.e15.	13.5	259
75	Dissection of progenitor compartments resolves developmental trajectories in B-lymphopoiesis. <i>Journal of Experimental Medicine</i> , 2018, 215, 1947-1963.	4.2	20
76	Single-Cell RNA Sequencing: A New Window into Cell Scale Dynamics. <i>Biophysical Journal</i> , 2018, 115, 429-435.	0.2	9
77	Sensitive and powerful single-cell RNA sequencing using mcSCR-seq. <i>Nature Communications</i> , 2018, 9, 2937.	5.8	183
78	Single-Cell Transcriptomics of a Human Kidney Allograft Biopsy Specimen Defines a Diverse Inflammatory Response. <i>Journal of the American Society of Nephrology: JASN</i> , 2018, 29, 2069-2080.	3.0	281
79	Large-Scale Single-Cell RNA-Seq Reveals Molecular Signatures of Heterogeneous Populations of Human Induced Pluripotent Stem Cell-Derived Endothelial Cells. <i>Circulation Research</i> , 2018, 123, 443-450.	2.0	110
80	NeuroSystematics and Periodic System of Neurons: Model vs Reference Species at Single-Cell Resolution. <i>ACS Chemical Neuroscience</i> , 2018, 9, 1884-1903.	1.7	31
81	Single cell transcriptomics in neuroscience: cell classification and beyond. <i>Current Opinion in Neurobiology</i> , 2018, 50, 242-249.	2.0	71
82	Single-Cell RNA Sequencing of Lymph Node Stromal Cells Reveals Niche-Associated Heterogeneity. <i>Immunity</i> , 2018, 48, 1014-1028.e6.	6.6	339
83	Boosting the power of single-cell analysis. <i>Nature Biotechnology</i> , 2018, 36, 408-409.	9.4	43
84	Co-expression in Single-Cell Analysis: Saving Grace or Original Sin?. <i>Trends in Genetics</i> , 2018, 34, 823-831.	2.9	34
85	Integrated measurement of intracellular proteins and transcripts in single cells. <i>Lab on A Chip</i> , 2018, 18, 3251-3262.	3.1	16
86	Neuro-evo-devo in the single cell sequencing era. <i>Current Opinion in Systems Biology</i> , 2018, 11, 32-40.	1.3	9
87	Allergic inflammatory memory in human respiratory epithelial progenitor cells. <i>Nature</i> , 2018, 560, 649-654.	13.7	368
88	A Single-Cell Transcriptomic Atlas of Thymus Organogenesis Resolves Cell Types and Developmental Maturation. <i>Immunity</i> , 2018, 48, 1258-1270.e6.	6.6	147
89	Computational approaches for high-throughput single-cell data analysis. <i>FEBS Journal</i> , 2019, 286, 1451-1467.	2.2	33
90	Functional Genomics via CRISPR-Cas. <i>Journal of Molecular Biology</i> , 2019, 431, 48-65.	2.0	62

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91	Cross-Species Analysis of Single-Cell Transcriptomic Data. <i>Frontiers in Cell and Developmental Biology</i> , 2019, 7, 175.	1.8	71
92	Molecular mechanisms of lineage decisions in metabolite-specific T cells. <i>Nature Immunology</i> , 2019, 20, 1244-1255.	7.0	74
93	Immuno-PET identifies the myeloid compartment as a key contributor to the outcome of the antitumor response under PD-1 blockade. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 16971-16980.	3.3	92
94	Locally renewing resident synovial macrophages provide a protective barrier for the joint. <i>Nature</i> , 2019, 572, 670-675.	13.7	345
95	Single-Cell Survey of Human Lymphatics Unveils Marked Endothelial Cell Heterogeneity and Mechanisms of Homing for Neutrophils. <i>Immunity</i> , 2019, 51, 561-572.e5.	6.6	149
96	Landscape of Intercellular Crosstalk in Healthy and NASH Liver Revealed by Single-Cell Secretome Gene Analysis. <i>Molecular Cell</i> , 2019, 75, 644-660.e5.	4.5	488
97	GATA2 Promotes Hematopoietic Development and Represses Cardiac Differentiation of Human Mesoderm. <i>Stem Cell Reports</i> , 2019, 13, 515-529.	2.3	27
98	A single-nuclei RNA sequencing study of Mendelian and sporadic AD in the human brain. <i>Alzheimer's Research and Therapy</i> , 2019, 11, 71.	3.0	131
99	BBKNN: fast batch alignment of single cell transcriptomes. <i>Bioinformatics</i> , 2020, 36, 964-965.	1.8	517
100	BERMUDA: a novel deep transfer learning method for single-cell RNA sequencing batch correction reveals hidden high-resolution cellular subtypes. <i>Genome Biology</i> , 2019, 20, 165.	3.8	94
101	Single-cell analysis reveals fibroblast heterogeneity and myofibroblasts in systemic sclerosis-associated interstitial lung disease. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 1379-1387.	0.5	178
102	Multimodal single-cell approaches shed light on T cell heterogeneity. <i>Current Opinion in Immunology</i> , 2019, 61, 17-25.	2.4	13
103	Single-cell RNA sequencing reveals cell type-specific HPV expression in hyperplastic skin lesions. <i>Virology</i> , 2019, 537, 14-19.	1.1	19
104	Single cell transcriptome analysis of developing arcuate nucleus neurons uncovers their key developmental regulators. <i>Nature Communications</i> , 2019, 10, 3696.	5.8	49
105	A general approach for detecting expressed mutations in AML cells using single cell RNA-sequencing. <i>Nature Communications</i> , 2019, 10, 3660.	5.8	147
106	scAlign: a tool for alignment, integration, and rare cell identification from scRNA-seq data. <i>Genome Biology</i> , 2019, 20, 166.	3.8	78
107	m6A RNA Methylation Maintains Hematopoietic Stem Cell Identity and Symmetric Commitment. <i>Cell Reports</i> , 2019, 28, 1703-1716.e6.	2.9	117
108	TrxG Complex Catalytic and Non-catalytic Activity Play Distinct Roles in Pancreas Progenitor Specification and Differentiation. <i>Cell Reports</i> , 2019, 28, 1830-1844.e6.	2.9	10

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109	A Thpok-Directed Transcriptional Circuitry Promotes Bcl6 and Maf Expression to Orchestrate T Follicular Helper Differentiation. <i>Immunity</i> , 2019, 51, 465-478.e6.	6.6	30
110	Defining the Identity and Dynamics of Adult Gastric Isthmus Stem Cells. <i>Cell Stem Cell</i> , 2019, 25, 342-356.e7.	5.2	97
111	An Nfil3- <i>Zeb2</i> -Id2 pathway imposes Irf8 enhancer switching during cDC1 development. <i>Nature Immunology</i> , 2019, 20, 1174-1185.	7.0	80
112	The E3 ubiquitin ligase SPOP controls resolution of systemic inflammation by triggering MYD88 degradation. <i>Nature Immunology</i> , 2019, 20, 1196-1207.	7.0	42
113	The Malaria Cell Atlas: Single parasite transcriptomes across the complete <i>Plasmodium</i> life cycle. <i>Science</i> , 2019, 365, .	6.0	198
114	A single-cell transcriptome atlas of the adult human retina. <i>EMBO Journal</i> , 2019, 38, e100811.	3.5	185
115	Innate Immune Response to Influenza Virus at Single-Cell Resolution in Human Epithelial Cells Revealed Paracrine Induction of Interferon Lambda 1. <i>Journal of Virology</i> , 2019, 93, .	1.5	65
116	SingleCellNet: A Computational Tool to Classify Single Cell RNA-Seq Data Across Platforms and Across Species. <i>Cell Systems</i> , 2019, 9, 207-213.e2.	2.9	225
117	scGen predicts single-cell perturbation responses. <i>Nature Methods</i> , 2019, 16, 715-721.	9.0	290
118	Nonparametric expression analysis using inferential replicate counts. <i>Nucleic Acids Research</i> , 2019, 47, e105-e105.	6.5	54
119	LTMG: a novel statistical modeling of transcriptional expression states in single-cell RNA-Seq data. <i>Nucleic Acids Research</i> , 2019, 47, e111-e111.	6.5	46
120	Alterations in Polyamine Metabolism in Patients With Lymphangiomyomatosis and Tuberous Sclerosis Complex 2-Deficient Cells. <i>Chest</i> , 2019, 156, 1137-1148.	0.4	18
121	<i>Nkx2-5</i> defines a subpopulation of pacemaker cells and is essential for the physiological function of the sinoatrial node in mice. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	23
122	Single-cell RNA Sequencing and Analysis of Human Pancreatic Islets. <i>Journal of Visualized Experiments</i> , 2019, , .	0.2	11
123	Single-cell transcriptional logic of cell-fate specification and axon guidance in early born retinal neurons. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	48
124	Systematic Immunotherapy Target Discovery Using Genome-Scale In Vivo CRISPR Screens in CD8+ T Cells. <i>Cell</i> , 2019, 178, 1189-1204.e23.	13.5	189
125	Glucose-Dependent Insulinotropic Polypeptide Receptor-Expressing Cells in the Hypothalamus Regulate Food Intake. <i>Cell Metabolism</i> , 2019, 30, 987-996.e6.	7.2	171
126	CONFINED: distinguishing biological from technical sources of variation by leveraging multiple methylation datasets. <i>Genome Biology</i> , 2019, 20, 138.	3.8	6

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127	Joint analysis of heterogeneous single-cell RNA-seq dataset collections. <i>Nature Methods</i> , 2019, 16, 695-698.	9.0	219
128	Single-cell reconstruction of follicular remodeling in the human adult ovary. <i>Nature Communications</i> , 2019, 10, 3164.	5.8	132
129	Canine osteosarcoma genome sequencing identifies recurrent mutations in DMD and the histone methyltransferase gene SETD2. <i>Communications Biology</i> , 2019, 2, 266.	2.0	77
130	A Tool for Visualization and Analysis of Single-Cell RNA-Seq Data Based on Text Mining. <i>Frontiers in Genetics</i> , 2019, 10, 734.	1.1	15
131	The Unmixing Problem: A Guide to Applying Single-Cell RNA Sequencing to Bone. <i>Journal of Bone and Mineral Research</i> , 2019, 34, 1207-1219.	3.1	34
132	A statistical simulator scDesign for rational scRNA-seq experimental design. <i>Bioinformatics</i> , 2019, 35, i41-i50.	1.8	48
133	Minnow: a principled framework for rapid simulation of dscRNA-seq data at the read level. <i>Bioinformatics</i> , 2019, 35, i136-i144.	1.8	17
134	Deconvolution of autoencoders to learn biological regulatory modules from single cell mRNA sequencing data. <i>BMC Bioinformatics</i> , 2019, 20, 379.	1.2	22
135	scOrange—a tool for hands-on training of concepts from single-cell data analytics. <i>Bioinformatics</i> , 2019, 35, i4-i12.	1.8	8
136	Single-Cell Signature Explorer for comprehensive visualization of single cell signatures across scRNA-seq datasets. <i>Nucleic Acids Research</i> , 2019, 47, e133-e133.	6.5	96
137	Single-Cell Analysis Reveals Regional Reprogramming During Adaptation to Massive Small Bowel Resection in Mice. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2019, 8, 407-426.	2.3	24
138	Transcriptomic Profiling of the Developing Cardiac Conduction System at Single-Cell Resolution. <i>Circulation Research</i> , 2019, 125, 379-397.	2.0	120
139	scSLAM-seq reveals core features of transcription dynamics in single cells. <i>Nature</i> , 2019, 571, 419-423.	13.7	153
140	Comprehensive single-cell transcriptome lineages of a proto-vertebrate. <i>Nature</i> , 2019, 571, 349-354.	13.7	162
141	Molecular Mechanisms Driving Switch Behavior in Xylem Cell Differentiation. <i>Cell Reports</i> , 2019, 28, 342-351.e4.	2.9	61
142	The Cytokine TNF Promotes Transcription Factor SREBP Activity and Binding to Inflammatory Genes to Activate Macrophages and Limit Tissue Repair. <i>Immunity</i> , 2019, 51, 241-257.e9.	6.6	91
143	A Single-Cell Transcriptomic Atlas of Human Neocortical Development during Mid-gestation. <i>Neuron</i> , 2019, 103, 785-801.e8.	3.8	361
144	Generation of Human PSC-Derived Kidney Organoids with Patterned Nephron Segments and a De Novo Vascular Network. <i>Cell Stem Cell</i> , 2019, 25, 373-387.e9.	5.2	219

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145	Genetic mapping of cell type specificity for complex traits. Nature Communications, 2019, 10, 3222.	5.8	212
146	Estimation of immune cell content in tumor using single-cell RNA-seq reference data. BMC Cancer, 2019, 19, 715.	1.1	32
147	Predicting bacterial infection outcomes using single cell RNA-sequencing analysis of human immune cells. Nature Communications, 2019, 10, 3266.	5.8	62
148	Early Detection of Peripheral Blood Cell Signature in Children Developing \hat{I}^2 -Cell Autoimmunity at a Young Age. Diabetes, 2019, 68, 2024-2034.	0.3	37
149	Efficient CD4Cre-Mediated Conditional KRas Expression in Alveolar Macrophages and Alveolar Epithelial Cells Causes Fatal Hyperproliferative Pneumonitis. Journal of Immunology, 2019, 203, 1208-1217.	0.4	2
150	Activation Dynamics and Immunoglobulin Evolution of Pre-existing and Newly Generated Human Memory B cell Responses to Influenza Hemagglutinin. Immunity, 2019, 51, 398-410.e5.	6.6	107
151	Single-cell analysis of cardiogenesis reveals basis for organ-level developmental defects. Nature, 2019, 572, 120-124.	13.7	197
152	Resolving medulloblastoma cellular architecture by single-cell genomics. Nature, 2019, 572, 74-79.	13.7	273
153	Intra- and Inter-cellular Rewiring of the Human Colon during Ulcerative Colitis. Cell, 2019, 178, 714-730.e22.	13.5	806
154	Stem cell differentiation trajectories in <i>Hydra</i> resolved at single-cell resolution. Science, 2019, 365, .	6.0	253
155	SCINA: Semi-Supervised Analysis of Single Cells in Silico. Genes, 2019, 10, 531.	1.0	150
156	DMSO cryopreservation is the method of choice to preserve cells for droplet-based single-cell RNA sequencing. Scientific Reports, 2019, 9, 10699.	1.6	78
157	Single-Cell RNA-Sequencing and Metabolomics Analyses Reveal the Contribution of Perivascular Adipose Tissue Stem Cells to Vascular Remodeling. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 2049-2066.	1.1	72
158	Understanding the kidney one cell at a time. Kidney International, 2019, 96, 862-870.	2.6	45
159	Computational approaches for characterizing the tumor immune microenvironment. Immunology, 2019, 158, 70-84.	2.0	30
160	Meeting the Challenges of High-Dimensional Single-Cell Data Analysis in Immunology. Frontiers in Immunology, 2019, 10, 1515.	2.2	67
161	Atheroprotective roles of smooth muscle cell phenotypic modulation and the TCF21 disease gene as revealed by single-cell analysis. Nature Medicine, 2019, 25, 1280-1289.	15.2	494
162	Clonal replacement of tumor-specific T cells following PD-1 blockade. Nature Medicine, 2019, 25, 1251-1259.	15.2	974

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163	Development of a Chimeric Model to Study and Manipulate Human Microglia In Vivo. <i>Neuron</i> , 2019, 103, 1016-1033.e10.	3.8	218
164	ACTINN: automated identification of cell types in single cell RNA sequencing. <i>Bioinformatics</i> , 2020, 36, 533-538.	1.8	140
165	Epigenomics and Single-Cell Sequencing Define a Developmental Hierarchy in Langerhans Cell Histiocytosis. <i>Cancer Discovery</i> , 2019, 9, 1406-1421.	7.7	42
166	RhoA in tyrosine hydroxylase neurones regulates food intake and body weight via altered sensitivity to peripheral hormones. <i>Journal of Neuroendocrinology</i> , 2019, 31, e12761.	1.2	10
167	Neutrophils Driving Unconventional T Cells Mediate Resistance against Murine Sarcomas and Selected Human Tumors. <i>Cell</i> , 2019, 178, 346-360.e24.	13.5	176
168	c-Kit-positive ILC2s exhibit an ILC3-like signature that may contribute to IL-17-mediated pathologies. <i>Nature Immunology</i> , 2019, 20, 992-1003.	7.0	142
169	Aberrant fucosylation enables breast cancer clusterin to interact with dendritic cell-specific ICAM-grabbing non-integrin (DC-SIGN). <i>OncoImmunology</i> , 2019, 8, e1629257.	2.1	18
170	Matrix-metalloproteinase expression and gelatinase activity in the avian retina and their influence on Müller glia proliferation. <i>Experimental Neurology</i> , 2019, 320, 112984.	2.0	24
171	Innate $\gamma\delta$ T Cells Mediate Antitumor Immunity by Orchestrating Immunogenic Macrophage Programming. <i>Cancer Discovery</i> , 2019, 9, 1288-1305.	7.7	19
172	Identification of Genes With Enriched Expression in Early Developing Mouse Cone Photoreceptors. , 2019, 60, 2787.		23
173	Somatic mutations and cell identity linked by Genotyping of Transcriptomes. <i>Nature</i> , 2019, 571, 355-360.	13.7	206
174	Inadequate DNA Damage Repair Promotes Mammary Transdifferentiation, Leading to BRCA1 Breast Cancer. <i>Cell</i> , 2019, 178, 135-151.e19.	13.5	60
175	Context-Specific Transcription Factor Functions Regulate Epigenomic and Transcriptional Dynamics during Cardiac Reprogramming. <i>Cell Stem Cell</i> , 2019, 25, 87-102.e9.	5.2	89
176	Single-cell RNA-seq highlights intra-tumoral heterogeneity and malignant progression in pancreatic ductal adenocarcinoma. <i>Cell Research</i> , 2019, 29, 725-738.	5.7	661
177	Nuclei multiplexing with barcoded antibodies for single-nucleus genomics. <i>Nature Communications</i> , 2019, 10, 2907.	5.8	117
178	Concepts and limitations for learning developmental trajectories from single cell genomics. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	177
179	Accurate estimation of cell-type composition from gene expression data. <i>Nature Communications</i> , 2019, 10, 2975.	5.8	125
180	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

#	ARTICLE	IF	CITATIONS
181	Single-cell RNA-sequencing of herpes simplex virus 1-infected cells connects NRF2 activation to an antiviral program. <i>Nature Communications</i> , 2019, 10, 4878.	5.8	96
182	Activation of Hedgehog Signaling Promotes Development of Mouse and Human Enteric Neural Crest Cells, Based on Single-Cell Transcriptome Analyses. <i>Gastroenterology</i> , 2019, 157, 1556-1571.e5.	0.6	31
183	PlanExp: intuitive integration of complex RNA-seq datasets with planarian omics resources. <i>Bioinformatics</i> , 2020, 36, 1889-1895.	1.8	12
184	Multimodal Analysis of Cell Types in a Hypothalamic Node Controlling Social Behavior. <i>Cell</i> , 2019, 179, 713-728.e17.	13.5	186
185	Single-Cell Analysis Reveals Regulatory Gene Expression Dynamics Leading to Lineage Commitment in Early T Cell Development. <i>Cell Systems</i> , 2019, 9, 321-337.e9.	2.9	80
186	Calcitonin Gene-Related Peptide Negatively Regulates Alarmin-Driven Type 2 Innate Lymphoid Cell Responses. <i>Immunity</i> , 2019, 51, 709-723.e6.	6.6	144
187	Characterization of dendritic cell subtypes in human cord blood by single-cell sequencing. <i>Biophysics Reports</i> , 2019, 5, 199-208.	0.2	9
188	Reconstruction of the Global Neural Crest Gene Regulatory Network In Vivo. <i>Developmental Cell</i> , 2019, 51, 255-276.e7.	3.1	108
189	CD24: a marker of granulosa cell subpopulation and a mediator of ovulation. <i>Cell Death and Disease</i> , 2019, 10, 791.	2.7	19
190	Genetic Control of Expression and Splicing in Developing Human Brain Informs Disease Mechanisms. <i>Cell</i> , 2019, 179, 750-771.e22.	13.5	174
191	Transcriptional Atlas of Intestinal Immune Cells Reveals that Neuropeptide \pm -CGRP Modulates Group 2 Innate Lymphoid Cell Responses. <i>Immunity</i> , 2019, 51, 696-708.e9.	6.6	154
192	Single-Cell RNA Sequencing Resolves Spatiotemporal Development of Pre-thymic Lymphoid Progenitors and Thymus Organogenesis in Human Embryos. <i>Immunity</i> , 2019, 51, 930-948.e6.	6.6	97
193	Myo-REG: A Portal for Signaling Interactions in Muscle Regeneration. <i>Frontiers in Physiology</i> , 2019, 10, 1216.	1.3	8
194	The human body at cellular resolution: the NIH Human Biomolecular Atlas Program. <i>Nature</i> , 2019, 574, 187-192.	13.7	393
195	Single-cell RNA sequencing reveals regulatory mechanism for trophoblast cell-fate divergence in human peri-implantation conceptuses. <i>PLoS Biology</i> , 2019, 17, e3000187.	2.6	60
196	Single-cell RNA-seq analysis of Mesp1-induced skeletal myogenic development. <i>Biochemical and Biophysical Research Communications</i> , 2019, 520, 284-290.	1.0	5
197	The brain-placental axis: Therapeutic and pharmacological relevancy to pregnancy. <i>Pharmacological Research</i> , 2019, 149, 104468.	3.1	31
198	Interleukin-36 β -producing macrophages drive IL-17-mediated fibrosis. <i>Science Immunology</i> , 2019, 4, .	5.6	123

#	ARTICLE	IF	CITATIONS
199	Machine Learning in Biology and Medicine. <i>Advances in Molecular Pathology</i> , 2019, 2, 143-152.	0.2	13
200	MetaCell: analysis of single-cell RNA-seq data using K-nn graph partitions. <i>Genome Biology</i> , 2019, 20, 206.	3.8	218
201	Resolving the fibrotic niche of human liver cirrhosis at single-cell level. <i>Nature</i> , 2019, 575, 512-518.	13.7	946
202	Oligodendrocyte Intrinsic miR-27a Controls Myelination and Remyelination. <i>Cell Reports</i> , 2019, 29, 904-919.e9.	2.9	40
203	Systems-level network modeling of Small Cell Lung Cancer subtypes identifies master regulators and destabilizers. <i>PLoS Computational Biology</i> , 2019, 15, e1007343.	1.5	77
204	Single-cell transcriptomics of the human retinal pigment epithelium and choroid in health and macular degeneration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24100-24107.	3.3	234
205	Clonally Expanded T Cells Reveal Immunogenicity of Rhabdoid Tumors. <i>Cancer Cell</i> , 2019, 36, 597-612.e8.	7.7	100
206	UCSC Genome Browser enters 20th year. <i>Nucleic Acids Research</i> , 2020, 48, D756-D761.	6.5	138
207	Single-Cell Sequencing of Mouse Heart Immune Infiltrate in Pressure Overload-Driven Heart Failure Reveals Extent of Immune Activation. <i>Circulation</i> , 2019, 140, 2089-2107.	1.6	212
208	UM171 induces a homeostatic inflammatory-detoxification response supporting human HSC self-renewal. <i>PLoS ONE</i> , 2019, 14, e0224900.	1.1	31
209	In vitro culture of cynomolgus monkey embryos beyond early gastrulation. <i>Science</i> , 2019, 366, .	6.0	149
210	A Subset of Olfactory Sensory Neurons Express Forkhead Box J1-Driven eGFP. <i>Chemical Senses</i> , 2019, 44, 663-671.	1.1	4
211	Omics Approaches to Understanding Muscle Biology. , 2019, , .		3
212	Single-Cell Profiling Reveals Sex, Lineage, and Regional Diversity in the Mouse Kidney. <i>Developmental Cell</i> , 2019, 51, 399-413.e7.	3.1	266
213	Comparison of whole blood and spleen transcriptional signatures over the course of an experimental malaria infection. <i>Scientific Reports</i> , 2019, 9, 15853.	1.6	6
214	Gene Expression-Based Identification of Antigen-Responsive CD8+ T Cells on a Single-Cell Level. <i>Frontiers in Immunology</i> , 2019, 10, 2568.	2.2	25
215	Activity of caspase-8 determines plasticity between cell death pathways. <i>Nature</i> , 2019, 575, 679-682.	13.7	215
216	Subsets of mononuclear phagocytes are enriched in the inflamed colons of patients with IBD. <i>BMC Immunology</i> , 2019, 20, 42.	0.9	47

#	ARTICLE	IF	CITATIONS
217	Quantifying pluripotency landscape of cell differentiation from scRNA-seq data by continuous birth-death process. <i>PLoS Computational Biology</i> , 2019, 15, e1007488.	1.5	11
218	B Cells and T Follicular Helper Cells Mediate Response to Checkpoint Inhibitors in High Mutation Burden Mouse Models of Breast Cancer. <i>Cell</i> , 2019, 179, 1191-1206.e21.	13.5	291
219	A Bayesian mixture model for the analysis of allelic expression in single cells. <i>Nature Communications</i> , 2019, 10, 5188.	5.8	18
220	Single-cell transcriptomics reveals expansion of cytotoxic CD4 T cells in supercentenarians. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24242-24251.	3.3	215
221	Dissecting primate early post-implantation development using long-term in vitro embryo culture. <i>Science</i> , 2019, 366, .	6.0	137
222	Platelet regulation of myeloid suppressor of cytokine signaling 3 accelerates atherosclerosis. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	85
223	Building gene regulatory networks from scATAC-seq and scRNA-seq using Linked Self Organizing Maps. <i>PLoS Computational Biology</i> , 2019, 15, e1006555.	1.5	56
224	DoubletDecon: Deconvoluting Doublets from Single-Cell RNA-Sequencing Data. <i>Cell Reports</i> , 2019, 29, 1718-1727.e8.	2.9	134
225	Photic generation of 11-cis-retinal in bovine retinal pigment epithelium. <i>Journal of Biological Chemistry</i> , 2019, 294, 19137-19154.	1.6	33
226	Mucosal Profiling of Pediatric-Onset Colitis and IBD Reveals Common Pathogenics and Therapeutic Pathways. <i>Cell</i> , 2019, 179, 1160-1176.e24.	13.5	163
227	Serotonin is essential for eye regeneration in planaria <i>Schmidtea mediterranea</i> . <i>FEBS Letters</i> , 2019, 593, 3198-3209.	1.3	9
228	Valid Post-clustering Differential Analysis for Single-Cell RNA-Seq. <i>Cell Systems</i> , 2019, 9, 383-392.e6.	2.9	45
229	Stem-cell-derived human microglia transplanted in mouse brain to study human disease. <i>Nature Neuroscience</i> , 2019, 22, 2111-2116.	7.1	176
230	Single-cell study of neural stem cells derived from human iPSCs reveals distinct progenitor populations with neurogenic and gliogenic potential. <i>Genes To Cells</i> , 2019, 24, 836-847.	0.5	24
231	RBPJ-dependent Notch signaling initiates the T cell program in a subset of thymus-seeding progenitors. <i>Nature Immunology</i> , 2019, 20, 1456-1468.	7.0	61
232	Guidelines for the use of flow cytometry and cell sorting in immunological studies (second edition). <i>European Journal of Immunology</i> , 2019, 49, 1457-1973.	1.6	766
233	Biological process activity transformation of single cell gene expression for cross-species alignment. <i>Nature Communications</i> , 2019, 10, 4899.	5.8	29
234	Induction of metabolic quiescence defines the transitional to follicular B cell switch. <i>Science Signaling</i> , 2019, 12, .	1.6	35

#	ARTICLE	IF	CITATIONS
235	Tissue-specific deconvolution of immune cell composition by integrating bulk and single-cell transcriptomes. <i>Bioinformatics</i> , 2020, 36, 819-827.	1.8	13
236	An In Vitro Human Segmentation Clock Model Derived from Embryonic Stem Cells. <i>Cell Reports</i> , 2019, 28, 2247-2255.e5.	2.9	57
237	Network modeling of single-cell omics data: challenges, opportunities, and progresses. <i>Emerging Topics in Life Sciences</i> , 2019, 3, 379-398.	1.1	48
238	Current best practices in single-cell RNA-seq analysis: a tutorial. <i>Molecular Systems Biology</i> , 2019, 15, e8746.	3.2	1,322
239	B1 oligomerization regulates PML nuclear body biogenesis and leukemogenesis. <i>Nature Communications</i> , 2019, 10, 3789.	5.8	30
240	The cross-talk between TGF- β 2 and PDGFR β signaling pathways regulates stromal fibro/adipogenic progenitors' fate. <i>Journal of Cell Science</i> , 2019, 132, .	1.2	70
241	Conserved cell types with divergent features in human versus mouse cortex. <i>Nature</i> , 2019, 573, 61-68.	13.7	1,198
242	Ageing promotes reorganization of the CD4 T cell landscape toward extreme regulatory and effector phenotypes. <i>Science Advances</i> , 2019, 5, eaaw8330.	4.7	182
243	Peripheral blood DNA methylation differences in twin pairs discordant for Alzheimer's disease. <i>Clinical Epigenetics</i> , 2019, 11, 130.	1.8	29
244	Unified single-cell analysis of testis gene regulation and pathology in five mouse strains. <i>ELife</i> , 2019, 8, .	2.8	102
245	Defining HLA-II Ligand Processing and Binding Rules with Mass Spectrometry Enhances Cancer Epitope Prediction. <i>Immunity</i> , 2019, 51, 766-779.e17.	6.6	187
246	Nucleome Dynamics during Retinal Development. <i>Neuron</i> , 2019, 104, 512-528.e11.	3.8	70
247	Regulatory T cells in skin are uniquely poised to suppress profibrotic immune responses. <i>Science Immunology</i> , 2019, 4, .	5.6	78
248	Spatial and temporal tools for building a human cell atlas. <i>Molecular Biology of the Cell</i> , 2019, 30, 2435-2438.	0.9	3
249	Single-Cell Transcriptomic Map of the Human and Mouse Bladders. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 2159-2176.	3.0	90
250	Single-cell transcriptomics reveals multi-step adaptations to endocrine therapy. <i>Nature Communications</i> , 2019, 10, 3840.	5.8	93
251	A large pool of actively cycling progenitors orchestrates self-renewal and injury repair of an ectodermal appendage. <i>Nature Cell Biology</i> , 2019, 21, 1102-1112.	4.6	67
252	A pooled single-cell genetic screen identifies regulatory checkpoints in the continuum of the epithelial-to-mesenchymal transition. <i>Nature Genetics</i> , 2019, 51, 1389-1398.	9.4	150

#	ARTICLE	IF	CITATIONS
253	Single Cell Explorer, collaboration-driven tools to leverage large-scale single cell RNA-seq data. BMC Genomics, 2019, 20, 676.	1.2	20
254	PanoView: An iterative clustering method for single-cell RNA sequencing data. PLoS Computational Biology, 2019, 15, e1007040.	1.5	16
255	Single-Cell Analysis of Human Mononuclear Phagocytes Reveals Subset-Defining Markers and Identifies Circulating Inflammatory Dendritic Cells. Immunity, 2019, 51, 573-589.e8.	6.6	336
256	Complex Oscillatory Waves Emerging from Cortical Organoids Model Early Human Brain Network Development. Cell Stem Cell, 2019, 25, 558-569.e7.	5.2	520
257	Non-classical tissue monocytes and two functionally distinct populations of interstitial macrophages populate the mouse lung. Nature Communications, 2019, 10, 3964.	5.8	206
258	Heterogeneity of human bone marrow and blood natural killer cells defined by single-cell transcriptome. Nature Communications, 2019, 10, 3931.	5.8	178
259	Self-organizing neuruloids model developmental aspects of Huntingtonâ€™s disease in the ectodermal compartment. Nature Biotechnology, 2019, 37, 1198-1208.	9.4	116
260	Probabilistic cell-type assignment of single-cell RNA-seq for tumor microenvironment profiling. Nature Methods, 2019, 16, 1007-1015.	9.0	241
261	Spectrum: fast density-aware spectral clustering for single and multi-omic data. Bioinformatics, 2020, 36, 1159-1166.	1.8	57
262	Expression of Bitter Taste Receptors and Solitary Chemosensory Cell Markers in the Human Sinonasal Cavity. Chemical Senses, 2019, 44, 483-495.	1.1	17
263	rCASC: reproducible classification analysis of single-cell sequencing data. GigaScience, 2019, 8, .	3.3	26
264	Machine learning predicts putative hematopoietic stem cells within large single-cell transcriptomics data sets. Experimental Hematology, 2019, 78, 11-20.	0.2	39
265	Controlled modelling of human epiblast and amnion development using stem cells. Nature, 2019, 573, 421-425.	13.7	338
266	ascend: R package for analysis of single-cell RNA-seq data. GigaScience, 2019, 8, .	3.3	36
267	A comparison of automatic cell identification methods for single-cell RNA sequencing data. Genome Biology, 2019, 20, 194.	3.8	402
268	Next-generation computational tools for interrogating cancer immunity. Nature Reviews Genetics, 2019, 20, 724-746.	7.7	131
269	B cells sustain inflammation and predict response to immune checkpoint blockade in human melanoma. Nature Communications, 2019, 10, 4186.	5.8	236
270	Interleukin 1 beta and Matrix Metalloproteinase 3 Contribute to Development of Epidermal Growth Factor Receptorâ€“Dependent Serrated Polyps in Mouse Cecum. Gastroenterology, 2019, 157, 1572-1583.e8.	0.6	7

#	ARTICLE	IF	CITATIONS
271	Sour Sensing from the Tongue to the Brain. <i>Cell</i> , 2019, 179, 392-402.e15.	13.5	158
272	Digitaldsorter: Deep-Learning on scRNA-Seq to Deconvolute Gene Expression Data. <i>Frontiers in Genetics</i> , 2019, 10, 978.	1.1	22
273	Independent Component Analysis for Unraveling the Complexity of Cancer Omics Datasets. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4414.	1.8	62
274	Rapid Generation of Somatic Mouse Mosaics with Locus-Specific, Stably Integrated Transgenic Elements. <i>Cell</i> , 2019, 179, 251-267.e24.	13.5	40
275	Systems biology approaches to measure and model phenotypic heterogeneity in cancer. <i>Current Opinion in Systems Biology</i> , 2019, 17, 35-40.	1.3	17
276	MGKA: A genetic algorithm-based clustering technique for genomic data. , 2019, , .		4
277	Adult bone marrow progenitors become decidual cells and contribute to embryo implantation and pregnancy. <i>PLoS Biology</i> , 2019, 17, e3000421.	2.6	47
278	Seuratâ€™s Dots: A Shot Heard â€™Round the Art Worldâ€™ Fired by an Artist, Inspired by a Scientist. <i>Cell</i> , 2019, 179, 46-50.	13.5	3
279	Cell type-specific transcriptional programs in mouse prefrontal cortex during adolescence and addiction. <i>Nature Communications</i> , 2019, 10, 4169.	5.8	100
280	Mapping human cell phenotypes to genotypes with single-cell genomics. <i>Science</i> , 2019, 365, 1401-1405.	6.0	71
281	The Phenotypes of Proliferating Glioblastoma Cells Reside on a Single Axis of Variation. <i>Cancer Discovery</i> , 2019, 9, 1708-1719.	7.7	205
282	Urothelial organoids originating from Cd49fhigh mouse stem cells display Notch-dependent differentiation capacity. <i>Nature Communications</i> , 2019, 10, 4407.	5.8	42
283	IKAPâ€™Identifying K mAjor cell Population groups in single-cell RNA-sequencing analysis. <i>GigaScience</i> , 2019, 8, .	3.3	16
284	Latent cellular analysis robustly reveals subtle diversity in large-scale single-cell RNA-seq data. <i>Nucleic Acids Research</i> , 2019, 47, e143-e143.	6.5	26
285	An Efficient and Flexible Method for Deconvoluting Bulk RNA-Seq Data with Single-Cell RNA-Seq Data. <i>Cells</i> , 2019, 8, 1161.	1.8	17
286	Tumor Cell Biodiversity Drives Microenvironmental Reprogramming in Liver Cancer. <i>Cancer Cell</i> , 2019, 36, 418-430.e6.	7.7	433
287	A novel approach to remove the batch effect of single-cell data. <i>Cell Discovery</i> , 2019, 5, 46.	3.1	37
288	Spatiotemporal immune zonation of the human kidney. <i>Science</i> , 2019, 365, 1461-1466.	6.0	281

#	ARTICLE	IF	CITATIONS
289	Single-cell transcriptomics reveal polyclonal memory T-cell responses in skin with positive abacavir patch test results. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 1413-1416.e7.	1.5	19
290	Diesel exhaust particles dysregulate multiple immunological pathways in murine macrophages: Lessons from microarray and scRNA-seq technologies. <i>Archives of Biochemistry and Biophysics</i> , 2019, 678, 108116.	1.4	10
291	Deciphering Brain Complexity Using Single-cell Sequencing. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 344-366.	3.0	52
292	bayNorm: Bayesian gene expression recovery, imputation and normalization for single-cell RNA-sequencing data. <i>Bioinformatics</i> , 2020, 36, 1174-1181.	1.8	79
293	CDK2 kinase activity is a regulator of male germ cell fate. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	15
294	Single-cell RNA-Sequencing in Neuroscience. <i>Neuroforum</i> , 2019, 25, 251-258.	0.2	2
295	Single-Cell Chromatin Analysis of Mammary Gland Development Reveals Cell-State Transcriptional Regulators and Lineage Relationships. <i>Cell Reports</i> , 2019, 29, 495-510.e6.	2.9	66
296	Meta-Analysis of Human and Mouse Biliary Epithelial Cell Gene Profiles. <i>Cells</i> , 2019, 8, 1117.	1.8	8
297	Memory CD4+ T cells are generated in the human fetal intestine. <i>Nature Immunology</i> , 2019, 20, 301-312.	7.0	132
298	Integrative single-cell analysis. <i>Nature Reviews Genetics</i> , 2019, 20, 257-272.	7.7	932
299	Single-cell transcriptomes reveal molecular specializations of neuronal cell types in the developing cerebellum. <i>Journal of Molecular Cell Biology</i> , 2019, 11, 636-648.	1.5	38
300	Neuronal cell types in the fly: single-cell anatomy meets single-cell genomics. <i>Current Opinion in Neurobiology</i> , 2019, 56, 125-134.	2.0	64
301	Homeostatic Control of Sebaceous Glands by Innate Lymphoid Cells Regulates Commensal Bacteria Equilibrium. <i>Cell</i> , 2019, 176, 982-997.e16.	13.5	159
302	Molecular Classification and Comparative Taxonomics of Foveal and Peripheral Cells in Primate Retina. <i>Cell</i> , 2019, 176, 1222-1237.e22.	13.5	347
303	Optimal-Transport Analysis of Single-Cell Gene Expression Identifies Developmental Trajectories in Reprogramming. <i>Cell</i> , 2019, 176, 928-943.e22.	13.5	411
304	High-Parameter Single-Cell Analysis. <i>Annual Review of Analytical Chemistry</i> , 2019, 12, 411-430.	2.8	23
305	Machine Learning and Integrative Analysis of Biomedical Big Data. <i>Genes</i> , 2019, 10, 87.	1.0	208
306	Revolutionizing Cancer Immunology: The Power of Next-Generation Sequencing Technologies. <i>Cancer Immunology Research</i> , 2019, 7, 168-173.	1.6	10

#	ARTICLE	IF	CITATIONS
307	Single-cell transcriptome provides novel insights into antler stem cells, a cell type capable of mammalian organ regeneration. <i>Functional and Integrative Genomics</i> , 2019, 19, 555-564.	1.4	8
308	The Short Chain Fatty Acid Butyrate Imprints an Antimicrobial Program in Macrophages. <i>Immunity</i> , 2019, 50, 432-445.e7.	6.6	612
309	Single-cell analysis reveals congruence between kidney organoids and human fetal kidney. <i>Genome Medicine</i> , 2019, 11, 3.	3.6	158
310	The Neonatal and Adult Human Testis Defined at the Single-Cell Level. <i>Cell Reports</i> , 2019, 26, 1501-1517.e4.	2.9	224
311	A single-cell transcriptomic atlas of the developing chicken limb. <i>BMC Genomics</i> , 2019, 20, 401.	1.2	38
312	Single-Cell RNA-seq: Introduction to Bioinformatics Analysis. <i>Current Protocols in Molecular Biology</i> , 2019, 127, e92.	2.9	10
313	Benchmarking single cell RNA-sequencing analysis pipelines using mixture control experiments. <i>Nature Methods</i> , 2019, 16, 479-487.	9.0	259
314	Single cell RNA-seq in the sea urchin embryo show marked cell-type specificity in the Delta/Notch pathway. <i>Molecular Reproduction and Development</i> , 2019, 86, 931-934.	1.0	14
315	Myc and Dnmt1 impede the pluripotent to totipotent state transition in embryonic stem cells. <i>Nature Cell Biology</i> , 2019, 21, 835-844.	4.6	82
316	Single-cell RNA-seq reveals TOX as a key regulator of CD8+ T cell persistence in chronic infection. <i>Nature Immunology</i> , 2019, 20, 890-901.	7.0	361
317	A cellular census of human lungs identifies novel cell states in health and in asthma. <i>Nature Medicine</i> , 2019, 25, 1153-1163.	15.2	631
318	Defective Tmprss3-Associated Hair Cell Degeneration in Inner Ear Organoids. <i>Stem Cell Reports</i> , 2019, 13, 147-162.	2.3	52
319	MULTI-seq: sample multiplexing for single-cell RNA sequencing using lipid-tagged indices. <i>Nature Methods</i> , 2019, 16, 619-626.	9.0	421
320	Single-Cell RNA Sequencing-Based Computational Analysis to Describe Disease Heterogeneity. <i>Frontiers in Genetics</i> , 2019, 10, 629.	1.1	20
321	Fc μ r regulates mononuclear phagocyte control of anti-tumor immunity. <i>Nature Communications</i> , 2019, 10, 2678.	5.8	14
322	p73 regulates epidermal wound healing and induced keratinocyte programming. <i>PLoS ONE</i> , 2019, 14, e0218458.	1.1	20
323	Single-Cell Transcriptomics Identifies the Adaptation of Scart1+ V β 36+ T Cells to Skin Residency as Activated Effector Cells. <i>Cell Reports</i> , 2019, 27, 3657-3671.e4.	2.9	79
324	Enhancement of LIN28B-induced hematopoietic reprogramming by IGF2BP3. <i>Genes and Development</i> , 2019, 33, 1048-1068.	2.7	53

#	ARTICLE	IF	CITATIONS
325	Navigating the Depths and Avoiding the Shallows of Pancreatic Islet Cell Transcriptomes. <i>Diabetes</i> , 2019, 68, 1380-1393.	0.3	73
326	R-spondin-3 induces secretory, antimicrobial Lgr5+ cells in the stomach. <i>Nature Cell Biology</i> , 2019, 21, 812-823.	4.6	53
327	Prolactin receptor expression in mouse dorsal root ganglia neuronal subtypes is sex-dependent. <i>Journal of Neuroendocrinology</i> , 2019, 31, e12759.	1.2	34
328	Subpopulation Detection and Their Comparative Analysis across Single-Cell Experiments with scPopCorn. <i>Cell Systems</i> , 2019, 8, 506-513.e5.	2.9	13
329	Loss of the interleukin-6 receptor causes immunodeficiency, atopy, and abnormal inflammatory responses. <i>Journal of Experimental Medicine</i> , 2019, 216, 1986-1998.	4.2	153
330	CHETAH: a selective, hierarchical cell type identification method for single-cell RNA sequencing. <i>Nucleic Acids Research</i> , 2019, 47, e95-e95.	6.5	169
331	Transcriptional dynamics of pluripotent stem cell-derived endothelial cell differentiation revealed by single-cell RNA sequencing. <i>European Heart Journal</i> , 2020, 41, 1024-1036.	1.0	43
332	Developmental kinetics and transcriptome dynamics of stem cell specification in the spermatogenic lineage. <i>Nature Communications</i> , 2019, 10, 2787.	5.8	77
333	Functional genomics in cancer immunotherapy: computational approaches for biomarker and drug discovery. <i>Molecular Systems Design and Engineering</i> , 2019, 4, 689-700.	1.7	3
334	Cell-Intrinsic Wnt4 Influences Conventional Dendritic Cell Fate Determination to Suppress Type 2 Immunity. <i>Journal of Immunology</i> , 2019, 203, 511-519.	0.4	6
335	Learning common and specific patterns from data of multiple interrelated biological scenarios with matrix factorization. <i>Nucleic Acids Research</i> , 2019, 47, 6606-6617.	6.5	28
336	Single-Cell Multi-omic Integration Compares and Contrasts Features of Brain Cell Identity. <i>Cell</i> , 2019, 177, 1873-1887.e17.	13.5	844
337	Comprehensive Integration of Single-Cell Data. <i>Cell</i> , 2019, 177, 1888-1902.e21.	13.5	9,755
338	Geometric Sketching Compactly Summarizes the Single-Cell Transcriptomic Landscape. <i>Cell Systems</i> , 2019, 8, 483-493.e7.	2.9	95
339	Agouti-Related Protein 2 Is a New Player in the Teleost Stress Response System. <i>Current Biology</i> , 2019, 29, 2009-2019.e7.	1.8	35
340	Distinct fibroblast subsets drive inflammation and damage in arthritis. <i>Nature</i> , 2019, 570, 246-251.	13.7	550
341	Single Cell RNA Sequencing Identifies Subsets of Hepatic Stellate Cells and Myofibroblasts in Liver Fibrosis. <i>Cells</i> , 2019, 8, 503.	1.8	153
342	Single cell expression analysis reveals anatomical and cell cycle-dependent transcriptional shifts during heart development. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	71

#	ARTICLE	IF	CITATIONS
343	Single-Cell Analysis of the Normal Mouse Aorta Reveals Functionally Distinct Endothelial Cell Populations. <i>Circulation</i> , 2019, 140, 147-163.	1.6	231
344	NeuroMesodermal Progenitors (NMPs): a comparative study between Pluripotent Stem Cells and Embryo derived populations. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	29
345	Single-cell transcriptomes of murine bone marrow stromal cells reveal niche-associated heterogeneity. <i>European Journal of Immunology</i> , 2019, 49, 1372-1379.	1.6	28
346	A single-cell transcriptional roadmap for cardiopharyngeal fate diversification. <i>Nature Cell Biology</i> , 2019, 21, 674-686.	4.6	78
347	A transcriptomic roadmap to alpha- and beta cell differentiation in the embryonic pancreas. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	17
348	A case study on the detailed reproducibility of a Human Cell Atlas project. <i>Quantitative Biology</i> , 2019, 7, 162-169.	0.3	6
349	Individual brain organoids reproducibly form cell diversity of the human cerebral cortex. <i>Nature</i> , 2019, 570, 523-527.	13.7	649
350	Migrant memory B cells secrete luminal antibody in the vagina. <i>Nature</i> , 2019, 571, 122-126.	13.7	77
351	Integration of Single-Cell Genomics Datasets. <i>Cell</i> , 2019, 177, 1677-1679.	13.5	21
352	Leader β^2 -cells coordinate Ca^{2+} dynamics across pancreatic islets in vivo. <i>Nature Metabolism</i> , 2019, 1, 615-629.	5.1	128
353	Simulating multiple faceted variability in single cell RNA sequencing. <i>Nature Communications</i> , 2019, 10, 2611.	5.8	89
354	An Atlas of Vagal Sensory Neurons and Their Molecular Specialization. <i>Cell Reports</i> , 2019, 27, 2508-2523.e4.	2.9	259
355	Decomposing Cell Identity for Transfer Learning across Cellular Measurements, Platforms, Tissues, and Species. <i>Cell Systems</i> , 2019, 8, 395-411.e8.	2.9	121
356	Single cell analysis of the developing mouse kidney provides deeper insight into marker gene expression and ligand-receptor crosstalk. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	123
357	Single-cell RNA sequencing unveils the shared and the distinct cytotoxic hallmarks of human TCRV α 1 and TCRV α 2 β 1 T lymphocytes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11906-11915.	3.3	152
358	Chromatin Decondensation by FOXP2 Promotes Human Neuron Maturation and Expression of Neurodevelopmental Disease Genes. <i>Cell Reports</i> , 2019, 27, 1699-1711.e9.	2.9	40
359	The Hippo Pathway Blocks Mammalian Retinal Müller Glial Cell Reprogramming. <i>Cell Reports</i> , 2019, 27, 1637-1649.e6.	2.9	92
360	Further Defining the Human Virome using NGS: Identification of Redondoviridae. <i>Cell Host and Microbe</i> , 2019, 25, 634-635.	5.1	10

#	ARTICLE	IF	CITATIONS
361	Single cell RNA sequencing and its promise in reconstructing plant vascular cell lineages. <i>Current Opinion in Plant Biology</i> , 2019, 48, 47-56.	3.5	20
362	scRNA-Seq reveals distinct stem cell populations that drive hair cell regeneration after loss of Fgf and Notch signaling. <i>ELife</i> , 2019, 8, .	2.8	130
363	Establishment of an Integrated Computational Workflow for Single Cell RNA-Seq Dataset. , 2019, , .		0
364	CellTag Indexing: genetic barcode-based sample multiplexing for single-cell genomics. <i>Genome Biology</i> , 2019, 20, 90.	3.8	61
365	diffcyt: Differential discovery in high-dimensional cytometry via high-resolution clustering. <i>Communications Biology</i> , 2019, 2, 183.	2.0	162
366	Identification of enhancer of mRNA decapping 4 as a novel fusion partner of MLL in acute myeloid leukemia. <i>Blood Advances</i> , 2019, 3, 761-765.	2.5	3
367	Single-cell expression profiling reveals dynamic flux of cardiac stromal, vascular and immune cells in health and injury. <i>ELife</i> , 2019, 8, .	2.8	379
368	Low ambient humidity impairs barrier function and innate resistance against influenza infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10905-10910.	3.3	235
369	A Gene Signature Predicting Natural Killer Cell Infiltration and Improved Survival in Melanoma Patients. <i>Cancer Immunology Research</i> , 2019, 7, 1162-1174.	1.6	201
370	High-Throughput Single-Cell Transcriptome Profiling of Plant Cell Types. <i>Cell Reports</i> , 2019, 27, 2241-2247.e4.	2.9	279
371	Mesenchymal Stromal Cells Are Required for Regeneration and Homeostatic Maintenance of Skeletal Muscle. <i>Cell Reports</i> , 2019, 27, 2029-2035.e5.	2.9	235
372	Distinct modes of cell competition shape mammalian tissue morphogenesis. <i>Nature</i> , 2019, 569, 497-502.	13.7	112
373	Tracing the origin of adult intestinal stem cells. <i>Nature</i> , 2019, 570, 107-111.	13.7	107
374	Performance Assessment and Selection of Normalization Procedures for Single-Cell RNA-Seq. <i>Cell Systems</i> , 2019, 8, 315-328.e8.	2.9	117
375	Molecular characterization of foveal versus peripheral human retina by single-cell RNA sequencing. <i>Experimental Eye Research</i> , 2019, 184, 234-242.	1.2	102
376	The selective estrogen receptor modulator raloxifene mitigates the effect of all-trans-retinal toxicity in photoreceptor degeneration. <i>Journal of Biological Chemistry</i> , 2019, 294, 9461-9475.	1.6	11
377	Molecular recording of mammalian embryogenesis. <i>Nature</i> , 2019, 570, 77-82.	13.7	257
378	Proneural factors <i>Ascl1</i> and <i>Neurog2</i> contribute to neuronal subtype identities by establishing distinct chromatin landscapes. <i>Nature Neuroscience</i> , 2019, 22, 897-908.	7.1	99

#	ARTICLE	IF	CITATIONS
379	Perivascular adipose tissue-derived stromal cells contribute to vascular remodeling during aging. <i>Aging Cell</i> , 2019, 18, e12969.	3.0	40
380	Identification of a regeneration-organizing cell in the <i>Xenopus</i> tail. <i>Science</i> , 2019, 364, 653-658.	6.0	108
381	scNPF: an integrative framework assisted by network propagation and network fusion for preprocessing of single-cell RNA-seq data. <i>BMC Genomics</i> , 2019, 20, 347.	1.2	11
382	Focused multidimensional scaling: interactive visualization for exploration of high-dimensional data. <i>BMC Bioinformatics</i> , 2019, 20, 221.	1.2	12
383	Single-Cell Transcriptomics Analyses of Neural Stem Cell Heterogeneity and Contextual Plasticity in a Zebrafish Brain Model of Amyloid Toxicity. <i>Cell Reports</i> , 2019, 27, 1307-1318.e3.	2.9	87
384	The Major Risk Factors for Alzheimer's Disease: Age, Sex, and Genes Modulate the Microglia Response to A β Plaques. <i>Cell Reports</i> , 2019, 27, 1293-1306.e6.	2.9	527
385	Notch Signaling Mediates Secondary Senescence. <i>Cell Reports</i> , 2019, 27, 997-1007.e5.	2.9	82
386	Neocortical Projection Neurons Instruct Inhibitory Interneuron Circuit Development in a Lineage-Dependent Manner. <i>Neuron</i> , 2019, 102, 960-975.e6.	3.8	51
387	Single-cell transcriptomes of the regenerating intestine reveal a revival stem cell. <i>Nature</i> , 2019, 569, 121-125.	13.7	327
388	Multiplexed detection of proteins, transcriptomes, clonotypes and CRISPR perturbations in single cells. <i>Nature Methods</i> , 2019, 16, 409-412.	9.0	364
389	Efficient integration of heterogeneous single-cell transcriptomes using Scanorama. <i>Nature Biotechnology</i> , 2019, 37, 685-691.	9.4	557
390	Determining cell type abundance and expression from bulk tissues with digital cytometry. <i>Nature Biotechnology</i> , 2019, 37, 773-782.	9.4	2,396
391	LAMBDA: label ambiguous domain adaptation dataset integration reduces batch effects and improves subtype detection. <i>Bioinformatics</i> , 2019, 35, 4696-4706.	1.8	31
392	Single-cell transcriptomic landscape of nucleated cells in umbilical cord blood. <i>GigaScience</i> , 2019, 8, .	3.3	24
393	RIG-I Activation by a Designer Short RNA Ligand Protects Human Immune Cells against Dengue Virus Infection without Causing Cytotoxicity. <i>Journal of Virology</i> , 2019, 93, .	1.5	11
394	A 3D Atlas of Hematopoietic Stem and Progenitor Cell Expansion by Multi-dimensional RNA-Seq Analysis. <i>Cell Reports</i> , 2019, 27, 1567-1578.e5.	2.9	45
395	Childhood cerebellar tumours mirror conserved fetal transcriptional programs. <i>Nature</i> , 2019, 572, 67-73.	13.7	293
396	Tanycyte-Independent Control of Hypothalamic Leptin Signaling. <i>Frontiers in Neuroscience</i> , 2019, 13, 240.	1.4	46

#	ARTICLE	IF	CITATIONS
397	Single-Cell RNA-Sequencing-Based CRISPRi Screening Resolves Molecular Drivers of Early Human Endoderm Development. <i>Cell Reports</i> , 2019, 27, 708-718.e10.	2.9	81
398	DC Respond to Cognate T Cell Interaction in the Antigen-Challenged Lymph Node. <i>Frontiers in Immunology</i> , 2019, 10, 863.	2.2	16
399	Origin and differentiation trajectories of fibroblastic reticular cells in the splenic white pulp. <i>Nature Communications</i> , 2019, 10, 1739.	5.8	73
400	A niche-dependent myeloid transcriptome signature defines dormant myeloma cells. <i>Blood</i> , 2019, 134, 30-43.	0.6	99
401	Embracing systems toxicology at single-cell resolution. <i>Current Opinion in Toxicology</i> , 2019, 16, 49-57.	2.6	24
402	scMerge leverages factor analysis, stable expression, and pseudoreplication to merge multiple single-cell RNA-seq datasets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9775-9784.	3.3	130
403	Single-Cell RNA-Sequencing of Peripheral Blood Mononuclear Cells with ddSEQ. <i>Methods in Molecular Biology</i> , 2019, 1979, 155-176.	0.4	19
404	A Bioinformatic Toolkit for Single-Cell mRNA Analysis. <i>Methods in Molecular Biology</i> , 2019, 1979, 433-455.	0.4	2
405	Molecular profiling of resident and infiltrating mononuclear phagocytes during rapid adult retinal degeneration using single-cell RNA sequencing. <i>Scientific Reports</i> , 2019, 9, 4858.	1.6	67
406	Dynamic transcriptome profiles within spermatogonial and spermatocyte populations during postnatal testis maturation revealed by single-cell sequencing. <i>PLoS Genetics</i> , 2019, 15, e1007810.	1.5	80
407	Spatiotemporal Developmental Trajectories in the Arabidopsis Root Revealed Using High-Throughput Single-Cell RNA Sequencing. <i>Developmental Cell</i> , 2019, 48, 840-852.e5.	3.1	367
408	High-Dimensional Single-Cell Cartography Reveals Novel Skeletal Muscle-Resident Cell Populations. <i>Molecular Cell</i> , 2019, 74, 609-621.e6.	4.5	271
409	Precise Gene Editing Preserves Hematopoietic Stem Cell Function following Transient p53-Mediated DNA Damage Response. <i>Cell Stem Cell</i> , 2019, 24, 551-565.e8.	5.2	237
410	Scalable analysis of cell-type composition from single-cell transcriptomics using deep recurrent learning. <i>Nature Methods</i> , 2019, 16, 311-314.	9.0	142
411	Single-cell analysis of adult skeletal muscle stem cells in homeostatic and regenerative conditions. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	135
413	Growth Plate Borderline Chondrocytes Behave as Transient Mesenchymal Precursor Cells. <i>Journal of Bone and Mineral Research</i> , 2019, 34, 1387-1392.	3.1	44
414	Single-Cell RNA Profiling of Glomerular Cells Shows Dynamic Changes in Experimental Diabetic Kidney Disease. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 533-545.	3.0	133
415	Generation and persistence of human tissue-resident memory T cells in lung transplantation. <i>Science Immunology</i> , 2019, 4, .	5.6	203

#	ARTICLE	IF	CITATIONS
416	Kidney micro-organoids in suspension culture as a scalable source of human pluripotent stem cell-derived kidney cells. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	97
417	SinNLRR: a robust subspace clustering method for cell type detection by non-negative and low-rank representation. <i>Bioinformatics</i> , 2019, 35, 3642-3650.	1.8	112
418	Epithelial endoplasmic reticulum stress orchestrates a protective IgA response. <i>Science</i> , 2019, 363, 993-998.	6.0	51
419	Single-Cell RNA Sequencing of Oligodendrocyte Lineage Cells from the Mouse Central Nervous System. <i>Methods in Molecular Biology</i> , 2019, 1936, 1-21.	0.4	6
420	Therapeutic resistance and susceptibility is shaped by cooperative multi-compartment tumor adaptation. <i>Cell Death and Differentiation</i> , 2019, 26, 2416-2429.	5.0	25
421	Osteogenesis depends on commissioning of a network of stem cell transcription factors that act as repressors of adipogenesis. <i>Nature Genetics</i> , 2019, 51, 716-727.	9.4	156
422	Single-Cell Heterogeneity Analysis and CRISPR Screen Identify Key $\hat{2}$ -Cell-Specific Disease Genes. <i>Cell Reports</i> , 2019, 26, 3132-3144.e7.	2.9	90
423	Predicting Cell Populations in Single Cell Mass Cytometry Data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2019, 95, 769-781.	1.1	54
424	Defining developmental diversification of diencephalon neurons through single-cell gene expression profiling. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	28
425	Single-Cell Transcriptome Analysis of CD34+ Stem Cell-Derived Myeloid Cells Infected With Human Cytomegalovirus. <i>Frontiers in Microbiology</i> , 2019, 10, 577.	1.5	25
426	Single cell RNA-seq study of wild type and Hox9,10,11 mutant developing uterus. <i>Scientific Reports</i> , 2019, 9, 4557.	1.6	44
427	Convergent Identification and Interrogation of Tumor-Intrinsic Factors that Modulate Cancer Immunity In Vivo. <i>Cell Systems</i> , 2019, 8, 136-151.e7.	2.9	14
428	Microglial Function Is Distinct in Different Anatomical Locations during Retinal Homeostasis and Degeneration. <i>Immunity</i> , 2019, 50, 723-737.e7.	6.6	235
429	Reporter-based fate mapping in human kidney organoids confirms nephron lineage relationships and reveals synchronous nephron formation. <i>EMBO Reports</i> , 2019, 20, .	2.0	52
430	Evaluating measures of association for single-cell transcriptomics. <i>Nature Methods</i> , 2019, 16, 381-386.	9.0	109
431	Single Molecule and Single Cell Sequencing. <i>Advances in Experimental Medicine and Biology</i> , 2019, , .	0.8	7
432	Beyond bulk: a review of single cell transcriptomics methodologies and applications. <i>Current Opinion in Biotechnology</i> , 2019, 58, 129-136.	3.3	235
433	An Informative Approach to Single-Cell Sequencing Analysis. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1129, 81-96.	0.8	3

#	ARTICLE	IF	CITATIONS
434	The bone marrow microenvironment at single-cell resolution. <i>Nature</i> , 2019, 569, 222-228.	13.7	624
435	TSEE: an elastic embedding method to visualize the dynamic gene expression patterns of time series single-cell RNA sequencing data. <i>BMC Genomics</i> , 2019, 20, 224.	1.2	17
436	Research in Computational Molecular Biology. <i>Lecture Notes in Computer Science</i> , 2019, , .	1.0	0
437	Single-Cell RNA Sequencing Identifies Candidate Renal Resident Macrophage Gene Expression Signatures across Species. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 767-781.	3.0	126
438	Interleukin-1 β Induces mtDNA Release to Activate Innate Immune Signaling via cGAS-STING. <i>Molecular Cell</i> , 2019, 74, 801-815.e6.	4.5	203
439	Adventitial Cell Atlas of wt (Wild Type) and ApoE (Apolipoprotein E)-Deficient Mice Defined by Single-Cell RNA Sequencing. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2019, 39, 1055-1071.	1.1	78
440	DoubletFinder: Doublet Detection in Single-Cell RNA Sequencing Data Using Artificial Nearest Neighbors. <i>Cell Systems</i> , 2019, 8, 329-337.e4.	2.9	1,648
441	PanglaoDB: a web server for exploration of mouse and human single-cell RNA sequencing data. Database: the <i>Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	762
442	MYRF haploinsufficiency causes 46,XY and 46,XX disorders of sex development: bioinformatics consideration. <i>Human Molecular Genetics</i> , 2019, 28, 2319-2329.	1.4	25
443	A component overlapping attribute clustering (COAC) algorithm for single-cell RNA sequencing data analysis and potential pathobiological implications. <i>PLoS Computational Biology</i> , 2019, 15, e1006772.	1.5	14
444	Single-cell RNA sequencing reveals midbrain dopamine neuron diversity emerging during mouse brain development. <i>Nature Communications</i> , 2019, 10, 581.	5.8	189
445	Single-Cell RNA Sequencing Resolves Molecular Relationships Among Individual Plant Cells. <i>Plant Physiology</i> , 2019, 179, 1444-1456.	2.3	348
446	Establishing Cerebral Organoids as Models of Human-Specific Brain Evolution. <i>Cell</i> , 2019, 176, 743-756.e17.	13.5	423
447	CellFishing.jl: an ultrafast and scalable cell search method for single-cell RNA sequencing. <i>Genome Biology</i> , 2019, 20, 31.	3.8	22
448	Lymphocyte innateness defined by transcriptional states reflects a balance between proliferation and effector functions. <i>Nature Communications</i> , 2019, 10, 687.	5.8	136
449	Human Fetal TNF- α -Cytokine-Producing CD4+ Effector Memory T Cells Promote Intestinal Development and Mediate Inflammation Early in Life. <i>Immunity</i> , 2019, 50, 462-476.e8.	6.6	146
450	Multimodal Single-Cell Analysis Reveals Physiological Maturation in the Developing Human Neocortex. <i>Neuron</i> , 2019, 102, 143-158.e7.	3.8	61
451	Combined quantification of intracellular (phospho-)proteins and transcriptomics from fixed single cells. <i>Scientific Reports</i> , 2019, 9, 1469.	1.6	73

#	ARTICLE	IF	CITATIONS
452	SuperCT: a supervised-learning framework for enhanced characterization of single-cell transcriptomic profiles. <i>Nucleic Acids Research</i> , 2019, 47, e48-e48.	6.5	52
453	Colonic epithelial cell diversity in health and inflammatory bowel disease. <i>Nature</i> , 2019, 567, 49-55.	13.7	486
454	Rate of Progression through a Continuum of Transit-Amplifying Progenitor Cell States Regulates Blood Cell Production. <i>Developmental Cell</i> , 2019, 49, 118-129.e7.	3.1	22
455	Non-lytic clearance of influenza B virus from infected cells preserves epithelial barrier function. <i>Nature Communications</i> , 2019, 10, 779.	5.8	26
456	Targeted Elimination of Senescent Beta Cells Prevents Type 1 Diabetes. <i>Cell Metabolism</i> , 2019, 29, 1045-1060.e10.	7.2	232
457	Altered human oligodendrocyte heterogeneity in multiple sclerosis. <i>Nature</i> , 2019, 566, 543-547.	13.7	522
458	Resolving Cell Fate Decisions during Somatic Cell Reprogramming by Single-Cell RNA-Seq. <i>Molecular Cell</i> , 2019, 73, 815-829.e7.	4.5	79
459	Spatial and temporal heterogeneity of mouse and human microglia at single-cell resolution. <i>Nature</i> , 2019, 566, 388-392.	13.7	853
460	Diabetes relief in mice by glucose-sensing insulin-secreting human β -cells. <i>Nature</i> , 2019, 567, 43-48.	13.7	188
461	Identification of Cell Types from Single-Cell Transcriptomic Data. <i>Methods in Molecular Biology</i> , 2019, 1935, 45-77.	0.4	16
462	Estimating Differentiation Potency of Single Cells Using Single-Cell Entropy (SCENT). <i>Methods in Molecular Biology</i> , 2019, 1935, 125-139.	0.4	12
463	Single cell immune profiling in transplantation research. <i>American Journal of Transplantation</i> , 2019, 19, 1278-1287.	2.6	7
464	Early adaptive immune activation detected in monozygotic twins with prodromal multiple sclerosis. <i>Journal of Clinical Investigation</i> , 2019, 129, 4758-4768.	3.9	81
465	Single-cell analysis of ROR γ tracer mouse lung reveals ILC progenitors and effector ILC2 subsets. <i>Journal of Experimental Medicine</i> , 0, , .	4.2	0
466	Generation and function of progenitor T cells from StemRegenin-1 β -expanded CD34 $^{+}$ human hematopoietic progenitor cells. <i>Blood Advances</i> , 2019, 3, 2934-2948.	2.5	14
467	Integrative Modeling and Novel Technologies in Human Genomics. , 2019, , 155-189.		0
468	Myeloid translocation gene CBFA2T3 directs a relapse gene program and determines patient-specific outcomes in AML. <i>Blood Advances</i> , 2019, 3, 1379-1393.	2.5	15
469	Heterogeneous beta-catenin activation is sufficient to cause hepatocellular carcinoma in zebrafish. <i>Biology Open</i> , 2019, 8, .	0.6	13

#	ARTICLE	IF	CITATIONS
470	Dynamic MAPK signaling activity underlies a transition from growth arrest to proliferation in <i>Drosophila scribble</i> mutant tumors. <i>DMM Disease Models and Mechanisms</i> , 2019, 12, .	1.2	19
471	Dropout imputation and batch effect correction for single-cell RNA sequencing data. <i>Journal of Bio-X Research</i> , 2019, 2, 169-177.	0.3	2
472	Single-cell analysis of bone marrow-derived CD34+ cells from children with sickle cell disease and thalassemia. <i>Blood</i> , 2019, 134, 2111-2115.	0.6	21
473	Low oxygen enhances trophoblast column growth by potentiating differentiation of the extravillous lineage and promoting LOX activity. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	20
474	AIK-Means: A Novel Clustering Method for Single-Cell RNA Sequencing Data. , 2019, , .		0
475	MicroRNA-155 coordinates the immunological landscape within murine melanoma and correlates with immunity in human cancers. <i>JCI Insight</i> , 2019, 4, .	2.3	31
476	Neuronal maturation reduces the type I IFN response to orthobunyavirus infection and leads to increased apoptosis of human neurons. <i>Journal of Neuroinflammation</i> , 2019, 16, 229.	3.1	22
477	Single-Cell RNA Sequencing of Plant-Associated Bacterial Communities. <i>Frontiers in Microbiology</i> , 2019, 10, 2452.	1.5	10
478	ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. <i>PLoS ONE</i> , 2019, 14, e0224693.	1.1	19
479	Single-cell reconstruction of differentiation trajectory reveals a critical role of ETS1 in human cardiac lineage commitment. <i>BMC Biology</i> , 2019, 17, 89.	1.7	31
480	Sertoli cell-only phenotype and scRNA-seq define PRAMEF12 as a factor essential for spermatogenesis in mice. <i>Nature Communications</i> , 2019, 10, 5196.	5.8	35
481	scRNA-seq in medulloblastoma shows cellular heterogeneity and lineage expansion support resistance to SHH inhibitor therapy. <i>Nature Communications</i> , 2019, 10, 5829.	5.8	77
482	Single-cell analysis of CD8 T lymphocyte diversity during adaptive immunity. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2020, 12, e1475.	6.6	3
483	Human Primordial Germ Cells Are Specified from Lineage-Primed Progenitors. <i>Cell Reports</i> , 2019, 29, 4568-4582.e5.	2.9	114
484	Using transfer learning from prior reference knowledge to improve the clustering of single-cell RNA-Seq data. <i>Scientific Reports</i> , 2019, 9, 20353.	1.6	23
485	Elite control of HIV is associated with distinct functional and transcriptional signatures in lymphoid tissue CD8 T cells. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	81
486	Single-cell RNA sequencing reveals compartmental remodeling of tumor-infiltrating immune cells induced by anti-CD47 targeting in pancreatic cancer. <i>Journal of Hematology and Oncology</i> , 2019, 12, 124.	6.9	95
487	Automated optimized parameters for T-distributed stochastic neighbor embedding improve visualization and analysis of large datasets. <i>Nature Communications</i> , 2019, 10, 5415.	5.8	277

#	ARTICLE	IF	CITATIONS
488	Single-cell transcriptomics of the naked mole-rat reveals unexpected features of mammalian immunity. PLoS Biology, 2019, 17, e3000528.	2.6	80
489	Single cell census of human kidney organoids shows reproducibility and diminished off-target cells after transplantation. Nature Communications, 2019, 10, 5462.	5.8	133
490	A cancer rainbow mouse for visualizing the functional genomics of oncogenic clonal expansion. Nature Communications, 2019, 10, 5490.	5.8	31
491	Myc controls a distinct transcriptional program in fetal thymic epithelial cells that determines thymus growth. Nature Communications, 2019, 10, 5498.	5.8	39
492	Single-Cell Profiling Defines Transcriptomic Signatures Specific to Tumor-Reactive versus Virus-Responsive CD4+ T Cells. Cell Reports, 2019, 29, 3019-3032.e6.	2.9	50
493	Single cell transcriptome dynamics from pluripotency to FLK1+ mesoderm. Development (Cambridge), 2019, 146, .	1.2	11
494	MTGO-SC, A Tool to Explore Gene Modules in Single-Cell RNA Sequencing Data. Frontiers in Genetics, 2019, 10, 953.	1.1	3
495	Stalled developmental programs at the root of pediatric brain tumors. Nature Genetics, 2019, 51, 1702-1713.	9.4	136
496	Early chromatin shaping predetermines multipotent vagal neural crest into neural, neuronal and mesenchymal lineages. Nature Cell Biology, 2019, 21, 1504-1517.	4.6	41
497	c-Jun overexpression in CAR T cells induces exhaustion resistance. Nature, 2019, 576, 293-300.	13.7	480
498	Resistance to autosomal dominant Alzheimer's disease in an APOE3 Christchurch homozygote: a case report. Nature Medicine, 2019, 25, 1680-1683.	15.2	328
499	Prenatal androgen exposure and transgenerational susceptibility to polycystic ovary syndrome. Nature Medicine, 2019, 25, 1894-1904.	15.2	193
500	Fast, sensitive and accurate integration of single-cell data with Harmony. Nature Methods, 2019, 16, 1289-1296.	9.0	3,494
501	An ultra high-throughput method for single-cell joint analysis of open chromatin and transcriptome. Nature Structural and Molecular Biology, 2019, 26, 1063-1070.	3.6	239
502	The human tissue-resident CCR5 ⁺ T cell compartment maintains protective and functional properties during inflammation. Science Translational Medicine, 2019, 11, .	5.8	41
503	Feature selection and dimension reduction for single-cell RNA-Seq based on a multinomial model. Genome Biology, 2019, 20, 295.	3.8	288
504	Normalization and variance stabilization of single-cell RNA-seq data using regularized negative binomial regression. Genome Biology, 2019, 20, 296.	3.8	2,460
505	Single-cell Transcriptomics and Solid Organ Transplantation. Transplantation, 2019, 103, 1776-1782.	0.5	28

#	ARTICLE	IF	CITATIONS
506	Meta-Analysis of in vitro-Differentiated Macrophages Identifies Transcriptomic Signatures That Classify Disease Macrophages in vivo. <i>Frontiers in Immunology</i> , 2019, 10, 2887.	2.2	30
507	Emerging deep learning methods for single-cell RNA-seq data analysis. <i>Quantitative Biology</i> , 2019, 7, 247-254.	0.3	25
508	The Cellular Diversity and Transcription Factor Code of <i>Drosophila</i> Enteroendocrine Cells. <i>Cell Reports</i> , 2019, 29, 4172-4185.e5.	2.9	82
509	Theory of cell fate. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2020, 12, e1471.	6.6	19
510	Electrical and synaptic integration of glioma into neural circuits. <i>Nature</i> , 2019, 573, 539-545.	13.7	706
511	Organoid single-cell genomic atlas uncovers human-specific features of brain development. <i>Nature</i> , 2019, 574, 418-422.	13.7	496
512	Heterogeneity in old fibroblasts is linked to variability in reprogramming and wound healing. <i>Nature</i> , 2019, 574, 553-558.	13.7	187
513	Exploring single-cell data with deep multitasking neural networks. <i>Nature Methods</i> , 2019, 16, 1139-1145.	9.0	222
514	A repeated molecular architecture across thalamic pathways. <i>Nature Neuroscience</i> , 2019, 22, 1925-1935.	7.1	132
515	Single-cell transcriptomic profiling of the aging mouse brain. <i>Nature Neuroscience</i> , 2019, 22, 1696-1708.	7.1	432
516	scPred: accurate supervised method for cell-type classification from single-cell RNA-seq data. <i>Genome Biology</i> , 2019, 20, 264.	3.8	263
517	Single Cell Analysis of Endothelial Cells Identified Organ-Specific Molecular Signatures and Heart-Specific Cell Populations and Molecular Features. <i>Frontiers in Cardiovascular Medicine</i> , 2019, 6, 165.	1.1	76
518	A Study of High-Grade Serous Ovarian Cancer Origins Implicates the SOX18 Transcription Factor in Tumor Development. <i>Cell Reports</i> , 2019, 29, 3726-3735.e4.	2.9	39
519	<p>SSBP1 Upregulation In Colorectal Cancer Regulates Mitochondrial Mass</p>. <i>Cancer Management and Research</i> , 2019, Volume 11, 10093-10106.	0.9	9
520	Toward a Common Coordinate Framework for the Human Body. <i>Cell</i> , 2019, 179, 1455-1467.	13.5	81
521	A Galaxy-based training resource for single-cell RNA-sequencing quality control and analyses. <i>GigaScience</i> , 2019, 8, .	3.3	4
522	Sensory coding mechanisms revealed by optical tagging of physiologically defined neuronal types. <i>Science</i> , 2019, 366, 1384-1389.	6.0	21
523	Accuracy, robustness and scalability of dimensionality reduction methods for single-cell RNA-seq analysis. <i>Genome Biology</i> , 2019, 20, 269.	3.8	140

#	ARTICLE	IF	CITATIONS
524	Heterogeneity and dynamics of active Kras-induced dysplastic lineages from mouse corpus stomach. Nature Communications, 2019, 10, 5549.	5.8	28
525	GCN2 drives macrophage and MDSC function and immunosuppression in the tumor microenvironment. Science Immunology, 2019, 4, .	5.6	85
526	Single-cell multiomic analysis identifies regulatory programs in mixed-phenotype acute leukemia. Nature Biotechnology, 2019, 37, 1458-1465.	9.4	321
527	A single-cell atlas of entorhinal cortex from individuals with Alzheimer's disease reveals cell-type-specific gene expression regulation. Nature Neuroscience, 2019, 22, 2087-2097.	7.1	591
528	Single-cell connectomic analysis of adult mammalian lungs. Science Advances, 2019, 5, eaaw3851.	4.7	156
529	Innate $\gamma\delta$ T-Cells Mediate Anti-Tumor Immunity by Orchestrating Immunogenic Macrophage Programming. Journal of the American College of Surgeons, 2019, 229, S266-S267.	0.2	0
530	Single-cell transcriptomics from human pancreatic islets: sample preparation matters. Biology Methods and Protocols, 2019, 4, bpz019.	1.0	15
531	Single-Cell RNA Sequencing of the Cardiovascular System: New Looks for Old Diseases. Frontiers in Cardiovascular Medicine, 2019, 6, 173.	1.1	47
532	Species-Specific miRNAs in Human Brain Development and Disease. Frontiers in Cellular Neuroscience, 2019, 13, 559.	1.8	26
533	Temporal patterning of neocortical progenitor cells: How do they know the right time?. Neuroscience Research, 2019, 138, 3-11.	1.0	22
534	A Genome-wide Framework for Mapping Gene Regulation via Cellular Genetic Screens. Cell, 2019, 176, 377-390.e19.	13.5	379
535	Single-Cell Analysis Reveals a Hair Follicle Dermal Niche Molecular Differentiation Trajectory that Begins Prior to Morphogenesis. Developmental Cell, 2019, 48, 17-31.e6.	3.1	90
536	Method to Synchronize Cell Cycle of Human Pluripotent Stem Cells without Affecting Their Fundamental Characteristics. Stem Cell Reports, 2019, 12, 165-179.	2.3	35
537	Single-cell RNA-Seq of follicular lymphoma reveals malignant B-cell types and coexpression of T-cell immune checkpoints. Blood, 2019, 133, 1119-1129.	0.6	99
538	Coupled Single-Cell CRISPR Screening and Epigenomic Profiling Reveals Causal Gene Regulatory Networks. Cell, 2019, 176, 361-376.e17.	13.5	215
539	Single-Cell RNA-Seq of the Pancreatic Islets "a Promise Not yet Fulfilled?. Cell Metabolism, 2019, 29, 539-544.	7.2	98
540	Evaluation of variability in human kidney organoids. Nature Methods, 2019, 16, 79-87.	9.0	176
541	A test metric for assessing single-cell RNA-seq batch correction. Nature Methods, 2019, 16, 43-49.	9.0	278

#	ARTICLE	IF	CITATIONS
542	scFTD-seq: freeze-thaw lysis based, portable approach toward highly distributed single-cell 3â€² mRNA profiling. <i>Nucleic Acids Research</i> , 2019, 47, e16-e16.	6.5	117
543	Single-cell analyses identify distinct and intermediate states of zebrafish pancreatic islet development. <i>Journal of Molecular Cell Biology</i> , 2019, 11, 435-447.	1.5	9
544	pyNVR: investigating factors affecting feature selection from scRNA-seq data for lineage reconstruction. <i>Bioinformatics</i> , 2019, 35, 2335-2337.	1.8	15
545	A complex auxiliary: IL-17/Th17 signaling during type 1 diabetes progression. <i>Molecular Immunology</i> , 2019, 105, 16-31.	1.0	14
546	Single-Cell RNA Sequencing of Microglia throughout the Mouse Lifespan and in the Injured Brain Reveals Complex Cell-State Changes. <i>Immunity</i> , 2019, 50, 253-271.e6.	6.6	1,351
547	Comparative Analysis of Droplet-Based Ultra-High-Throughput Single-Cell RNA-Seq Systems. <i>Molecular Cell</i> , 2019, 73, 130-142.e5.	4.5	283
548	ClusterMap: compare multiple single cell RNA-Seq datasets across different experimental conditions. <i>Bioinformatics</i> , 2019, 35, 3038-3045.	1.8	31
549	The Myeloid Cell Compartmentâ€”Cell by Cell. <i>Annual Review of Immunology</i> , 2019, 37, 269-293.	9.5	140
550	Single-Cell Applications of Next-Generation Sequencing. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2019, 9, a026898.	2.9	23
551	Single cell RNA-sequencing: replicability of cell types. <i>Current Opinion in Neurobiology</i> , 2019, 56, 69-77.	2.0	13
552	The Emergence and Functional Fitness of Memory CD4+ T Cells Require the Transcription Factor Thpok. <i>Immunity</i> , 2019, 50, 91-105.e4.	6.6	94
553	Challenges in unsupervised clustering of single-cell RNA-seq data. <i>Nature Reviews Genetics</i> , 2019, 20, 273-282.	7.7	780
554	The Septate Junction Protein Tsp2A Restricts Intestinal Stem Cell Activity via Endocytic Regulation of aPKC and Hippo Signaling. <i>Cell Reports</i> , 2019, 26, 670-688.e6.	2.9	43
555	Multi-omics at single-cell resolution: comparison of experimental and data fusion approaches. <i>Current Opinion in Biotechnology</i> , 2019, 55, 159-166.	3.3	25
556	A conditionally immortalized Gli1-positive kidney mesenchymal cell line models myofibroblast transition. <i>American Journal of Physiology - Renal Physiology</i> , 2019, 316, F63-F75.	1.3	20
557	Perspectives on defining cell types in the brain. <i>Current Opinion in Neurobiology</i> , 2019, 56, 61-68.	2.0	44
558	Self-renewing resident cardiac macrophages limit adverse remodeling following myocardial infarction. <i>Nature Immunology</i> , 2019, 20, 29-39.	7.0	537
559	Deconstructing Retinal Organoids: Single Cell RNA-Seq Reveals the Cellular Components of Human Pluripotent Stem Cell-Derived Retina. <i>Stem Cells</i> , 2019, 37, 593-598.	1.4	106

#	ARTICLE	IF	CITATIONS
560	Commensal-specific T cell plasticity promotes rapid tissue adaptation to injury. <i>Science</i> , 2019, 363, .	6.0	219
561	Dimensionality reduction for visualizing single-cell data using UMAP. <i>Nature Biotechnology</i> , 2019, 37, 38-44.	9.4	3,254
562	Advantages of Single-Nucleus over Single-Cell RNA Sequencing of Adult Kidney: Rare Cell Types and Novel Cell States Revealed in Fibrosis. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 23-32.	3.0	493
563	Recovery and analysis of transcriptome subsets from pooled single-cell RNA-seq libraries. <i>Nucleic Acids Research</i> , 2019, 47, e20-e20.	6.5	16
564	Machine learning for integrating data in biology and medicine: Principles, practice, and opportunities. <i>Information Fusion</i> , 2019, 50, 71-91.	11.7	340
565	Transcriptomics and single-cell RNA sequencing. <i>Respirology</i> , 2019, 24, 29-36.	1.3	77
566	Myeloid cells in liver and bone marrow acquire a functionally distinct inflammatory phenotype during obesity-related steatohepatitis. <i>Gut</i> , 2020, 69, 551-563.	6.1	142
567	Machine learning and statistical methods for clustering single-cell RNA-sequencing data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1209-1223.	3.2	146
568	Single-cell transcriptome-based multilayer network biomarker for predicting prognosis and therapeutic response of gliomas. <i>Briefings in Bioinformatics</i> , 2020, 21, 1080-1097.	3.2	62
569	A spatially restricted fibrotic niche in pulmonary fibrosis is sustained by M-CSF/M-CSFR signalling in monocyte-derived alveolar macrophages. <i>European Respiratory Journal</i> , 2020, 55, 1900646.	3.1	188
570	Clarin-1 expression in adult mouse and human retina highlights a role of Müller glia in Usher syndrome. <i>Journal of Pathology</i> , 2020, 250, 195-204.	2.1	15
571	Role of thrombomodulin expression on hematopoietic stem cells. <i>Journal of Thrombosis and Haemostasis</i> , 2020, 18, 123-135.	1.9	3
572	Transcriptional profiling of circulating tumor cells in multiple myeloma: a new model to understand disease dissemination. <i>Leukemia</i> , 2020, 34, 589-603.	3.3	41
573	High-dimensional cytometric analysis of colorectal cancer reveals novel mediators of antitumour immunity. <i>Gut</i> , 2020, 69, 691-703.	6.1	92
574	MCPyV Large T Antigen-Induced Atonal Homolog 1 Is a Lineage-Dependency Oncogene in Merkel Cell Carcinoma. <i>Journal of Investigative Dermatology</i> , 2020, 140, 56-65.e3.	0.3	35
575	Interneuron Types as Attractors and Controllers. <i>Annual Review of Neuroscience</i> , 2020, 43, 1-30.	5.0	127
576	scds: computational annotation of doublets in single-cell RNA sequencing data. <i>Bioinformatics</i> , 2020, 36, 1150-1158.	1.8	139
577	scRCMF: Identification of Cell Subpopulations and Transition States From Single-Cell Transcriptomes. <i>IEEE Transactions on Biomedical Engineering</i> , 2020, 67, 1418-1428.	2.5	13

#	ARTICLE	IF	CITATIONS
578	VirtualCytometry: a webserver for evaluating immune cell differentiation using single-cell RNA sequencing data. <i>Bioinformatics</i> , 2020, 36, 546-551.	1.8	8
579	Single-Cell RNA Sequencing Identifies Yes-Associated Protein 1-Dependent Hepatic Mesothelial Progenitors in Fibrolamellar Carcinoma. <i>American Journal of Pathology</i> , 2020, 190, 93-107.	1.9	10
580	Defining Transcriptional Signatures of Human Hair Follicle Cell States. <i>Journal of Investigative Dermatology</i> , 2020, 140, 764-773.e4.	0.3	42
581	Cortical Foxp2 Supports Behavioral Flexibility and Developmental Dopamine D1 Receptor Expression. <i>Cerebral Cortex</i> , 2020, 30, 1855-1870.	1.6	27
582	Cellular Plasticity in Musculoskeletal Development, Regeneration, and Disease. <i>Journal of Orthopaedic Research</i> , 2020, 38, 708-718.	1.2	4
583	Apoptotic Cell Exclusion and Bias-Free Single-Cell Selection Are Important Quality Control Requirements for Successful Single-Cell Sequencing Applications. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2020, 97, 156-167.	1.1	15
584	Migraine-associated gene expression in cell types of the central and peripheral nervous system. <i>Cephalalgia</i> , 2020, 40, 517-523.	1.8	9
585	Neuron-glia interaction through Serotonin-BDNF-NGFR axis enables regenerative neurogenesis in Alzheimer's model of adult zebrafish brain. <i>PLoS Biology</i> , 2020, 18, e3000585.	2.6	73
586	Identification of a LIF-Responsive, Replication-Competent Subpopulation of Human \hat{I}^2 Cells. <i>Cell Metabolism</i> , 2020, 31, 327-338.e6.	7.2	17
587	The emergence and promise of single-cell temporal-omics approaches. <i>Current Opinion in Biotechnology</i> , 2020, 63, 70-78.	3.3	34
588	FLOW-MAP: a graph-based, force-directed layout algorithm for trajectory mapping in single-cell time course datasets. <i>Nature Protocols</i> , 2020, 15, 398-420.	5.5	17
589	Siah2 control of T-regulatory cells limits anti-tumor immunity. <i>Nature Communications</i> , 2020, 11, 99.	5.8	15
590	Single-cell reconstruction of the adult human heart during heart failure and recovery reveals the cellular landscape underlying cardiac function. <i>Nature Cell Biology</i> , 2020, 22, 108-119.	4.6	270
591	Genetic modifiers of risk and age at onset in GBA associated Parkinson's disease and Lewy body dementia. <i>Brain</i> , 2020, 143, 234-248.	3.7	149
592	The Dynamic Transcriptional Cell Atlas of Testis Development during Human Puberty. <i>Cell Stem Cell</i> , 2020, 26, 262-276.e4.	5.2	155
593	Clonally expanded CD8 T cells patrol the cerebrospinal fluid in Alzheimer's disease. <i>Nature</i> , 2020, 577, 399-404.	13.7	537
594	Enteric Nervous System-Derived IL-18 Orchestrates Mucosal Barrier Immunity. <i>Cell</i> , 2020, 180, 50-63.e12.	13.5	120
595	Prox1-positive cells monitor and sustain the murine intestinal epithelial cholinergic niche. <i>Nature Communications</i> , 2020, 11, 111.	5.8	40

#	ARTICLE	IF	CITATIONS
596	Clonal kinetics and single-cell transcriptional profiling of CAR-T cells in patients undergoing CD19 CAR-T immunotherapy. <i>Nature Communications</i> , 2020, 11, 219.	5.8	167
597	A single-cell atlas of the developing <i>Drosophila</i> ovary identifies follicle stem cell progenitors. <i>Genes and Development</i> , 2020, 34, 239-249.	2.7	62
598	Cell shape determines gene expression: cardiomyocyte morphotypic transcriptomes. <i>Basic Research in Cardiology</i> , 2020, 115, 7.	2.5	14
599	CDK7 Inhibition Potentiates Genome Instability Triggering Anti-tumor Immunity in Small Cell Lung Cancer. <i>Cancer Cell</i> , 2020, 37, 37-54.e9.	7.7	138
600	Allergen-specific IgG+ memory B cells are temporally linked to IgE memory responses. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 146, 180-191.	1.5	46
601	Single cell RNA-sequencing reveals cellular heterogeneity and trajectories of lineage specification during murine embryonic limb development. <i>Matrix Biology</i> , 2020, 89, 1-10.	1.5	53
602	Combined single-cell and spatial transcriptomics reveal the molecular, cellular and spatial bone marrow niche organization. <i>Nature Cell Biology</i> , 2020, 22, 38-48.	4.6	521
603	Highly multiplexed single-cell RNA-seq by DNA oligonucleotide tagging of cellular proteins. <i>Nature Biotechnology</i> , 2020, 38, 35-38.	9.4	83
604	Microglial microRNAs mediate sex-specific responses to tau pathology. <i>Nature Neuroscience</i> , 2020, 23, 167-171.	7.1	79
605	Single-cell analysis of human adipose tissue identifies depot- and disease-specific cell types. <i>Nature Metabolism</i> , 2020, 2, 97-109.	5.1	272
606	Evaluation of single-cell classifiers for single-cell RNA sequencing data sets. <i>Briefings in Bioinformatics</i> , 2020, 21, 1581-1595.	3.2	63
607	Causal network perturbations for instance-specific analysis of single cell and disease samples. <i>Bioinformatics</i> , 2020, 36, 2515-2521.	1.8	14
608	SAME-clustering: Single-cell Aggregated Clustering via Mixture Model Ensemble. <i>Nucleic Acids Research</i> , 2020, 48, 86-95.	6.5	55
609	Distinct epigenetic features of tumor-reactive CD8+ T cells in colorectal cancer patients revealed by genome-wide DNA methylation analysis. <i>Genome Biology</i> , 2020, 21, 2.	3.8	77
610	Chemical Cocktail Induces Hematopoietic Reprogramming and Expands Hematopoietic Stem/Progenitor Cells. <i>Advanced Science</i> , 2020, 7, 1901785.	5.6	12
611	Multipotent RAG1+ progenitors emerge directly from haemogenic endothelium in human pluripotent stem cell-derived haematopoietic organoids. <i>Nature Cell Biology</i> , 2020, 22, 60-73.	4.6	37
612	Immune Landscape of Viral- and Carcinogen-Driven Head and Neck Cancer. <i>Immunity</i> , 2020, 52, 183-199.e9.	6.6	383
613	Precursors for Nonlymphoid-Tissue Treg Cells Reside in Secondary Lymphoid Organs and Are Programmed by the Transcription Factor BATF. <i>Immunity</i> , 2020, 52, 295-312.e11.	6.6	140

#	ARTICLE	IF	CITATIONS
614	schex avoids overplotting for large single-cell RNA-sequencing datasets. <i>Bioinformatics</i> , 2020, 36, 2291-2292.	1.8	10
615	NicheNet: modeling intercellular communication by linking ligands to target genes. <i>Nature Methods</i> , 2020, 17, 159-162.	9.0	904
616	Macrophage-tumor cell interaction promotes ATRT progression and chemoresistance. <i>Acta Neuropathologica</i> , 2020, 139, 913-936.	3.9	24
617	Using single-cell technologies to map the human immune system – implications for nephrology. <i>Nature Reviews Nephrology</i> , 2020, 16, 112-128.	4.1	39
618	BMP10-mediated ALK1 signaling is continuously required for vascular development and maintenance. <i>Angiogenesis</i> , 2020, 23, 203-220.	3.7	52
619	Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , 2020, 17, 137-145.	9.0	488
620	Understanding the complexity of retina and pluripotent stem cell derived retinal organoids with single cell RNA sequencing: current progress, remaining challenges and future prospective. <i>Current Eye Research</i> , 2020, 45, 385-396.	0.7	22
621	FLASH Irradiation Spares Lung Progenitor Cells and Limits the Incidence of Radio-induced Senescence. <i>Clinical Cancer Research</i> , 2020, 26, 1497-1506.	3.2	148
622	Differential Contributions of Pre- and Post-EMT Tumor Cells in Breast Cancer Metastasis. <i>Cancer Research</i> , 2020, 80, 163-169.	0.4	62
623	Data generation and network reconstruction strategies for single cell transcriptomic profiles of CRISPR-mediated gene perturbations. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194441.	0.9	4
624	Single-Cell Transcriptomics: A High-Resolution Avenue for Plant Functional Genomics. <i>Trends in Plant Science</i> , 2020, 25, 186-197.	4.3	128
625	Commensal microbiota drive the functional diversification of colon macrophages. <i>Mucosal Immunology</i> , 2020, 13, 216-229.	2.7	70
626	A single-cell transcriptome atlas for zebrafish development. <i>Developmental Biology</i> , 2020, 459, 100-108.	0.9	191
627	<i>CellBench</i> : <i>R/Bioconductor</i> software for comparing single-cell RNA-seq analysis methods. <i>Bioinformatics</i> , 2020, 36, 2288-2290.	1.8	20
628	Single-cell transcriptional analyses of spasmolytic polypeptide-expressing metaplasia arising from acute drug injury and chronic inflammation in the stomach. <i>Gut</i> , 2020, 69, 1027-1038.	6.1	50
629	Single-cell transcriptome analysis reveals differential nutrient absorption functions in human intestine. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	227
630	Cerebro: interactive visualization of scRNA-seq data. <i>Bioinformatics</i> , 2020, 36, 2311-2313.	1.8	53
631	Dissecting the human immune system with single cell RNA sequencing technology. <i>Journal of Leukocyte Biology</i> , 2020, 107, 613-623.	1.5	13

#	ARTICLE	IF	CITATIONS
632	Modeling population heterogeneity from microbial communities to immune response in cells. Cellular and Molecular Life Sciences, 2020, 77, 415-432.	2.4	5
633	Single-Cell Expression Variability Implies Cell Function. Cells, 2020, 9, 14.	1.8	27
634	Single-cell RNA sequencing analysis reveals alginate oligosaccharides preventing chemotherapy-induced mucositis. Mucosal Immunology, 2020, 13, 437-448.	2.7	38
635	Dimensionality reduction for single cell RNA sequencing data using constrained robust non-negative matrix factorization. NAR Genomics and Bioinformatics, 2020, 2, lqaa064.	1.5	10
636	Probing single-cell metabolism reveals prognostic value of highly metabolically active circulating stromal cells in prostate cancer. Science Advances, 2020, 6, .	4.7	22
637	Regulatory T cell control of systemic immunity and immunotherapy response in liver metastasis. Science Immunology, 2020, 5, .	5.6	148
638	Single-Cell RNA Sequencing Reveals the Diversity of the Immunological Landscape following Central Nervous System Infection by a Murine Coronavirus. Journal of Virology, 2020, 94, .	1.5	19
639	Profiling the Resident and Infiltrating Monocyte/Macrophages during Rejection following Kidney Transplantation. Journal of Immunology Research, 2020, 2020, 1-14.	0.9	7
641	Stromal cell diversity associated with immune evasion in human triple-negative breast cancer. EMBO Journal, 2020, 39, e104063.	3.5	224
642	Signaling molecules orchestrating liver regenerative medicine. Journal of Tissue Engineering and Regenerative Medicine, 2020, 14, 1715-1737.	1.3	6
643	Single-Cell Transcriptome Profiling Reveals β 2 Cell Maturation in Stem Cell-Derived Islets after Transplantation. Cell Reports, 2020, 32, 108067.	2.9	103
644	Benchmarking algorithms for pathway activity transformation of single-cell RNA-seq data. Computational and Structural Biotechnology Journal, 2020, 18, 2953-2961.	1.9	43
645	Pan-neuroblastoma analysis reveals age- and signature-associated driver alterations. Nature Communications, 2020, 11, 5183.	5.8	87
646	A new lymphoid-primed progenitor marked by Dach1 downregulation identified with single cell multi-omics. Nature Immunology, 2020, 21, 1574-1584.	7.0	20
647	MARS: discovering novel cell types across heterogeneous single-cell experiments. Nature Methods, 2020, 17, 1200-1206.	9.0	90
648	scLRTD : A Novel Low Rank Tensor Decomposition Method for Imputing Missing Values in Single-Cell Multi-Omics Sequencing Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1144-1153.	1.9	5
649	Reactivating latent HIV with PKC agonists induces resistance to apoptosis and is associated with phosphorylation and activation of BCL2. PLoS Pathogens, 2020, 16, e1008906.	2.1	25
650	Single-Cell Analyses Identify Brain Mural Cells Expressing CD19 as Potential Off-Tumor Targets for CAR-T Immunotherapies. Cell, 2020, 183, 126-142.e17.	13.5	269

#	ARTICLE	IF	CITATIONS
652	Paneth Cell-Derived Lysozyme Defines the Composition of Mucolytic Microbiota and the Inflammatory Tone of the Intestine. <i>Immunity</i> , 2020, 53, 398-416.e8.	6.6	97
653	Microglia and Astrocytes in Disease: Dynamic Duo or Partners in Crime?. <i>Trends in Immunology</i> , 2020, 41, 820-835.	2.9	146
654	Cell-Autonomous versus Systemic Akt Isoform Deletions Uncovered New Roles for Akt1 and Akt2 in Breast Cancer. <i>Molecular Cell</i> , 2020, 80, 87-101.e5.	4.5	32
655	Intrinsic Endocardial Defects Contribute to Hypoplastic Left Heart Syndrome. <i>Cell Stem Cell</i> , 2020, 27, 574-589.e8.	5.2	89
656	Delineation of a molecularly distinct terminally differentiated memory CD8 T cell population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25667-25678.	3.3	73
657	Kidney Single-Cell Atlas Reveals Myeloid Heterogeneity in Progression and Regression of Kidney Disease. <i>Journal of the American Society of Nephrology: JASN</i> , 2020, 31, 2833-2854.	3.0	113
658	Model-based autoencoders for imputing discrete single-cell RNA-seq data. <i>Methods</i> , 2021, 192, 112-119.	1.9	10
659	STAT3- <i>BDNF</i> - <i>TrkB</i> signalling promotes alveolar epithelial regeneration after lung injury. <i>Nature Cell Biology</i> , 2020, 22, 1197-1210.	4.6	71
660	Transposon expression in the <i>Drosophila</i> brain is driven by neighboring genes and diversifies the neural transcriptome. <i>Genome Research</i> , 2020, 30, 1559-1569.	2.4	17
661	Single-Cell Transcriptome Analysis of Colon Cancer Cell Response to 5-Fluorouracil-Induced DNA Damage. <i>Cell Reports</i> , 2020, 32, 108077.	2.9	40
662	Landscape of Exhausted Virus-Specific CD8 ⁺ T Cells in Chronic LCMV Infection. <i>Cell Reports</i> , 2020, 32, 108078.	2.9	45
663	SERGIO: A Single-Cell Expression Simulator Guided by Gene Regulatory Networks. <i>Cell Systems</i> , 2020, 11, 252-271.e11.	2.9	59
664	RIPK1 gene variants associate with obesity in humans and can be therapeutically silenced to reduce obesity in mice. <i>Nature Metabolism</i> , 2020, 2, 1113-1125.	5.1	34
665	Microanatomy of the Human Atherosclerotic Plaque by Single-Cell Transcriptomics. <i>Circulation Research</i> , 2020, 127, 1437-1455.	2.0	283
666	A Unique Population of Regulatory T Cells in Heart Potentiates Cardiac Protection From Myocardial Infarction. <i>Circulation</i> , 2020, 142, 1956-1973.	1.6	104
667	Single-Cell Genomics Reveals a Novel Cell State During Smooth Muscle Cell Phenotypic Switching and Potential Therapeutic Targets for Atherosclerosis in Mouse and Human. <i>Circulation</i> , 2020, 142, 2060-2075.	1.6	292
668	Biological insights from multi-omic analysis of 31 genomic risk loci for adult hearing difficulty. <i>PLoS Genetics</i> , 2020, 16, e1009025.	1.5	42
669	Single-Nucleus RNA-Seq Is Not Suitable for Detection of Microglial Activation Genes in Humans. <i>Cell Reports</i> , 2020, 32, 108189.	2.9	201

#	ARTICLE	IF	CITATIONS
670	Gene regulatory networks controlling vertebrate retinal regeneration. <i>Science</i> , 2020, 370, .	6.0	248
671	Single-cell transcriptome analysis of tumor and stromal compartments of pancreatic ductal adenocarcinoma primary tumors and metastatic lesions. <i>Genome Medicine</i> , 2020, 12, 80.	3.6	134
672	Sequencing dropout-and-batch effect normalization for single-cell mRNA profiles: a survey and comparative analysis. <i>Briefings in Bioinformatics</i> , 2020, 22, .	3.2	4
673	The role of SCF Skp2 and SCF β -TrCP1/2 in the cerebellar granule cell precursors. <i>Genes To Cells</i> , 2020, 25, 796-810.	0.5	0
674	Single-Cell Transcriptomics of Engineered Cardiac Tissues From Patient-Specific Induced Pluripotent Stem Cell-Derived Cardiomyocytes Reveals Abnormal Developmental Trajectory and Intrinsic Contractile Defects in Hypoplastic Right Heart Syndrome. <i>Journal of the American Heart Association</i> , 2020, 9, e016528.	1.6	30
675	What has single-cell RNA sequencing revealed about microglial neuroimmunology?. <i>Immunity, Inflammation and Disease</i> , 2020, 8, 825-839.	1.3	18
676	PAI-1-Dependent Inactivation of SMAD4-Modulated Junction and Adhesion Complex in Obese Endometrial Cancer. <i>Cell Reports</i> , 2020, 33, 108253.	2.9	6
677	The role of neutrophil extracellular traps and TLR signaling in skeletal muscle ischemia reperfusion injury. <i>FASEB Journal</i> , 2020, 34, 15753-15770.	0.2	21
678	Agonist-induced functional analysis and cell sorting associated with single-cell transcriptomics characterizes cell subtypes in normal and pathological brain. <i>Genome Research</i> , 2020, 30, 1633-1642.	2.4	7
679	MiR-302 Regulates Glycolysis to Control Cell-Cycle during Neural Tube Closure. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7534.	1.8	17
680	Co-option of Neutrophil Fates by Tissue Environments. <i>Cell</i> , 2020, 183, 1282-1297.e18.	13.5	246
681	Regulation of meiotic progression by Sertoli-cell androgen signaling. <i>Molecular Biology of the Cell</i> , 2020, 31, 2841-2862.	0.9	24
682	Identification of epilepsy-associated neuronal subtypes and gene expression underlying epileptogenesis. <i>Nature Communications</i> , 2020, 11, 5038.	5.8	80
683	Tissue distributions of antiviral drugs affect their capabilities of reducing viral loads in COVID-19 treatment. <i>European Journal of Pharmacology</i> , 2020, 889, 173634.	1.7	35
684	A gene expression signature of TREM2hi macrophages and β 1 T cells predicts immunotherapy response. <i>Nature Communications</i> , 2020, 11, 5084.	5.8	90
685	Astrocytes regulate brain extracellular pH via a neuronal activity-dependent bicarbonate shuttle. <i>Nature Communications</i> , 2020, 11, 5073.	5.8	72
686	Single-cell RNA sequencing highlights the role of inflammatory cancer-associated fibroblasts in bladder urothelial carcinoma. <i>Nature Communications</i> , 2020, 11, 5077.	5.8	281
688	Purification of Human CD34+CD90+ HSCs Reduces Target Cell Population and Improves Lentiviral Transduction for Gene Therapy. <i>Molecular Therapy - Methods and Clinical Development</i> , 2020, 18, 679-691.	1.8	28

#	ARTICLE	IF	CITATIONS
689	An Agonistic Anti-CD137 Antibody Disrupts Lymphoid Follicle Structure and T-Cell-Dependent Antibody Responses. <i>Cell Reports Medicine</i> , 2020, 1, 100035.	3.3	3
690	Single-Cell Analyses Identify Dysfunctional CD16+ CD8 ⁺ T Cells in Smokers. <i>Cell Reports Medicine</i> , 2020, 1, 100054.	3.3	21
691	AP-1 and TGF β cooperativity drives non-canonical Hedgehog signaling in resistant basal cell carcinoma. <i>Nature Communications</i> , 2020, 11, 5079.	5.8	47
692	Succinate Produced by Intestinal Microbes Promotes Specification of Tuft Cells to Suppress Ileal Inflammation. <i>Gastroenterology</i> , 2020, 159, 2101-2115.e5.	0.6	123
693	Spectacle: An interactive resource for ocular single-cell RNA sequencing data analysis. <i>Experimental Eye Research</i> , 2020, 200, 108204.	1.2	47
694	Interleukin-10 Prevents Pathological Microglia Hyperactivation following Peripheral Endotoxin Challenge. <i>Immunity</i> , 2020, 53, 1033-1049.e7.	6.6	93
695	An era of single-cell genomics consortia. <i>Experimental and Molecular Medicine</i> , 2020, 52, 1409-1418.	3.2	12
696	Type 2 and interferon inflammation regulate SARS-CoV-2 entry factor expression in the airway epithelium. <i>Nature Communications</i> , 2020, 11, 5139.	5.8	131
697	Single-cell RNA cap and tail sequencing (scRCAT-seq) reveals subtype-specific isoforms differing in transcript demarcation. <i>Nature Communications</i> , 2020, 11, 5148.	5.8	14
698	Gli1+ mesenchymal stromal cells form a pathological niche to promote airway progenitor metaplasia in the fibrotic lung. <i>Nature Cell Biology</i> , 2020, 22, 1295-1306.	4.6	62
699	Anti-GD2 CAR-NKT cells in patients with relapsed or refractory neuroblastoma: an interim analysis. <i>Nature Medicine</i> , 2020, 26, 1686-1690.	15.2	159
700	Reading the heart at single-cell resolution. <i>Journal of Molecular and Cellular Cardiology</i> , 2020, 148, 34-45.	0.9	6
701	Inherited myeloproliferative neoplasm risk affects haematopoietic stem cells. <i>Nature</i> , 2020, 586, 769-775.	13.7	101
702	Transcriptome dynamics of CD4+ T cells during malaria maps gradual transit from effector to memory. <i>Nature Immunology</i> , 2020, 21, 1597-1610.	7.0	43
703	Stress-induced RNA ³ chromatin interactions promote endothelial dysfunction. <i>Nature Communications</i> , 2020, 11, 5211.	5.8	39
704	The cellular basis of distinct thirst modalities. <i>Nature</i> , 2020, 588, 112-117.	13.7	48
705	Capillary cell-type specialization in the alveolus. <i>Nature</i> , 2020, 586, 785-789.	13.7	231
706	Flow-Induced Transcriptomic Remodeling of Endothelial Cells Derived From Human Induced Pluripotent Stem Cells. <i>Frontiers in Physiology</i> , 2020, 11, 591450.	1.3	13

#	ARTICLE	IF	CITATIONS
707	Leveraging Uncertainty in Machine Learning Accelerates Biological Discovery and Design. <i>Cell Systems</i> , 2020, 11, 461-477.e9.	2.9	92
708	Emergence of Neuronal Diversity during Vertebrate Brain Development. <i>Neuron</i> , 2020, 108, 1058-1074.e6.	3.8	51
709	Patient-derived organoids and orthotopic xenografts of primary and recurrent gliomas represent relevant patient avatars for precision oncology. <i>Acta Neuropathologica</i> , 2020, 140, 919-949.	3.9	72
710	Rapid Enhancer Remodeling and Transcription Factor Repurposing Enable High Magnitude Gene Induction upon Acute Activation of NK Cells. <i>Immunity</i> , 2020, 53, 745-758.e4.	6.6	46
711	Circadian VIPergic Neurons of the Suprachiasmatic Nuclei Sculpt the Sleep-Wake Cycle. <i>Neuron</i> , 2020, 108, 486-499.e5.	3.8	55
712	Glioma-derived IL-33 orchestrates an inflammatory brain tumor microenvironment that accelerates glioma progression. <i>Nature Communications</i> , 2020, 11, 4997.	5.8	109
713	Highly interconnected enhancer communities control lineage-determining genes in human mesenchymal stem cells. <i>Nature Genetics</i> , 2020, 52, 1227-1238.	9.4	57
714	Characteristics of anti-CD19 CAR T cell infusion products associated with efficacy and toxicity in patients with large B cell lymphomas. <i>Nature Medicine</i> , 2020, 26, 1878-1887.	15.2	321
715	Single-nucleus transcriptome analysis reveals dysregulation of angiogenic endothelial cells and neuroprotective glia in Alzheimer's disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25800-25809.	3.3	238
716	Metformin rescues Parkinson's disease phenotypes caused by hyperactive mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 26438-26447.	3.3	95
717	A spectral clustering with self-weighted multiple kernel learning method for single-cell RNA-seq data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	25
718	The activation trajectory of plasmacytoid dendritic cells in vivo during a viral infection. <i>Nature Immunology</i> , 2020, 21, 983-997.	7.0	58
719	Basal-like and classical cells coexist in pancreatic cancer revealed by single-cell analysis on biopsy-derived pancreatic cancer organoids from the classical subtype. <i>FASEB Journal</i> , 2020, 34, 12214-12228.	0.2	83
720	Comparative analysis of cell lineage differentiation during hepatogenesis in humans and mice at the single-cell transcriptome level. <i>Cell Research</i> , 2020, 30, 1109-1126.	5.7	60
721	Microglia Require CD4 ⁺ T Cells to Complete the Fetal-to-Adult Transition. <i>Cell</i> , 2020, 182, 625-640.e24.	13.5	191
722	Parallel bimodal single-cell sequencing of transcriptome and chromatin accessibility. <i>Genome Research</i> , 2020, 30, 1027-1039.	2.4	52
723	Searching large-scale scRNA-seq databases via unbiased cell embedding with Cell BLAST. <i>Nature Communications</i> , 2020, 11, 3458.	5.8	81
724	Impaired mitochondrial oxidative phosphorylation limits the self-renewal of T cells exposed to persistent antigen. <i>Nature Immunology</i> , 2020, 21, 1022-1033.	7.0	227

#	ARTICLE	IF	CITATIONS
725	Scirpy: a Scanpy extension for analyzing single-cell T-cell receptor-sequencing data. <i>Bioinformatics</i> , 2020, 36, 4817-4818.	1.8	88
726	Ageing hallmarks exhibit organ-specific temporal signatures. <i>Nature</i> , 2020, 583, 596-602.	13.7	317
727	qSNE: quadratic rate t-SNE optimizer with automatic parameter tuning for large datasets. <i>Bioinformatics</i> , 2020, 36, 5086-5092.	1.8	3
728	Single-Cell RNA-Seq Reveals Cellular Hierarchies and Impaired Developmental Trajectories in Pediatric Ependymoma. <i>Cancer Cell</i> , 2020, 38, 44-59.e9.	7.7	94
729	The Intestinal Microbiome Restricts Alphavirus Infection and Dissemination through a Bile Acid-Type I IFN Signaling Axis. <i>Cell</i> , 2020, 182, 901-918.e18.	13.5	98
730	Plasma Cell Fate Is Orchestrated by Elaborate Changes in Genome Compartmentalization and Inter-chromosomal Hubs. <i>Cell Reports</i> , 2020, 31, 107470.	2.9	14
731	Distinct Transcriptomic Cell Types and Neural Circuits of the Subiculum and Prosubiculum along the Dorsal-Ventral Axis. <i>Cell Reports</i> , 2020, 31, 107648.	2.9	49
732	Integrated Transcriptome and Network Analysis Reveals Spatiotemporal Dynamics of Calvarial Suturogenesis. <i>Cell Reports</i> , 2020, 32, 107871.	2.9	42
733	Baseline Frequency of Inflammatory Cxcl9-Expressing Tumor-Associated Macrophages Predicts Response to Avelumab Treatment. <i>Cell Reports</i> , 2020, 32, 107873.	2.9	42
734	Interleukin 27 Protects From Gastric Atrophy and Metaplasia During Chronic Autoimmune Gastritis. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2020, 10, 561-579.	2.3	15
735	A Random Matrix Theory Approach to Denoise Single-Cell Data. <i>Patterns</i> , 2020, 1, 100035.	3.1	30
736	Cancer cells undergoing epigenetic transition show short-term resistance and are transformed into cells with medium-term resistance by drug treatment. <i>Experimental and Molecular Medicine</i> , 2020, 52, 1102-1115.	3.2	10
737	Resistance to PD1 blockade in the absence of metalloprotease-mediated LAG3 shedding. <i>Science Immunology</i> , 2020, 5, .	5.6	36
738	Stem Cell Pluripotency Genes Klf4 and Oct4 Regulate Complex SMC Phenotypic Changes Critical in Late-Stage Atherosclerotic Lesion Pathogenesis. <i>Circulation</i> , 2020, 142, 2045-2059.	1.6	221
739	Gene expression and <i>in situ</i> protein profiling of candidate SARS-CoV-2 receptors in human airway epithelial cells and lung tissue. <i>European Respiratory Journal</i> , 2020, 56, 2001123.	3.1	138
740	Single-Cell Sequencing of Peripheral Mononuclear Cells Reveals Distinct Immune Response Landscapes of COVID-19 and Influenza Patients. <i>Immunity</i> , 2020, 53, 685-696.e3.	6.6	299
741	DNA methylation and gene expression signatures are associated with ataxia-telangiectasia phenotype. <i>Scientific Reports</i> , 2020, 10, 7479.	1.6	13
742	Anti-integrin αv therapy improves cardiac fibrosis after myocardial infarction by blunting cardiac PW1+ stromal cells. <i>Scientific Reports</i> , 2020, 10, 11404.	1.6	28

#	ARTICLE	IF	CITATIONS
743	DISC: a highly scalable and accurate inference of gene expression and structure for single-cell transcriptomes using semi-supervised deep learning. <i>Genome Biology</i> , 2020, 21, 170.	3.8	26
744	Endocrine Significance of SARS-CoV-2's Reliance on ACE2. <i>Endocrinology</i> , 2020, 161, .	1.4	120
745	Single-Cell RNA Sequencing Unravels Heterogeneity of the Stromal Niche in Cutaneous Melanoma Heterogeneous Spheroids. <i>Cancers</i> , 2020, 12, 3324.	1.7	19
746	Characterisation of CD4+ T-cell subtypes using single cell RNA sequencing and the impact of cell number and sequencing depth. <i>Scientific Reports</i> , 2020, 10, 19825.	1.6	17
747	Genetic and structural analysis of the in vivo functional redundancy between murine NANOS2 and NANOS3. <i>Development (Cambridge)</i> , 2020, 148, .	1.2	8
748	Integrated Single-Cell RNA-Sequencing Analysis of Aquaporin 5-Expressing Mouse Lung Epithelial Cells Identifies GPRC5A as a Novel Validated Type I Cell Surface Marker. <i>Cells</i> , 2020, 9, 2460.	1.8	8
749	Tau Pathology Drives Dementia Risk-Associated Gene Networks toward Chronic Inflammatory States and Immunosuppression. <i>Cell Reports</i> , 2020, 33, 108398.	2.9	57
750	Distinct oligodendrocyte populations have spatial preference and different responses to spinal cord injury. <i>Nature Communications</i> , 2020, 11, 5860.	5.8	84
751	A molecular cell atlas of the human lung from single-cell RNA sequencing. <i>Nature</i> , 2020, 587, 619-625.	13.7	963
752	D-EE: Distributed software for visualizing intrinsic structure of large-scale single-cell data. <i>GigaScience</i> , 2020, 9, .	3.3	1
753	Expression of SARS-CoV-2 Entry Factors in the Pancreas of Normal Organ Donors and Individuals with COVID-19. <i>Cell Metabolism</i> , 2020, 32, 1041-1051.e6.	7.2	135
754	Mutations in BRCA1 and BRCA2 differentially affect the tumor microenvironment and response to checkpoint blockade immunotherapy. <i>Nature Cancer</i> , 2020, 1, 1188-1203.	5.7	114
755	Human innate lymphoid cell precursors express CD48 that modulates ILC differentiation through 2B4 signaling. <i>Science Immunology</i> , 2020, 5, .	5.6	10
756	A Conserved TCR ^{hi} Signature Dominates a Highly Polyclonal T-Cell Expansion During the Acute Phase of a Murine Malaria Infection. <i>Frontiers in Immunology</i> , 2020, 11, 587756.	2.2	9
757	Requisite Chromatin Remodeling for Myeloid and Erythroid Lineage Differentiation from Erythromyeloid Progenitors. <i>Cell Reports</i> , 2020, 33, 108395.	2.9	6
758	An Integrated Epigenomic and Transcriptomic Map of Mouse and Human $\hat{\pm}$ T Cell Development. <i>Immunity</i> , 2020, 53, 1182-1201.e8.	6.6	49
759	Androgen Signaling Regulates SARS-CoV-2 Receptor Levels and Is Associated with Severe COVID-19 Symptoms in Men. <i>Cell Stem Cell</i> , 2020, 27, 876-889.e12.	5.2	167
760	An IL-27-Driven Transcriptional Network Identifies Regulators of IL-10 Expression across T Helper Cell Subsets. <i>Cell Reports</i> , 2020, 33, 108433.	2.9	54

#	ARTICLE	IF	CITATIONS
761	gCAnno: a graph-based single cell type annotation method. BMC Genomics, 2020, 21, 823.	1.2	0
762	In vivo Perturb-Seq reveals neuronal and glial abnormalities associated with autism risk genes. Science, 2020, 370, .	6.0	155
763	Liver Immune Profiling Reveals Pathogenesis and Therapeutics for Biliary Atresia. Cell, 2020, 183, 1867-1883.e26.	13.5	70
764	Longitudinal Multi-omics Analyses Identify Responses of Megakaryocytes, Erythroid Cells, and Plasmablasts as Hallmarks of Severe COVID-19. Immunity, 2020, 53, 1296-1314.e9.	6.6	278
765	Pik3c3 deficiency in myeloid cells imparts partial resistance to experimental autoimmune encephalomyelitis associated with reduced IL-1 β production. Cellular and Molecular Immunology, 2021, 18, 2024-2039.	4.8	12
766	SSMD: a semi-supervised approach for a robust cell type identification and deconvolution of mouse transcriptomics data. Briefings in Bioinformatics, 2021, 22, .	3.2	3
767	Robustifying genomic classifiers to batch effects via ensemble learning. Bioinformatics, 2021, 37, 1521-1527.	1.8	13
768	Deep feature extraction of single-cell transcriptomes by generative adversarial network. Bioinformatics, 2021, 37, 1345-1351.	1.8	20
769	An allosteric interleukin-1 receptor modulator mitigates inflammation and photoreceptor toxicity in a model of retinal degeneration. Journal of Neuroinflammation, 2020, 17, 359.	3.1	10
770	Expression Partitioning of Duplicate Genes at Single Cell Resolution in Arabidopsis Roots. Frontiers in Genetics, 2020, 11, 596150.	1.1	23
771	Single cell RNA sequencing of human microglia uncovers a subset associated with Alzheimer's disease. Nature Communications, 2020, 11, 6129.	5.8	371
772	muscat detects subpopulation-specific state transitions from multi-sample multi-condition single-cell transcriptomics data. Nature Communications, 2020, 11, 6077.	5.8	223
773	Thick PCL Fibers Improving Host Remodeling of PGS/PCL Composite Grafts Implanted in Rat Common Carotid Arteries. Small, 2020, 16, e2004133.	5.2	29
774	Histone H3.3G34-Mutant Interneuron Progenitors Co-opt PDGFRA for Gliomagenesis. Cell, 2020, 183, 1617-1633.e22.	13.5	93
775	Fibrosis: from mechanisms to medicines. Nature, 2020, 587, 555-566.	13.7	746
776	Generation of human striatal organoids and cortico-striatal assembloids from human pluripotent stem cells. Nature Biotechnology, 2020, 38, 1421-1430.	9.4	206
777	Low-Avidity CD4+ T Cell Responses to SARS-CoV-2 in Unexposed Individuals and Humans with Severe COVID-19. Immunity, 2020, 53, 1258-1271.e5.	6.6	255
778	Single-cell RNA-seq reveals CD16+ monocytes as key regulators of human monocyte transcriptional response to Toxoplasma. Scientific Reports, 2020, 10, 21047.	1.6	8

#	ARTICLE	IF	CITATIONS
779	Single-cell transcriptome profiling of an adult human cell atlas of 15 major organs. <i>Genome Biology</i> , 2020, 21, 294.	3.8	118
780	Conserved Epigenetic Regulatory Logic Infers Genes Governing Cell Identity. <i>Cell Systems</i> , 2020, 11, 625-639.e13.	2.9	31
781	Coupled co-clustering-based unsupervised transfer learning for the integrative analysis of single-cell genomic data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	9
782	SITC cancer immunotherapy resource document: a compass in the land of biomarker discovery. , 2020, 8, e000705.		20
783	Reconstitution of prospermatogonial specification in vitro from human induced pluripotent stem cells. <i>Nature Communications</i> , 2020, 11, 5656.	5.8	75
784	Persistent transcriptional programmes are associated with remote memory. <i>Nature</i> , 2020, 587, 437-442.	13.7	61
785	Group 3 Innate Lymphoid Cells Program a Distinct Subset of IL-22BP-Producing Dendritic Cells Demarcating Solitary Intestinal Lymphoid Tissues. <i>Immunity</i> , 2020, 53, 1015-1032.e8.	6.6	41
786	FunRes: resolving tissue-specific functional cell states based on a cell-cell communication network model. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	7
787	Comprehensive mapping of the human cytokine gene regulatory network. <i>Nucleic Acids Research</i> , 2020, 48, 12055-12073.	6.5	20
788	High-Spatial-Resolution Multi-Omics Sequencing via Deterministic Barcoding in Tissue. <i>Cell</i> , 2020, 183, 1665-1681.e18.	13.5	423
789	A single-cell atlas and lineage analysis of the adult <i>Drosophila</i> ovary. <i>Nature Communications</i> , 2020, 11, 5628.	5.8	89
790	A human cell atlas of fetal chromatin accessibility. <i>Science</i> , 2020, 370, .	6.0	265
791	Type I interferons drive the maturation of human DC3s with a distinct costimulatory profile characterized by high GITRL. <i>Science Immunology</i> , 2020, 5, .	5.6	14
792	SARS-CoV-2 Cell Entry Factors ACE2 and TMPRSS2 Are Expressed in the Microvasculature and Ducts of Human Pancreas but Are Not Enriched in Î² Cells. <i>Cell Metabolism</i> , 2020, 32, 1028-1040.e4.	7.2	148
793	Heterogeneity of midgut cells and their differential responses to blood meal ingestion by the mosquito, <i>Aedes aegypti</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2020, 127, 103496.	1.2	20
794	Ocular macrophage origin and heterogeneity during steady state and experimental choroidal neovascularization. <i>Journal of Neuroinflammation</i> , 2020, 17, 341.	3.1	16
795	Human and Mouse Transcriptome Profiling Identifies Cross-Species Homology in Pulmonary and Lymph Node Mononuclear Phagocytes. <i>Cell Reports</i> , 2020, 33, 108337.	2.9	38
796	Characterization of iCell cardiomyocytes using single-cell RNA-sequencing methods. <i>Journal of Pharmacological and Toxicological Methods</i> , 2020, 106, 106915.	0.3	10

#	ARTICLE	IF	CITATIONS
797	Assessment of statistical methods from single cell, bulk RNA-seq, and metagenomics applied to microbiome data. <i>Genome Biology</i> , 2020, 21, 191.	3.8	67
798	Profiling Microglia From Alzheimer's Disease Donors and Non-demented Elderly in Acute Human Postmortem Cortical Tissue. <i>Frontiers in Molecular Neuroscience</i> , 2020, 13, 134.	1.4	51
799	A Distinct Transcriptional Program in Human CAR T Cells Bearing the 4-1BB Signaling Domain Revealed by scRNA-Seq. <i>Molecular Therapy</i> , 2020, 28, 2577-2592.	3.7	58
800	Integration of GWAS Summary Statistics and Gene Expression Reveals Target Cell Types Underlying Kidney Function Traits. <i>Journal of the American Society of Nephrology: JASN</i> , 2020, 31, 2326-2340.	3.0	23
801	Single-cell analysis of two severe COVID-19 patients reveals a monocyte-associated and tocilizumab-responding cytokine storm. <i>Nature Communications</i> , 2020, 11, 3924.	5.8	180
802	Single-Cell Transcriptome Analysis Profile of Meniscal Tissue Macrophages in Human Osteoarthritis. <i>Journal of Immunology Research</i> , 2020, 2020, 1-16.	0.9	7
803	Integrated Skin Transcriptomics and Serum Multiplex Assays Reveal Novel Mechanisms of Wound Healing in Diabetic Foot Ulcers. <i>Diabetes</i> , 2020, 69, 2157-2169.	0.3	68
804	Advances in single cell technologies in immunology. <i>BioTechniques</i> , 2020, 69, 226-236.	0.8	9
805	TREM2 Modulation Remodels the Tumor Myeloid Landscape Enhancing Anti-PD-1 Immunotherapy. <i>Cell</i> , 2020, 182, 886-900.e17.	13.5	309
806	Efficient Strategies for Microglia Replacement in the Central Nervous System. <i>Cell Reports</i> , 2020, 32, 108041.	2.9	68
807	Network Approaches for Dissecting the Immune System. <i>IScience</i> , 2020, 23, 101354.	1.9	28
808	Resolving Fates and Single-Cell Transcriptomes of Hematopoietic Stem Cell Clones by PolyloxExpress Barcoding. <i>Cell Stem Cell</i> , 2020, 27, 383-395.e8.	5.2	88
809	Metabolic conditioning of CD8+ effector T cells for adoptive cell therapy. <i>Nature Metabolism</i> , 2020, 2, 703-716.	5.1	83
810	Tuft Cells Inhibit Pancreatic Tumorigenesis in Mice by Producing Prostaglandin D2. <i>Gastroenterology</i> , 2020, 159, 1866-1881.e8.	0.6	45
811	Single-Cell Transcriptomic Profiling of Vascular Smooth Muscle Cell Phenotype Modulation in Marfan Syndrome Aortic Aneurysm. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2020, 40, 2195-2211.	1.1	126
812	Impact of Local Alloimmunity and Recipient Cells in Transplant Arteriosclerosis. <i>Circulation Research</i> , 2020, 127, 974-993.	2.0	17
813	Biological and Medical Importance of Cellular Heterogeneity Deciphered by Single-Cell RNA Sequencing. <i>Cells</i> , 2020, 9, 1751.	1.8	31
814	Single-Cell Reconstruction of Human Basal Cell Diversity in Normal and Idiopathic Pulmonary Fibrosis Lungs. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 202, 1540-1550.	2.5	107

#	ARTICLE	IF	CITATIONS
815	Emergence of a High-Plasticity Cell State during Lung Cancer Evolution. <i>Cancer Cell</i> , 2020, 38, 229-246.e13.	7.7	210
816	A robust nonlinear low-dimensional manifold for single cell RNA-seq data. <i>BMC Bioinformatics</i> , 2020, 21, 324.	1.2	12
817	Brain Endothelial Cells Are Exquisite Sensors of Age-Related Circulatory Cues. <i>Cell Reports</i> , 2020, 30, 4418-4432.e4.	2.9	133
818	High-dimensional single-cell analysis delineates radiofrequency ablation induced immune microenvironmental remodeling in pancreatic cancer. <i>Cell Death and Disease</i> , 2020, 11, 589.	2.7	34
819	Cycling Stem Cells Are Radioresistant and Regenerate the Intestine. <i>Cell Reports</i> , 2020, 32, 107952.	2.9	37
820	Single-cell RNA-seq analysis revealed long-lasting adverse effects of tamoxifen on neurogenesis in prenatal and adult brains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19578-19589.	3.3	33
821	The safety and clinical effects of administering a multiantigen-targeted T cell therapy to patients with multiple myeloma. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	25
822	A Single-Cell Atlas of the Human Healthy Airways. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 202, 1636-1645.	2.5	282
823	Bayesian model selection reveals biological origins of zero inflation in single-cell transcriptomics. <i>Genome Biology</i> , 2020, 21, 183.	3.8	45
824	Epigenomically Bistable Regions across Neuron-Specific Genes Govern Neuron Eligibility to a Coding Ensemble in the Hippocampus. <i>Cell Reports</i> , 2020, 31, 107789.	2.9	9
825	PHF7 Modulates BRDT Stability and Histone-to-Protamine Exchange during Spermiogenesis. <i>Cell Reports</i> , 2020, 32, 107950.	2.9	23
826	InÂVivo Chimeric Alzheimerâ€™s Disease Modeling of Apolipoprotein E4 Toxicity in Human Neurons. <i>Cell Reports</i> , 2020, 32, 107962.	2.9	30
827	Butyrophilin-like proteins display combinatorial diversity in selecting and maintaining signature intraepithelial Î³Î± T cell compartments. <i>Nature Communications</i> , 2020, 11, 3769.	5.8	44
828	Immunoprophylactic and immunotherapeutic control of hormone receptor-positive breast cancer. <i>Nature Communications</i> , 2020, 11, 3819.	5.8	71
829	The hepatocyte clock and feeding control chronophysiology of multiple liver cell types. <i>Science</i> , 2020, 369, 1388-1394.	6.0	103
830	Interactions of Monocytes, HIV, and ART Identified by an Innovative scRNAseq Pipeline: Pathways to Reservoirs and HIV-Associated Comorbidities. <i>MBio</i> , 2020, 11, .	1.8	17
831	Regenerative Reprogramming of the Intestinal Stem Cell State via Hippo Signaling Suppresses Metastatic Colorectal Cancer. <i>Cell Stem Cell</i> , 2020, 27, 590-604.e9.	5.2	112
832	Notch activation in the mouse mammary luminal lineage leads to ductal hyperplasia and altered partitioning of luminal cell subtypes. <i>Experimental Cell Research</i> , 2020, 395, 112156.	1.2	7

#	ARTICLE	IF	CITATIONS
833	Epigenetic regulator function through mouse gastrulation. <i>Nature</i> , 2020, 584, 102-108.	13.7	89
834	GMM-Demux: sample demultiplexing, multiplet detection, experiment planning, and novel cell-type verification in single cell sequencing. <i>Genome Biology</i> , 2020, 21, 188.	3.8	37
835	Single-Cell Isolation from Regenerating Murine Muscles for RNA-Sequencing Analysis. <i>STAR Protocols</i> , 2020, 1, 100051.	0.5	8
836	Histone deacetylase 3 controls lung alveolar macrophage development and homeostasis. <i>Nature Communications</i> , 2020, 11, 3822.	5.8	22
837	Severe COVID-19 Is Marked by a Dysregulated Myeloid Cell Compartment. <i>Cell</i> , 2020, 182, 1419-1440.e23.	13.5	1,162
838	Complex Autoinflammatory Syndrome Unveils Fundamental Principles of JAK1 Kinase Transcriptional and Biochemical Function. <i>Immunity</i> , 2020, 53, 672-684.e11.	6.6	66
839	Inflammatory Signals Induce AT2 Cell-Derived Damage-Associated Transient Progenitors that Mediate Alveolar Regeneration. <i>Cell Stem Cell</i> , 2020, 27, 366-382.e7.	5.2	303
840	Early pathogenesis of cystic fibrosis gallbladder disease in a porcine model. <i>Laboratory Investigation</i> , 2020, 100, 1388-1399.	1.7	12
841	A Widespread Neurogenic Potential of Neocortical Astrocytes Is Induced by Injury. <i>Cell Stem Cell</i> , 2020, 27, 605-617.e5.	5.2	77
842	Human Stem Cell Resources Are an Inroad to Neandertal DNA Functions. <i>Stem Cell Reports</i> , 2020, 15, 214-225.	2.3	18
843	Human Tumor-Infiltrating MAIT Cells Display Hallmarks of Bacterial Antigen Recognition in Colorectal Cancer. <i>Cell Reports Medicine</i> , 2020, 1, 100039.	3.3	32
844	Robust gene expression programs underlie recurrent cell states and phenotype switching in melanoma. <i>Nature Cell Biology</i> , 2020, 22, 986-998.	4.6	148
845	Two distinct pathways of pregranulosa cell differentiation support follicle formation in the mouse ovary. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20015-20026.	3.3	137
846	Transcriptomic comparison of human and mouse brain microvessels. <i>Scientific Reports</i> , 2020, 10, 12358.	1.6	89
847	Efficiency and Target Derepression of Anti-miR-92a: Results of a First in Human Study. <i>Nucleic Acid Therapeutics</i> , 2020, 30, 335-345.	2.0	93
848	Status and Potential of Single-Cell Transcriptomics for Understanding Plant Development and Functional Biology. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2020, 97, 997-1006.	1.1	7
849	Single-cell transcriptomic analysis in a mouse model deciphers cell transition states in the multistep development of esophageal cancer. <i>Nature Communications</i> , 2020, 11, 3715.	5.8	79
850	Differential expression of tissue-restricted antigens among mTEC is associated with distinct autoreactive T cell fates. <i>Nature Communications</i> , 2020, 11, 3734.	5.8	12

#	ARTICLE	IF	CITATIONS
851	Single-cell transcriptome profiling reveals neutrophil heterogeneity in homeostasis and infection. <i>Nature Immunology</i> , 2020, 21, 1119-1133.	7.0	380
852	Single-cell RNA sequencing reveals the landscape of early female germ cell development. <i>FASEB Journal</i> , 2020, 34, 12634-12645.	0.2	38
853	Complex Genetics in Pancreatitis. <i>Pancreas</i> , 2020, 49, 983-998.	0.5	8
854	Demystifying "drop-outs" in single-cell UMI data. <i>Genome Biology</i> , 2020, 21, 196.	3.8	72
855	Loss of NARS1 impairs progenitor proliferation in cortical brain organoids and leads to microcephaly. <i>Nature Communications</i> , 2020, 11, 4038.	5.8	44
856	Single-cell landscape of immunological responses in patients with COVID-19. <i>Nature Immunology</i> , 2020, 21, 1107-1118.	7.0	508
857	Single-Cell RNA-seq Reveals Obesity-Induced Alterations in the Brca1-Mutated Mammary Gland Microenvironment. <i>Cancers</i> , 2020, 12, 2235.	1.7	5
858	Immature neutrophil signature associated with the sexual dimorphism of systemic juvenile idiopathic arthritis. <i>Journal of Leukocyte Biology</i> , 2020, 108, 1319-1327.	1.5	6
859	Single-Cell Profiling Shows Murine Forebrain Neural Stem Cells Reacquire a Developmental State when Activated for Adult Neurogenesis. <i>Cell Reports</i> , 2020, 32, 108022.	2.9	40
860	Comparison of Human Antral Follicles of Xenograft versus Ovarian Origin Reveals Disparate Molecular Signatures. <i>Cell Reports</i> , 2020, 32, 108027.	2.9	21
861	Adaptive immune responses to SARS-CoV-2 infection in severe versus mild individuals. <i>Signal Transduction and Targeted Therapy</i> , 2020, 5, 156.	7.1	134
862	Distinct fibroblast subsets regulate lacteal integrity through YAP/TAZ-induced VEGF-C in intestinal villi. <i>Nature Communications</i> , 2020, 11, 4102.	5.8	36
863	An interpretable deep-learning architecture of capsule networks for identifying cell-type gene expression programs from single-cell RNA-sequencing data. <i>Nature Machine Intelligence</i> , 2020, 2, 693-703.	8.3	40
864	A Systems Biology Approach to Identifying a Master Regulator That Can Transform the Fast Growing Cellular State to a Slowly Growing One in Early Colorectal Cancer Development Model. <i>Frontiers in Genetics</i> , 2020, 11, 570546.	1.1	12
865	Single-Cell Transcriptome Profiling of Immune Cell Repertoire of the Atlantic Cod Which Naturally Lacks the Major Histocompatibility Class II System. <i>Frontiers in Immunology</i> , 2020, 11, 559555.	2.2	24
866	Single-Cell Transcriptomics Reveals Early Emergence of Liver Parenchymal and Non-parenchymal Cell Lineages. <i>Cell</i> , 2020, 183, 702-716.e14.	13.5	52
867	Comparative Neurobiology of Biogenic Amines in Animal Models in Deuterostomes. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	7
868	Adaptation and selection shape clonal evolution of tumors during residual disease and recurrence. <i>Nature Communications</i> , 2020, 11, 5017.	5.8	28

#	ARTICLE	IF	CITATIONS
869	Developmental and cellular age direct conversion of CD4 ⁺ T cells into ROR γ ⁺ or Helios ⁺ colon Treg cells. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	50
870	Single-cell RNA sequencing of murine islets shows high cellular complexity at all stages of autoimmune diabetes. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	78
871	Controlled Cycling and Quiescence Enables Efficient HDR in Engraftment-Enriched Adult Hematopoietic Stem and Progenitor Cells. <i>Cell Reports</i> , 2020, 32, 108093.	2.9	54
872	Overcoming primary and acquired resistance to anti-PD-L1 therapy by induction and activation of tumor-residing cDC1s. <i>Nature Communications</i> , 2020, 11, 5415.	5.8	85
873	Single-cell analysis of ROR γ [±] tracer mouse lung reveals ILC progenitors and effector ILC2 subsets. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	74
874	Probing infectious disease by single-cell RNA sequencing: Progresses and perspectives. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2962-2971.	1.9	32
875	Enzymatic Dissociation Induces Transcriptional and Proteotype Bias in Brain Cell Populations. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7944.	1.8	72
876	Dissecting heterogeneous cell populations across drug and disease conditions with PopAlign. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28784-28794.	3.3	20
877	Persistent STAT5 activation reprograms the epigenetic landscape in CD4 ⁺ T cells to drive polyfunctionality and antitumor immunity. <i>Science Immunology</i> , 2020, 5, .	5.6	40
878	The role of nicotinic receptors in SARS-CoV-2 receptor ACE2 expression in intestinal epithelia. <i>Bioelectronic Medicine</i> , 2020, 6, 20.	1.0	5
879	Transcriptional Programs of Circuit Assembly in the Drosophila Visual System. <i>Neuron</i> , 2020, 108, 1045-1057.e6.	3.8	115
880	A review of computational strategies for denoising and imputation of single-cell transcriptomic data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	27
881	Limiting Self-Renewal of the Basal Compartment by PKA Activation Induces Differentiation and Alters the Evolution of Mammary Tumors. <i>Developmental Cell</i> , 2020, 55, 544-557.e6.	3.1	20
882	Murine interfollicular epidermal differentiation is gradualistic with GRHL3 controlling progression from stem to transition cell states. <i>Nature Communications</i> , 2020, 11, 5434.	5.8	33
883	Marcksl1 modulates endothelial cell mechanoresponse to haemodynamic forces to control blood vessel shape and size. <i>Nature Communications</i> , 2020, 11, 5476.	5.8	23
884	Single-cell analysis of copy-number alterations in serous ovarian cancer reveals substantial heterogeneity in both low- and high-grade tumors. <i>Cell Cycle</i> , 2020, 19, 3154-3166.	1.3	13
885	Single-cell RNA Sequencing Data Clustering by Low-Rank Subspace Ensemble Framework. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, PP, 1-1.	1.9	10
886	Leukemia-on-a-chip: Dissecting the chemoresistance mechanisms in B cell acute lymphoblastic leukemia bone marrow niche. <i>Science Advances</i> , 2020, 6, .	4.7	44

#	ARTICLE	IF	CITATIONS
887	Single symbiotic cell transcriptome sequencing of coral. <i>Genomics</i> , 2020, 112, 5305-5312.	1.3	5
888	Spatial cell type composition in normal and Alzheimers human brains is revealed using integrated mouse and human single cell RNA sequencing. <i>Scientific Reports</i> , 2020, 10, 18014.	1.6	9
889	Single-cell profiling reveals an endothelium-mediated immunomodulatory pathway in the eye choroid. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	55
890	Dynamics of human monocytes and airway macrophages during healthy aging and after transplant. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	113
891	Constructing and deconstructing GATA2-regulated cell fate programs to establish developmental trajectories. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	28
892	A committed tissue-resident memory T cell precursor within the circulating CD8+ effector T cell pool. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	72
893	Anti-human TREM2 induces microglia proliferation and reduces pathology in an Alzheimerâ€™s disease model. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	223
894	Single-cell RNA sequencing identifies shared differentiation paths of mouse thymic innate T cells. <i>Nature Communications</i> , 2020, 11, 4367.	5.8	56
895	Inference and multiscale model of epithelial-to-mesenchymal transition via single-cell transcriptomic data. <i>Nucleic Acids Research</i> , 2020, 48, 9505-9520.	6.5	45
896	CSS: cluster similarity spectrum integration of single-cell genomics data. <i>Genome Biology</i> , 2020, 21, 224.	3.8	30
898	Suprachiasmatic VIP neurons are required for normal circadian rhythmicity and comprised of molecularly distinct subpopulations. <i>Nature Communications</i> , 2020, 11, 4410.	5.8	72
899	The cellular and molecular landscape of hypothalamic patterning and differentiation from embryonic to late postnatal development. <i>Nature Communications</i> , 2020, 11, 4360.	5.8	96
900	Î”9-Tetrahydrocannabinol Prevents Mortality from Acute Respiratory Distress Syndrome through the Induction of Apoptosis in Immune Cells, Leading to Cytokine Storm Suppression. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6244.	1.8	38
901	Characterization of Diabetic and Non-Diabetic Foot Ulcers Using Single-Cell RNA-Sequencing. <i>Micromachines</i> , 2020, 11, 815.	1.4	34
902	Tumor-Infiltrating Regulatory T-cell Accumulation in the Tumor Microenvironment Is Mediated by IL33/ST2 Signaling. <i>Cancer Immunology Research</i> , 2020, 8, 1393-1406.	1.6	28
903	Multi-omic single cell analysis resolves novel stromal cell populations in healthy and diseased human tendon. <i>Scientific Reports</i> , 2020, 10, 13939.	1.6	72
904	Identification of the key gene and pathways associated with osteoarthritis via single-cell RNA sequencing on synovial fibroblasts. <i>Medicine (United States)</i> , 2020, 99, e21707.	0.4	10
905	Anti-Inflammatory Actions of Soluble Ninjurin-1 Ameliorate Atherosclerosis. <i>Circulation</i> , 2020, 142, 1736-1751.	1.6	34

#	ARTICLE	IF	CITATIONS
906	Single-Cell Analysis of Neonatal HSC Ontogeny Reveals Gradual and Uncoordinated Transcriptional Reprogramming that Begins before Birth. <i>Cell Stem Cell</i> , 2020, 27, 732-747.e7.	5.2	53
907	Pharmacologically reversible zonation-dependent endothelial cell transcriptomic changes with neurodegenerative disease associations in the aged brain. <i>Nature Communications</i> , 2020, 11, 4413.	5.8	59
908	Single-cell RNA-seq data clustering: A survey with performance comparison study. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2040005.	0.3	16
909	Identification of hub genes in diabetic kidney disease via multiple-microarray analysis. <i>Annals of Translational Medicine</i> , 2020, 8, 997-997.	0.7	16
910	Presynaptic dysfunction in CASK-related neurodevelopmental disorders. <i>Translational Psychiatry</i> , 2020, 10, 312.	2.4	28
911	Molecular classification and immunologic characteristics of immunoreactive high-grade serous ovarian cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 8103-8114.	1.6	2
912	A single-cell RNA-seq atlas of <i>Schistosoma mansoni</i> identifies a key regulator of blood feeding. <i>Science</i> , 2020, 369, 1644-1649.	6.0	108
913	FUT9-Driven Programming of Colon Cancer Cells towards a Stem Cell-Like State. <i>Cancers</i> , 2020, 12, 2580.	1.7	15
914	Multiplatform genomic profiling and magnetic resonance imaging identify mechanisms underlying intratumor heterogeneity in meningioma. <i>Nature Communications</i> , 2020, 11, 4803.	5.8	56
915	The myeloid type I interferon response to myocardial infarction begins in bone marrow and is regulated by Nrf2-activated macrophages. <i>Science Immunology</i> , 2020, 5, .	5.6	43
916	H3.3 G34W Promotes Growth and Impedes Differentiation of Osteoblast-Like Mesenchymal Progenitors in Giant Cell Tumor of Bone. <i>Cancer Discovery</i> , 2020, 10, 1968-1987.	7.7	40
917	Single-Cell Characterization of Malignant Phenotypes and Developmental Trajectories of Adrenal Neuroblastoma. <i>Cancer Cell</i> , 2020, 38, 716-733.e6.	7.7	137
918	Oxidative Metabolism Drives Immortalization of Neural Stem Cells during Tumorigenesis. <i>Cell</i> , 2020, 182, 1490-1507.e19.	13.5	100
919	The Human and Mouse Enteric Nervous System at Single-Cell Resolution. <i>Cell</i> , 2020, 182, 1606-1622.e23.	13.5	287
920	Retinal homeostasis and metformin-induced protection are not affected by retina-specific Ppar γ knockout. <i>Redox Biology</i> , 2020, 37, 101700.	3.9	5
921	A single-cell survey of cellular hierarchy in acute myeloid leukemia. <i>Journal of Hematology and Oncology</i> , 2020, 13, 128.	6.9	45
922	GRACE: A Graph-Based Cluster Ensemble Approach for Single-Cell RNA-Seq Data Clustering. <i>IEEE Access</i> , 2020, 8, 166730-166741.	2.6	6
923	The causal effect of obesity on prediabetes and insulin resistance reveals the important role of adipose tissue in insulin resistance. <i>PLoS Genetics</i> , 2020, 16, e1009018.	1.5	29

#	ARTICLE	IF	CITATIONS
924	Functionally Diverse Inflammatory Responses in Peripheral and Liver Monocytes in Alcohol-Associated Hepatitis. <i>Hepatology Communications</i> , 2020, 4, 1459-1476.	2.0	19
925	Human Cell Atlas and cell-type authentication for regenerative medicine. <i>Experimental and Molecular Medicine</i> , 2020, 52, 1443-1451.	3.2	22
926	Single Cell RNA-seq Data Analysis Reveals the Potential Risk of SARS-CoV-2 Infection Among Different Respiratory System Conditions. <i>Frontiers in Genetics</i> , 2020, 11, 942.	1.1	7
927	The CNS Myelin Proteome: Deep Profile and Persistence After Post-mortem Delay. <i>Frontiers in Cellular Neuroscience</i> , 2020, 14, 239.	1.8	54
928	An atlas of immune cell exhaustion in HIV-infected individuals revealed by single-cell transcriptomics. <i>Emerging Microbes and Infections</i> , 2020, 9, 2333-2347.	3.0	48
929	StreamFlow: Cross-Breeding Cloud With HPC. <i>IEEE Transactions on Emerging Topics in Computing</i> , 2021, 9, 1723-1737.	3.2	27
930	VEGF-C protects the integrity of the bone marrow perivascular niche in mice. <i>Blood</i> , 2020, 136, 1871-1883.	0.6	38
931	Tuning parameters of dimensionality reduction methods for single-cell RNA-seq analysis. <i>Genome Biology</i> , 2020, 21, 212.	3.8	18
932	Heterotypic cell-cell communication regulates glandular stem cell multipotency. <i>Nature</i> , 2020, 584, 608-613.	13.7	82
933	Multiplexed single-cell transcriptional response profiling to define cancer vulnerabilities and therapeutic mechanism of action. <i>Nature Communications</i> , 2020, 11, 4296.	5.8	98
934	β 2 Integrins differentially regulate β 3 T cell subset thymic development and peripheral maintenance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22367-22377.	3.3	10
935	CIPHER-SC: Disease-Gene Association Inference Using Graph Convolution on a Context-Aware Network with Single-Cell Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, PP, 1-1.	1.9	8
936	Mosquito cellular immunity at single-cell resolution. <i>Science</i> , 2020, 369, 1128-1132.	6.0	68
937	KIAA1522 potentiates TNF α -NF κ B signaling to antagonize platinum-based chemotherapy in lung adenocarcinoma. <i>Journal of Experimental and Clinical Cancer Research</i> , 2020, 39, 170.	3.5	13
938	The Construction of Bone Metastasis-Specific Prognostic Model and Co-expressed Network of Alternative Splicing in Breast Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 790.	1.8	6
939	A clustering-independent method for finding differentially expressed genes in single-cell transcriptome data. <i>Nature Communications</i> , 2020, 11, 4318.	5.8	50
940	Identification of cell types from single cell data using stable clustering. <i>Scientific Reports</i> , 2020, 10, 12349.	1.6	28
941	Intracrine Testosterone Activation in Human Pancreatic β 2-Cells Stimulates Insulin Secretion. <i>Diabetes</i> , 2020, 69, 2392-2399.	0.3	13

#	ARTICLE	IF	CITATIONS
942	Wnt activation as a therapeutic strategy in medulloblastoma. <i>Nature Communications</i> , 2020, 11, 4323.	5.8	34
943	Single cell transcriptomics identifies a signaling network coordinating endoderm and mesoderm diversification during foregut organogenesis. <i>Nature Communications</i> , 2020, 11, 4158.	5.8	129
944	Conventional Co-Housing Modulates Murine Gut Microbiota and Hematopoietic Gene Expression. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6143.	1.8	10
945	Massively parallel and time-resolved RNA sequencing in single cells with scNT-seq. <i>Nature Methods</i> , 2020, 17, 991-1001.	9.0	103
946	Low tolerance for transcriptional variation at cohesin genes is accompanied by functional links to disease-relevant pathways. <i>Journal of Medical Genetics</i> , 2021, 58, 534-542.	1.5	3
947	Single-cell sequencing techniques from individual to multiomics analyses. <i>Experimental and Molecular Medicine</i> , 2020, 52, 1419-1427.	3.2	136
948	Meningeal β 1 T cells regulate anxiety-like behavior via IL-17a signaling in neurons. <i>Nature Immunology</i> , 2020, 21, 1421-1429.	7.0	225
949	Distinct evolutionary paths in chronic lymphocytic leukemia during resistance to the graft-versus-leukemia effect. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	17
950	Homeostatic mini-intestines through scaffold-guided organoid morphogenesis. <i>Nature</i> , 2020, 585, 574-578.	13.7	408
951	Reprogramming roadmap reveals route to human induced trophoblast stem cells. <i>Nature</i> , 2020, 586, 101-107.	13.7	131
952	β 4CB-seq: microfluidic cell barcoding and sequencing for high-resolution imaging and sequencing of single cells. <i>Lab on A Chip</i> , 2020, 20, 3899-3913.	3.1	16
953	Tumor-on-a-chip platform to interrogate the role of macrophages in tumor progression. <i>Integrative Biology (United Kingdom)</i> , 2020, 12, 221-232.	0.6	37
954	The immune response after noise damage in the cochlea is characterized by a heterogeneous mix of adaptive and innate immune cells. <i>Scientific Reports</i> , 2020, 10, 15167.	1.6	41
955	Autophagy promotes growth of tumors with high mutational burden by inhibiting a T-cell immune response. <i>Nature Cancer</i> , 2020, 1, 923-934.	5.7	67
956	Cardiac cellularity is dependent upon biological sex and is regulated by gonadal hormones. <i>Cardiovascular Research</i> , 2021, 117, 2252-2262.	1.8	26
957	Dysregulation of club cell biology in idiopathic pulmonary fibrosis. <i>PLoS ONE</i> , 2020, 15, e0237529.	1.1	25
958	Only Hyperuricemia with Crystalluria, but not Asymptomatic Hyperuricemia, Drives Progression of Chronic Kidney Disease. <i>Journal of the American Society of Nephrology: JASN</i> , 2020, 31, 2773-2792.	3.0	66
959	Single-cell RNA sequencing in <i>Drosophila</i> : Technologies and applications. <i>Wiley Interdisciplinary Reviews: Developmental Biology</i> , 2021, 10, e396.	5.9	47

#	ARTICLE	IF	CITATIONS
960	Transcriptomic analysis links diverse hypothalamic cell types to fibroblast growth factor 1-induced sustained diabetes remission. <i>Nature Communications</i> , 2020, 11, 4458.	5.8	34
961	p53 drives a transcriptional program that elicits a non-cell-autonomous response and alters cell state in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23663-23673.	3.3	26
962	Profiling APOL1 Nephropathy Risk Variants in Genome-Edited Kidney Organoids with Single-Cell Transcriptomics. <i>Kidney360</i> , 2020, 1, 203-215.	0.9	18
963	Single-cell transcriptomic analysis defines the interplay between tumor cells, viral infection, and the microenvironment in nasopharyngeal carcinoma. <i>Cell Research</i> , 2020, 30, 950-965.	5.7	111
964	Single-cell transcriptomes of pancreatic preinvasive lesions and cancer reveal acinar metaplastic cellsâ€™ heterogeneity. <i>Nature Communications</i> , 2020, 11, 4516.	5.8	117
965	Adaptable haemodynamic endothelial cells for organogenesis and tumorigenesis. <i>Nature</i> , 2020, 585, 426-432.	13.7	145
966	Deep-learning-assisted biophysical imaging cytometry at massive throughput delineates cell population heterogeneity. <i>Lab on A Chip</i> , 2020, 20, 3696-3708.	3.1	41
967	SMARCB1 loss interacts with neuronal differentiation state to block maturation and impact cell stability. <i>Genes and Development</i> , 2020, 34, 1316-1329.	2.7	30
968	Diversification of reprogramming trajectories revealed by parallel single-cell transcriptome and chromatin accessibility sequencing. <i>Science Advances</i> , 2020, 6, .	4.7	37
969	The protein expression profile of ACE2 in human tissues. <i>Molecular Systems Biology</i> , 2020, 16, e9610.	3.2	769
970	A single cell RNA sequencing resource for early sea urchin development. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	36
971	Visualizing Single-Cell RNA-seq Data with Semisupervised Principal Component Analysis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5797.	1.8	16
972	SARS-CoV-2 Receptor <i>ACE2</i> Is Enriched in a Subpopulation of Mouse Tongue Epithelial Cells in Nongustatory Papillae but Not in Taste Buds or Embryonic Oral Epithelium. <i>ACS Pharmacology and Translational Science</i> , 2020, 3, 749-758.	2.5	52
973	Gene editing and elimination of latent herpes simplex virus in vivo. <i>Nature Communications</i> , 2020, 11, 4148.	5.8	46
974	Integrative genomics approach identifies conserved transcriptomic networks in Alzheimerâ€™s disease. <i>Human Molecular Genetics</i> , 2020, 29, 2899-2919.	1.4	50
975	A single-cell transcriptome atlas of marsupial embryogenesis and Xâ€™inactivation. <i>Nature</i> , 2020, 586, 612-617.	13.7	34
976	Immune-evasive human islet-like organoids ameliorate diabetes. <i>Nature</i> , 2020, 586, 606-611.	13.7	192
977	Comparison of visualization tools for single-cell RNAseq data. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa052.	1.5	41

#	ARTICLE	IF	CITATIONS
978	Social reprogramming in ants induces longevity-associated glia remodeling. <i>Science Advances</i> , 2020, 6, eaba9869.	4.7	46
979	Neutrophil extracellular traps target senescent vasculature for tissue remodeling in retinopathy. <i>Science</i> , 2020, 369, .	6.0	139
980	Single-Nucleus RNA-Sequencing Profiling of Mouse Lung. Reduced Dissociation Bias and Improved Rare Cell-Type Detection Compared with Single-Cell RNA Sequencing. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2020, 63, 739-747.	1.4	39
981	Integrative analysis of scRNA-seq and GWAS data pinpoints periportal hepatocytes as the relevant liver cell types for blood lipids. <i>Human Molecular Genetics</i> , 2020, 29, 3145-3153.	1.4	2
982	Changes in Peripheral and Local Tumor Immunity after Neoadjuvant Chemotherapy Reshape Clinical Outcomes in Patients with Breast Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 5668-5681.	3.2	37
983	Heterogeneity and clonal relationships of adaptive immune cells in ulcerative colitis revealed by single-cell analyses. <i>Science Immunology</i> , 2020, 5, .	5.6	127
984	Reservoir of Fibroblasts Promotes Recovery From Limb Ischemia. <i>Circulation</i> , 2020, 142, 1647-1662.	1.6	33
985	A single-cell atlas of the human substantia nigra reveals cell-specific pathways associated with neurological disorders. <i>Nature Communications</i> , 2020, 11, 4183.	5.8	178
986	Single cell RNA sequencing identifies early diversity of sensory neurons forming via bi-potential intermediates. <i>Nature Communications</i> , 2020, 11, 4175.	5.8	45
987	Single-Cell Transcriptional Analyses Identify Lineage-Specific Epithelial Responses to Inflammation and Metaplastic Development in the Gastric Corpus. <i>Gastroenterology</i> , 2020, 159, 2116-2129.e4.	0.6	52
988	Transfer learning efficiently maps bone marrow cell types from mouse to human using single-cell RNA sequencing. <i>Communications Biology</i> , 2020, 3, 736.	2.0	18
989	Experimental and computational technologies to dissect the kidney at the single-cell level. <i>Nephrology Dialysis Transplantation</i> , 2022, 37, 628-637.	0.4	6
990	Spatiotemporal cellular movement and fate decisions during first pharyngeal arch morphogenesis. <i>Science Advances</i> , 2020, 6, .	4.7	28
991	Improved efficiency of urine cell image segmentation using droplet microfluidics technology. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2020, 99, 722-731.	1.1	2
992	Single-cell atlas of the first intra-mammalian developmental stage of the human parasite <i>Schistosoma mansoni</i> . <i>Nature Communications</i> , 2020, 11, 6411.	5.8	51
993	A multicenter study benchmarking single-cell RNA sequencing technologies using reference samples. <i>Nature Biotechnology</i> , 2021, 39, 1103-1114.	9.4	69
994	FR-Match: robust matching of cell type clusters from single cell RNA sequencing data using the Friedman-Rafsky non-parametric test. <i>Briefings in Bioinformatics</i> , 2020, 22, .	3.2	12
995	Human Pluripotent Stem Cell-Derived Kidney Organoids with Improved Collecting Duct Maturation and Injury Modeling. <i>Cell Reports</i> , 2020, 33, 108514.	2.9	79

#	ARTICLE	IF	CITATIONS
996	Optimized workflow for single-cell transcriptomics on infectious diseases including COVID-19. STAR Protocols, 2020, 1, 100233.	0.5	10
997	Single-Cell Transcriptional Profiling of Mouse Islets Following Short-Term Obesogenic Dietary Intervention. Metabolites, 2020, 10, 513.	1.3	14
998	Analyses of Avascular Mutants Reveal Unique Transcriptomic Signature of Non-conventional Endothelial Cells. Frontiers in Cell and Developmental Biology, 2020, 8, 589717.	1.8	6
999	Molecularly targeted photothermal ablation improves tumor specificity and immune modulation in a rat model of hepatocellular carcinoma. Communications Biology, 2020, 3, 783.	2.0	13
1000	Comprehensive Integration of Single-Cell Transcriptional Profiling Reveals the Heterogeneities of Non-cardiomyocytes in Healthy and Ischemic Hearts. Frontiers in Cardiovascular Medicine, 2020, 7, 615161.	1.1	23
1001	Generation of a Single-Cell RNAseq Atlas of Murine Salivary Gland Development. IScience, 2020, 23, 101838.	1.9	66
1002	Age-associated telomere attrition in adipocyte progenitors predisposes to metabolic disease. Nature Metabolism, 2020, 2, 1482-1497.	5.1	39
1003	Goals and approaches for each processing step for single-cell RNA sequencing data. Briefings in Bioinformatics, 2021, 22, .	3.2	31
1004	Human obstructive (postvasectomy) and nonobstructive azoospermia – Insights from scRNA-Seq and transcriptome analysis. Genes and Diseases, 2022, 9, 766-776.	1.5	13
1005	On the in vivo origin of human nasal mesenchymal stem cell cultures. Laryngoscope Investigative Otolaryngology, 2020, 5, 975-982.	0.6	3
1006	Generation of Functional Human 3D Cortico-Motor Assembloids. Cell, 2020, 183, 1913-1929.e26.	13.5	262
1007	Obesity Shapes Metabolism in the Tumor Microenvironment to Suppress Anti-Tumor Immunity. Cell, 2020, 183, 1848-1866.e26.	13.5	347
1008	Reduction of mNAT1/hNAT2 Contributes to Cerebral Endothelial Necroptosis and A β Accumulation in Alzheimer's Disease. Cell Reports, 2020, 33, 108447.	2.9	26
1009	Cell-Type-Specific Gene Regulatory Networks Underlying Murine Neonatal Heart Regeneration at Single-Cell Resolution. Cell Reports, 2020, 33, 108472.	2.9	99
1010	Transcriptomic Profiling of Human Pluripotent Stem Cell-derived Retinal Pigment Epithelium over Time. Genomics, Proteomics and Bioinformatics, 2021, 19, 223-242.	3.0	25
1011	Single-Cell Transcriptome Analysis Dissects the Replicating Process of Pancreatic Beta Cells in Partial Pancreatectomy Model. IScience, 2020, 23, 101774.	1.9	15
1012	Single-cell RNA landscape of intratumoral heterogeneity and immunosuppressive microenvironment in advanced osteosarcoma. Nature Communications, 2020, 11, 6322.	5.8	259
1013	Single-nucleus transcriptomics reveals functional compartmentalization in syncytial skeletal muscle cells. Nature Communications, 2020, 11, 6375.	5.8	122

#	ARTICLE	IF	CITATIONS
1014	Thymic iNKT single cell analyses unmask the common developmental program of mouse innate T cells. <i>Nature Communications</i> , 2020, 11, 6238.	5.8	47
1015	Blood and lymphatic systems are segregated by the FLCN tumor suppressor. <i>Nature Communications</i> , 2020, 11, 6314.	5.8	17
1016	FEATS: feature selection-based clustering of single-cell RNA-seq data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	13
1017	Mouse embryonic stem cells self-organize into trunk-like structures with neural tube and somites. <i>Science</i> , 2020, 370, .	6.0	193
1018	Stem-like CD8 T cells mediate response of adoptive cell immunotherapy against human cancer. <i>Science</i> , 2020, 370, 1328-1334.	6.0	273
1019	Single-Cell RNA Sequencing of a Postmenopausal Normal Breast Tissue Identifies Multiple Cell Types That Contribute to Breast Cancer. <i>Cancers</i> , 2020, 12, 3639.	1.7	15
1020	Transcriptional Trajectories in Mouse Limb Buds Reveal the Transition from Anterior-Posterior to Proximal-Distal Patterning at Early Limb Bud Stage. <i>Journal of Developmental Biology</i> , 2020, 8, 31.	0.9	11
1021	Gene set inference from single-cell sequencing data using a hybrid of matrix factorization and variational autoencoders. <i>Nature Machine Intelligence</i> , 2020, 2, 800-809.	8.3	5
1022	Single-Cell Profiling of AKI in a Murine Model Reveals Novel Transcriptional Signatures, Profibrotic Phenotype, and Epithelial-to-Stromal Crosstalk. <i>Journal of the American Society of Nephrology: JASN</i> , 2020, 31, 2793-2814.	3.0	108
1023	Transcriptional priming as a conserved mechanism of lineage diversification in the developing mouse and human neocortex. <i>Science Advances</i> , 2020, 6, .	4.7	43
1024	Investigating transcriptome-wide sex dimorphism by multi-level analysis of single-cell RNA sequencing data in ten mouse cell types. <i>Biology of Sex Differences</i> , 2020, 11, 61.	1.8	19
1025	T Follicular Regulatory Cellâ€Derived Fibrinogen-like Protein 2 Regulates Production of Autoantibodies and Induction of Systemic Autoimmunity. <i>Journal of Immunology</i> , 2020, 205, 3247-3262.	0.4	13
1026	A rank-based marker selection method for high throughput scRNA-seq data. <i>BMC Bioinformatics</i> , 2020, 21, 477.	1.2	29
1027	Functional module detection through integration of single-cell RNA sequencing data with proteinâ€protein interaction networks. <i>BMC Genomics</i> , 2020, 21, 756.	1.2	13
1028	Defining the Teratoma as a Model for Multi-lineage Human Development. <i>Cell</i> , 2020, 183, 1402-1419.e18.	13.5	32
1029	Toward a Consensus View of Mammalian Adipocyte Stem and Progenitor Cell Heterogeneity. <i>Trends in Cell Biology</i> , 2020, 30, 937-950.	3.6	69
1031	Single-Cell RNA-Seq Analysis Reveals Microenvironmental Infiltration of Plasma Cells and Hepatocytic Prognostic Markers in HCC With Cirrhosis. <i>Frontiers in Oncology</i> , 2020, 10, 596318.	1.3	46
1032	The bone marrow microenvironment of pre-B acute lymphoblastic leukemia at single-cell resolution. <i>Scientific Reports</i> , 2020, 10, 19173.	1.6	16

#	ARTICLE	IF	CITATIONS
1033	A map of tumor-host interactions in glioma at single-cell resolution. <i>GigaScience</i> , 2020, 9, .	3.3	32
1034	Single-cell transcriptomics of murine mural cells reveals cellular heterogeneity. <i>Science China Life Sciences</i> , 2020, 64, 1077-1086.	2.3	3
1035	Degenerative and regenerative pathways underlying Duchenne muscular dystrophy revealed by single-nucleus RNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 29691-29701.	3.3	90
1036	Single-cell analysis of germinal-center B cells informs on lymphoma cell of origin and outcome. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	117
1037	A Transcriptomics-Based Meta-Analysis Combined With Machine Learning Identifies a Secretary Biomarker Panel for Diagnosis of Pancreatic Adenocarcinoma. <i>Frontiers in Genetics</i> , 2020, 11, 572284.	1.1	15
1038	Rainbow Kaposi's Sarcoma-Associated Herpesvirus Revealed Heterogenic Replication with Dynamic Gene Expression. <i>Journal of Virology</i> , 2020, 94, .	1.5	13
1039	Regulatory T Cells License Macrophage Pro-Resolving Functions During Atherosclerosis Regression. <i>Circulation Research</i> , 2020, 127, 335-353.	2.0	130
1040	Single-cell resolution analysis of the human pancreatic ductal progenitor cell niche. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10876-10887.	3.3	109
1041	Reprogramming Axial Level Identity to Rescue Neural-Crest-Related Congenital Heart Defects. <i>Developmental Cell</i> , 2020, 53, 300-315.e4.	3.1	37
1042	Context specificity of the EMT transcriptional response. <i>Nature Communications</i> , 2020, 11, 2142.	5.8	156
1043	UHRF1 Controls Thymocyte Fate Decisions through the Epigenetic Regulation of EGR1 Expression. <i>Journal of Immunology</i> , 2020, 204, 3248-3261.	0.4	9
1044	A single-cell transcriptomic landscape of primate arterial aging. <i>Nature Communications</i> , 2020, 11, 2202.	5.8	95
1045	Single-nucleus RNA-seq identifies divergent populations of FSHD2 myotube nuclei. <i>PLoS Genetics</i> , 2020, 16, e1008754.	1.5	27
1046	Nascent transcript and single-cell RNA-seq analysis defines the mechanism of action of the LSD1 inhibitor INCB059872 in myeloid leukemia. <i>Gene</i> , 2020, 752, 144758.	1.0	17
1047	Single cell transcriptomics identifies stem cell-derived graft composition in a model of Parkinson's disease. <i>Nature Communications</i> , 2020, 11, 2434.	5.8	54
1048	Redundant and additive functions of the four <i>Lef/Tcf</i> transcription factors in lung epithelial progenitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12182-12191.	3.3	18
1049	Interindividual Variability in Lymphocyte Stimulation and Transcriptomic Response Predicts Mycophenolic Acid Sensitivity in Healthy Volunteers. <i>Clinical and Translational Science</i> , 2020, 13, 1137-1149.	1.5	2
1050	CIPR: a web-based R/shiny app and R package to annotate cell clusters in single cell RNA sequencing experiments. <i>BMC Bioinformatics</i> , 2020, 21, 191.	1.2	45

#	ARTICLE	IF	CITATIONS
1051	Trajectory and Functional Analysis of PD-1 ^{high} CD4 ⁺ CD8 ⁺ T Cells in Hepatocellular Carcinoma by Single-Cell Cytometry and Transcriptome Sequencing. <i>Advanced Science</i> , 2020, 7, 2000224.	5.6	62
1052	Type 1 Treg cells promote the generation of CD8 ⁺ tissue-resident memory T cells. <i>Nature Immunology</i> , 2020, 21, 766-776.	7.0	66
1053	Putative cell type discovery from single-cell gene expression data. <i>Nature Methods</i> , 2020, 17, 621-628.	9.0	91
1054	Remodeling of light and dark zone follicular dendritic cells governs germinal center responses. <i>Nature Immunology</i> , 2020, 21, 649-659.	7.0	80
1055	Single-cell-resolution transcriptome map of human, chimpanzee, bonobo, and macaque brains. <i>Genome Research</i> , 2020, 30, 776-789.	2.4	97
1056	Dissecting the cellular specificity of smoking effects and reconstructing lineages in the human airway epithelium. <i>Nature Communications</i> , 2020, 11, 2485.	5.8	166
1057	Single-cell analysis of childhood leukemia reveals a link between developmental states and ribosomal protein expression as a source of intra-individual heterogeneity. <i>Scientific Reports</i> , 2020, 10, 8079.	1.6	37
1058	Single-Cell Virtual Cytometer allows user-friendly and versatile analysis and visualization of multimodal single cell RNAseq datasets. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa025.	1.5	13
1059	Trichinella spiralis-induced mastocytosis and erythropoiesis are simultaneously supported by a bipotent mast cell/erythrocyte precursor cell. <i>PLoS Pathogens</i> , 2020, 16, e1008579.	2.1	15
1060	An Adaptive Sparse Subspace Clustering for Cell Type Identification. <i>Frontiers in Genetics</i> , 2020, 11, 407.	1.1	18
1061	Single-Cell RNA Sequencing of Hematopoietic Stem and Progenitor Cells Treated with Gemcitabine and Carboplatin. <i>Genes</i> , 2020, 11, 549.	1.0	2
1062	Single-Cell RNA Sequencing of Calvarial and Long-Bone Endocortical Cells. <i>Journal of Bone and Mineral Research</i> , 2020, 35, 1981-1991.	3.1	40
1063	A Single-Cell Transcriptional Roadmap of the Mouse and Human Lymph Node Lymphatic Vasculature. <i>Frontiers in Cardiovascular Medicine</i> , 2020, 7, 52.	1.1	97
1064	Adipogenesis of skeletal muscle fibro/adipogenic progenitors is affected by the WNT5a/GSK3 β -catenin axis. <i>Cell Death and Differentiation</i> , 2020, 27, 2921-2941.	5.0	69
1065	A method for the generation of human stem cell-derived alpha cells. <i>Nature Communications</i> , 2020, 11, 2241.	5.8	54
1066	Single-cell RNA sequencing demonstrates the molecular and cellular reprogramming of metastatic lung adenocarcinoma. <i>Nature Communications</i> , 2020, 11, 2285.	5.8	565
1067	Acquired resistance to combined BET and CDK4/6 inhibition in triple-negative breast cancer. <i>Nature Communications</i> , 2020, 11, 2350.	5.8	45
1068	A single-cell and single-nucleus RNA-Seq toolbox for fresh and frozen human tumors. <i>Nature Medicine</i> , 2020, 26, 792-802.	15.2	381

#	ARTICLE	IF	CITATIONS
1069	Toward Modeling Context-Specific EMT Regulatory Networks Using Temporal Single Cell RNA-Seq Data. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 54.	1.6	24
1070	Deep learning enables accurate clustering with batch effect removal in single-cell RNA-seq analysis. <i>Nature Communications</i> , 2020, 11, 2338.	5.8	180
1071	Single-cell RNA-seq analysis of human CSF microglia and myeloid cells in neuroinflammation. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2020, 7, .	3.1	65
1072	Single-Cell RNA Sequencing and Its Combination with Protein and DNA Analyses. <i>Cells</i> , 2020, 9, 1130.	1.8	42
1073	Characterization of the development of the mouse cochlear epithelium at the single cell level. <i>Nature Communications</i> , 2020, 11, 2389.	5.8	241
1074	BREM-SC: a bayesian random effects mixture model for joint clustering single cell multi-omics data. <i>Nucleic Acids Research</i> , 2020, 48, 5814-5824.	6.5	50
1075	APEC: an accession-based method for single-cell chromatin accessibility analysis. <i>Genome Biology</i> , 2020, 21, 116.	3.8	12
1076	A Quantitative Framework for Evaluating Single-Cell Data Structure Preservation by Dimensionality Reduction Techniques. <i>Cell Reports</i> , 2020, 31, 107576.	2.9	49
1077	Single-cell technologies in hepatology: new insights into liver biology and disease pathogenesis. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2020, 17, 457-472.	8.2	152
1078	Aggregating transcript-level analyses for single-cell differential gene expression. <i>Nature Methods</i> , 2020, 17, 583-585.	9.0	3
1079	CReSCENT: CanceR Single Cell ExpressioN Toolkit. <i>Nucleic Acids Research</i> , 2020, 48, W372-W379.	6.5	18
1080	SCSA: A Cell Type Annotation Tool for Single-Cell RNA-seq Data. <i>Frontiers in Genetics</i> , 2020, 11, 490.	1.1	88
1081	Computational Methods for Single-Cell RNA Sequencing. <i>Annual Review of Biomedical Data Science</i> , 2020, 3, 339-364.	2.8	81
1082	Macrophage Subpopulation Dynamics Shift following Intravenous Infusion of Mesenchymal Stromal Cells. <i>Molecular Therapy</i> , 2020, 28, 2007-2022.	3.7	15
1083	Hair-bearing human skin generated entirely from pluripotent stem cells. <i>Nature</i> , 2020, 582, 399-404.	13.7	236
1084	Therapeutic potential of lipids obtained from $\hat{1}^3$ -irradiated PBMCs in dendritic cell-mediated skin inflammation. <i>EBioMedicine</i> , 2020, 55, 102774.	2.7	18
1085	Neuronal activity increases translocator protein (TSPO) levels. <i>Molecular Psychiatry</i> , 2021, 26, 2025-2037.	4.1	70
1086	Toll-like receptor signaling in thymic epithelium controls monocyte-derived dendritic cell recruitment and Treg generation. <i>Nature Communications</i> , 2020, 11, 2361.	5.8	39

#	ARTICLE	IF	CITATIONS
1087	Transcriptional and Cellular Diversity of the Human Heart. <i>Circulation</i> , 2020, 142, 466-482.	1.6	326
1088	Unblending of Transcriptional Condensates in Human Repeat Expansion Disease. <i>Cell</i> , 2020, 181, 1062-1079.e30.	13.5	115
1089	Single-Cell Analysis of Human Retina Identifies Evolutionarily Conserved and Species-Specific Mechanisms Controlling Development. <i>Developmental Cell</i> , 2020, 53, 473-491.e9.	3.1	170
1090	The promise of single-cell genomics in plants. <i>Current Opinion in Plant Biology</i> , 2020, 54, 114-121.	3.5	26
1091	A Human Skeletal Muscle Atlas Identifies the Trajectories of Stem and Progenitor Cells across Development and from Human Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2020, 27, 158-176.e10.	5.2	97
1092	Single-Cell Transcriptome Analysis Reveals Intratumoral Heterogeneity in ccRCC, which Results in Different Clinical Outcomes. <i>Molecular Therapy</i> , 2020, 28, 1658-1672.	3.7	109
1093	Early precursors and molecular determinants of tissue-resident memory CD8 ⁺ T lymphocytes revealed by single-cell RNA sequencing. <i>Science Immunology</i> , 2020, 5, .	5.6	124
1094	Extraction of Distinct Neuronal Cell Types from within a Genetically Continuous Population. <i>Neuron</i> , 2020, 107, 274-282.e6.	3.8	88
1095	CNTF-STAT3-IL-6 Axis Mediates Neuroinflammatory Cascade across Schwann Cell-Neuron-Microglia. <i>Cell Reports</i> , 2020, 31, 107657.	2.9	77
1096	Expression of RUNX1-ETO Rapidly Alters the Chromatin Landscape and Growth of Early Human Myeloid Precursor Cells. <i>Cell Reports</i> , 2020, 31, 107691.	2.9	20
1097	A Multiplexed Barcodelet Single-Cell RNA-Seq Approach Elucidates Combinatorial Signaling Pathways that Drive ESC Differentiation. <i>Cell Stem Cell</i> , 2020, 26, 938-950.e6.	5.2	12
1098	Single cell transcriptomics reveals opioid usage evokes widespread suppression of antiviral gene program. <i>Nature Communications</i> , 2020, 11, 2611.	5.8	39
1099	Whole-exome sequencing of a large Chinese azoospermia and severe oligospermia cohort identifies novel infertility causative variants and genes. <i>Human Molecular Genetics</i> , 2020, 29, 2451-2459.	1.4	42
1100	ASAP 2020 update: an open, scalable and interactive web-based portal for (single-cell) omics analyses. <i>Nucleic Acids Research</i> , 2020, 48, W403-W414.	6.5	17
1101	MYC Drives Temporal Evolution of Small Cell Lung Cancer Subtypes by Reprogramming Neuroendocrine Fate. <i>Cancer Cell</i> , 2020, 38, 60-78.e12.	7.7	262
1102	scTPA: a web tool for single-cell transcriptome analysis of pathway activation signatures. <i>Bioinformatics</i> , 2020, 36, 4217-4219.	1.8	21
1103	Exploring dimension-reduced embeddings with Sleepwalk. <i>Genome Research</i> , 2020, 30, 749-756.	2.4	8
1104	Single-Cell Analysis Reveals Fibroblast Clusters Linked to Immunotherapy Resistance in Cancer. <i>Cancer Discovery</i> , 2020, 10, 1330-1351.	7.7	424

#	ARTICLE	IF	CITATIONS
1105	Distinct immune evasion in APOBEC-enriched, HPV-negative HNSCC. International Journal of Cancer, 2020, 147, 2293-2302.	2.3	10
1106	Extensive Remodeling of the Immune Microenvironment in B Cell Acute Lymphoblastic Leukemia. Cancer Cell, 2020, 37, 867-882.e12.	7.7	108
1107	Single-Cell Analysis of the Gene Expression Effects of Developmental Lead (Pb) Exposure on the Mouse Hippocampus. Toxicological Sciences, 2020, 176, 396-409.	1.4	24
1108	Functional role of kallikrein 5 and proteinase-activated receptor 2 in eosinophilic esophagitis. Science Translational Medicine, 2020, 12, .	5.8	36
1109	Unifying Developmental Programs for Embryonic and Post-Embryonic Neurogenesis in the Zebrafish Retina. Development (Cambridge), 2020, 147, .	1.2	33
1110	Quantitative single-cell interactomes in normal and virus-infected mouse lungs. DMM Disease Models and Mechanisms, 2020, 13, .	1.2	13
1111	Single-Cell Transcriptomic Analysis of Tumor-Derived Fibroblasts and Normal Tissue-Resident Fibroblasts Reveals Fibroblast Heterogeneity in Breast Cancer. Cancers, 2020, 12, 1307.	1.7	148
1112	Developments from Bulk Optogenetics to Single-Cell Strategies to Dissect the Neural Circuits that Underlie Aberrant Motivational States. Cold Spring Harbor Perspectives in Medicine, 2020, , a039792.	2.9	6
1113	CB2 improves power of cell detection in droplet-based single-cell RNA sequencing data. Genome Biology, 2020, 21, 137.	3.8	17
1114	Towards systems tissue engineering: Elucidating the dynamics, spatial coordination, and individual cells driving emergent behaviors. Biomaterials, 2020, 255, 120189.	5.7	8
1115	Bulk and single-cell gene expression analyses reveal aging human choriocapillaris has pro-inflammatory phenotype. Microvascular Research, 2020, 131, 104031.	1.1	34
1116	Neurons that regulate mouse torpor. Nature, 2020, 583, 115-121.	13.7	142
1117	Physiology-forward identification of bile acid-sensitive vomeronasal receptors. Science Advances, 2020, 6, eaaz6868.	4.7	11
1118	Dissecting intratumour heterogeneity of nodal B-cell lymphomas at the transcriptional, genetic and drug-response levels. Nature Cell Biology, 2020, 22, 896-906.	4.6	93
1119	Machine learning approaches to drug response prediction: challenges and recent progress. Npj Precision Oncology, 2020, 4, 19.	2.3	170
1120	Developmental Correlations of Head and Heart Musculature: Importance for Understanding Human Syndromes. Current Molecular Biology Reports, 2020, 6, 62-70.	0.8	1
1121	Activin A does not drive post-traumatic heterotopic ossification. Bone, 2020, 138, 115473.	1.4	22
1122	<i>Runx2</i> Regulates Mouse Tooth Root Development Via Activation of <i>WNT</i> Inhibitor <i>NOTUM</i> . Journal of Bone and Mineral Research, 2020, 35, 2252-2264.	3.1	43

#	ARTICLE	IF	CITATIONS
1123	Circulating immune cell phenotype dynamics reflect the strength of tumor-immune cell interactions in patients during immunotherapy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16072-16082.	3.3	60
1124	The polycomb proteins EZH1 and EZH2 co-regulate chromatin accessibility and nephron progenitor cell lifespan in mice. <i>Journal of Biological Chemistry</i> , 2020, 295, 11542-11558.	1.6	18
1125	Widespread transcript shortening through alternative polyadenylation in secretory cell differentiation. <i>Nature Communications</i> , 2020, 11, 3182.	5.8	34
1126	IL-18BP is a secreted immune checkpoint and barrier to IL-18 immunotherapy. <i>Nature</i> , 2020, 583, 609-614.	13.7	195
1127	Generation of self-organized sensory ganglion organoids and retinal ganglion cells from fibroblasts. <i>Science Advances</i> , 2020, 6, eaaz5858.	4.7	33
1128	Systematic assessment of tissue dissociation and storage biases in single-cell and single-nucleus RNA-seq workflows. <i>Genome Biology</i> , 2020, 21, 130.	3.8	342
1129	Trajectory mapping of human embryonic stem cell cardiogenesis reveals lineage branch points and an ISL1 progenitor-derived cardiac fibroblast lineage. <i>Stem Cells</i> , 2020, 38, 1267-1278.	1.4	15
1130	Loss of the transcription factor MAFB limits $\hat{2}$ -cell derivation from human PSCs. <i>Nature Communications</i> , 2020, 11, 2742.	5.8	37
1131	Single-cell transcriptomic analysis identifies the conversion of zebrafish Etv2-deficient vascular progenitors into skeletal muscle. <i>Nature Communications</i> , 2020, 11, 2796.	5.8	48
1132	Analysis of cell-associated DENV RNA by oligo(dT) primed 5 ^â capture scRNAseq. <i>Scientific Reports</i> , 2020, 10, 9047.	1.6	7
1133	Integrating multi-OMICS data through sparse canonical correlation analysis for the prediction of complex traits: a comparison study. <i>Bioinformatics</i> , 2020, 36, 4616-4625.	1.8	28
1134	Single-Cell RNA-Seq Mapping of Human Thymopoiesis Reveals Lineage Specification Trajectories and a Commitment Spectrum in T Cell Development. <i>Immunity</i> , 2020, 52, 1105-1118.e9.	6.6	58
1135	Hedgehog- $\hat{2}$ FGF signaling axis patterns anterior mesoderm during gastrulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 15712-15723.	3.3	21
1136	A Human Pluripotent Stem Cell-based Platform to Study SARS-CoV-2 Tropism and Model Virus Infection in Human Cells and Organoids. <i>Cell Stem Cell</i> , 2020, 27, 125-136.e7.	5.2	543
1137	A pan-cancer blueprint of the heterogeneous tumor microenvironment revealed by single-cell profiling. <i>Cell Research</i> , 2020, 30, 745-762.	5.7	391
1138	Radiation Triggers a Dynamic Sequence of Transient Microglial Alterations in Juvenile Brain. <i>Cell Reports</i> , 2020, 31, 107699.	2.9	23
1139	Distinct iNKT Cell Populations Use IFN $\hat{3}$ or ER Stress-Induced IL-10 to Control Adipose Tissue Homeostasis. <i>Cell Metabolism</i> , 2020, 32, 243-258.e6.	7.2	53
1140	A single-cell atlas of the peripheral immune response in patients with severe COVID-19. <i>Nature Medicine</i> , 2020, 26, 1070-1076.	15.2	1,300

#	ARTICLE	IF	CITATIONS
1141	Single-Cell Transcriptomics Analysis Identifies Nuclear Protein 1 as a Regulator of Docetaxel Resistance in Prostate Cancer Cells. <i>Molecular Cancer Research</i> , 2020, 18, 1290-1301.	1.5	25
1142	Analysis of Gene Signatures of Tumor Microenvironment Yields Insight Into Mechanisms of Resistance to Immunotherapy. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 348.	2.0	4
1143	Single-Cell RNA-Seq Analysis Uncovers Distinct Functional Human NKT Cell Sub-Populations in Peripheral Blood. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 384.	1.8	22
1144	Projected t-SNE for batch correction. <i>Bioinformatics</i> , 2020, 36, 3522-3527.	1.8	10
1145	Type 1 Interleukin-4 Signaling Obliterates Mouse Astroglia in vivo but Not in vitro. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 114.	1.8	16
1146	Defining Epidermal Basal Cell States during Skin Homeostasis and Wound Healing Using Single-Cell Transcriptomics. <i>Cell Reports</i> , 2020, 30, 3932-3947.e6.	2.9	139
1147	Astrocyte layers in the mammalian cerebral cortex revealed by a single-cell in situ transcriptomic map. <i>Nature Neuroscience</i> , 2020, 23, 500-509.	7.1	290
1148	A Multi-Omics Approach to Liver Diseases: Integration of Single Nuclei Transcriptomics with Proteomics and HiCap Bulk Data in Human Liver. <i>OMICS A Journal of Integrative Biology</i> , 2020, 24, 180-194.	1.0	26
1149	Lymphocyte Activation Gene (LAG)-3 Is Associated With Mucosal Inflammation and Disease Activity in Ulcerative Colitis. <i>Journal of Crohn's and Colitis</i> , 2020, 14, 1446-1461.	0.6	25
1150	Temporal specificity and heterogeneity of <i>Drosophila</i> immune cells. <i>EMBO Journal</i> , 2020, 39, e104486.	3.5	109
1151	Latent periodic process inference from single-cell RNA-seq data. <i>Nature Communications</i> , 2020, 11, 1441.	5.8	23
1152	Expression and Localization of Kcne2 in the Vertebrate Retina. , 2020, 61, 33.		1
1153	Long-Term Expansion of Pancreatic Islet Organoids from Resident Procr+ Progenitors. <i>Cell</i> , 2020, 180, 1198-1211.e19.	13.5	113
1154	In the rat pancreas, somatostatin tonically inhibits glucagon secretion and is required for glucose-induced inhibition of glucagon secretion. <i>Acta Physiologica</i> , 2020, 229, e13464.	1.8	31
1155	Deciphering Cell Fate Decision by Integrated Single-Cell Sequencing Analysis. <i>Annual Review of Biomedical Data Science</i> , 2020, 3, 1-22.	2.8	30
1156	Single-Cell Analysis of the Muscle Stem Cell Hierarchy Identifies Heterotypic Communication Signals Involved in Skeletal Muscle Regeneration. <i>Cell Reports</i> , 2020, 30, 3583-3595.e5.	2.9	227
1157	Single-cell RNA sequencing study of retinal immune regulators identified CD47 and CD59a expression in photoreceptors' Implications in subretinal immune regulation. <i>Journal of Neuroscience Research</i> , 2020, 98, 1498-1513.	1.3	19
1158	Mass Cytometry and Single-Cell RNA-seq Profiling of the Heterogeneity in Human Peripheral Blood Mononuclear Cells Interacting with Silver Nanoparticles. <i>Small</i> , 2020, 16, 1907674.	5.2	29

#	ARTICLE	IF	CITATIONS
1159	Single-Cell Transcriptomic Analysis. , 2020, 10, 767-783.		8
1160	Statistical significance of cluster membership for unsupervised evaluation of cell identities. <i>Bioinformatics</i> , 2020, 36, 3107-3114.	1.8	20
1161	The Integrated Transcriptome Bioinformatics Analysis Identifies Key Genes and Cellular Components for Spinal Cord Injury-Related Neuropathic Pain. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 101.	2.0	8
1162	Next-Generation Neuroimmunology: New Technologies to Understand Central Nervous System Autoimmunity. <i>Trends in Immunology</i> , 2020, 41, 341-354.	2.9	14
1163	Single-Cell Transcriptome Analysis of Mouse Liver Cell-Specific Tropism and Transcriptional Dysregulation Following Intravenous Administration of AAVrh.10 Vectors. <i>Human Gene Therapy</i> , 2020, 31, 590-604.	1.4	15
1164	Bayesian correlation is a robust gene similarity measure for single-cell RNA-seq data. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa002.	1.5	17
1165	Human Regulatory T Cells From Umbilical Cord Blood Display Increased Repertoire Diversity and Lineage Stability Relative to Adult Peripheral Blood. <i>Frontiers in Immunology</i> , 2020, 11, 611.	2.2	23
1166	An Effective Biclustering-based Framework for Identifying Cell Subpopulations from scRNA-seq Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 18, 1-1.	1.9	3
1167	Histone H3K27me3 demethylases regulate human Th17 cell development and effector functions by impacting on metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 6056-6066.	3.3	61
1168	T Cell-Expressed microRNA-155 Reduces Lifespan in a Mouse Model of Age-Related Chronic Inflammation. <i>Journal of Immunology</i> , 2020, 204, 2064-2075.	0.4	18
1169	IL-5R α marks nasal polyp IgG4- and IgE-expressing cells in aspirin-exacerbated respiratory disease. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 1574-1584.	1.5	55
1170	Integrated single-cell analysis of multicellular immune dynamics during hyperacute HIV-1 infection. <i>Nature Medicine</i> , 2020, 26, 511-518.	15.2	100
1171	B Cells Improve Overall Survival in HPV-Associated Squamous Cell Carcinomas and Are Activated by Radiation and PD-1 Blockade. <i>Clinical Cancer Research</i> , 2020, 26, 3345-3359.	3.2	117
1172	Resolving single-cell heterogeneity from hundreds of thousands of cells through sequential hybrid clustering and NMF. <i>Bioinformatics</i> , 2020, 36, 3773-3780.	1.8	42
1173	Platform Effects on Regeneration by Pulmonary Basal Cells as Evaluated by Single-Cell RNA Sequencing. <i>Cell Reports</i> , 2020, 30, 4250-4265.e6.	2.9	33
1174	Analysis of Dual Class I Histone Deacetylase and Lysine Demethylase Inhibitor Domatinostat (4SC-202) on Growth and Cellular and Genomic Landscape of Atypical Teratoid/Rhabdoid. <i>Cancers</i> , 2020, 12, 756.	1.7	25
1175	Integrative differential expression and gene set enrichment analysis using summary statistics for scRNA-seq studies. <i>Nature Communications</i> , 2020, 11, 1585.	5.8	43
1176	Dynamic Transcriptional Responses to Injury of Regenerative and Non-regenerative Cardiomyocytes Revealed by Single-Nucleus RNA Sequencing. <i>Developmental Cell</i> , 2020, 53, 102-116.e8.	3.1	95

#	ARTICLE	IF	CITATIONS
1177	Human iPSC-derived mature microglia retain their identity and functionally integrate in the chimeric mouse brain. <i>Nature Communications</i> , 2020, 11, 1577.	5.8	108
1178	Single-cell RNA sequencing in cardiovascular development, disease and medicine. <i>Nature Reviews Cardiology</i> , 2020, 17, 457-473.	6.1	174
1179	Tools for the analysis of high-dimensional single-cell RNA sequencing data. <i>Nature Reviews Nephrology</i> , 2020, 16, 408-421.	4.1	80
1180	Type I Interferons Act Directly on Nociceptors to Produce Pain Sensitization: Implications for Viral Infection-Induced Pain. <i>Journal of Neuroscience</i> , 2020, 40, 3517-3532.	1.7	62
1181	Tuning Macrophage Phenotype to Mitigate Skeletal Muscle Fibrosis. <i>Journal of Immunology</i> , 2020, 204, 2203-2215.	0.4	37
1182	Single-cell gene profiling and lineage tracing analyses revealed novel mechanisms of endothelial repair by progenitors. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 5299-5320.	2.4	24
1183	An organoid biobank for childhood kidney cancers that captures disease and tissue heterogeneity. <i>Nature Communications</i> , 2020, 11, 1310.	5.8	183
1184	Deep Phenotyping by Mass Cytometry and Single-Cell RNA-Sequencing Reveals LYN-Regulated Signaling Profiles Underlying Monocyte Subset Heterogeneity and Lifespan. <i>Circulation Research</i> , 2020, 126, e61-e79.	2.0	21
1185	Single-cell in vivo imaging of cellular circadian oscillators in zebrafish. <i>PLoS Biology</i> , 2020, 18, e3000435.	2.6	16
1186	Physical interactions between Gsx2 and Ascl1 balance progenitor expansion versus neurogenesis in the mouse lateral ganglionic eminence. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	14
1187	Dynamic Alternative Splicing During Mouse Preimplantation Embryo Development. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 35.	2.0	17
1188	Alginate oligosaccharides improve germ cell development and testicular microenvironment to rescue busulfan disrupted spermatogenesis. <i>Theranostics</i> , 2020, 10, 3308-3324.	4.6	72
1189	Genome-wide CRISPR screen identifies ZIC2 as an essential gene that controls the cell fate of early mesodermal precursors to human heart progenitors. <i>Stem Cells</i> , 2020, 38, 741-755.	1.4	15
1190	Single-Cell Analysis of Foxp1-Driven Mechanisms Essential for Striatal Development. <i>Cell Reports</i> , 2020, 30, 3051-3066.e7.	2.9	40
1191	Embracing the dropouts in single-cell RNA-seq analysis. <i>Nature Communications</i> , 2020, 11, 1169.	5.8	204
1192	Dynamic Interstitial Cell Response during Myocardial Infarction Predicts Resilience to Rupture in Genetically Diverse Mice. <i>Cell Reports</i> , 2020, 30, 3149-3163.e6.	2.9	123
1193	Transcriptomic evidence that von Economo neurons are regionally specialized extratelencephalic-projecting excitatory neurons. <i>Nature Communications</i> , 2020, 11, 1172.	5.8	70
1194	Sliced Human Cortical Organoids for Modeling Distinct Cortical Layer Formation. <i>Cell Stem Cell</i> , 2020, 26, 766-781.e9.	5.2	268

#	ARTICLE	IF	CITATIONS
1195	Transcriptional diversity and bioenergetic shift in human breast cancer metastasis revealed by single-cell RNA sequencing. <i>Nature Cell Biology</i> , 2020, 22, 310-320.	4.6	189
1196	Induced pluripotent stem cells as models of human neurodevelopmental disorders. , 2020, , 99-127.		0
1197	6-Color/1-Target Immuno-SERS Microscopy on the Same Single Cancer Cell. <i>ACS Applied Materials & Interfaces</i> , 2020, 12, 32321-32327.	4.0	15
1198	hubViz: A novel tool for hub-centric visualization. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2020, 203, 104071.	1.8	0
1199	Targeting CD70 with cusatuzumab eliminates acute myeloid leukemia stem cells in patients treated with hypomethylating agents. <i>Nature Medicine</i> , 2020, 26, 1459-1467.	15.2	122
1200	Sex differences in neutrophil biology modulate response to type I interferons and immunometabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16481-16491.	3.3	91
1201	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2020 update. <i>Nucleic Acids Research</i> , 2020, 48, W395-W402.	6.5	322
1202	Single-Cell Transcriptomic Analysis Identifies a Unique Pulmonary Lymphangioleiomyomatosis Cell. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 202, 1373-1387.	2.5	63
1203	Transcriptional and Functional Analysis of CD1c+ Human Dendritic Cells Identifies a CD163+ Subset Priming CD8+CD103+ T Cells. <i>Immunity</i> , 2020, 53, 335-352.e8.	6.6	206
1204	Physiological blood-brain transport is impaired with age by a shift in transcytosis. <i>Nature</i> , 2020, 583, 425-430.	13.7	243
1205	Robust principal component analysis for accurate outlier sample detection in RNA-Seq data. <i>BMC Bioinformatics</i> , 2020, 21, 269.	1.2	47
1206	mitch: multi-contrast pathway enrichment for multi-omics and single-cell profiling data. <i>BMC Genomics</i> , 2020, 21, 447.	1.2	34
1207	Analysis of endothelial-to-haematopoietic transition at the single cell level identifies cell cycle regulation as a driver of differentiation. <i>Genome Biology</i> , 2020, 21, 157.	3.8	35
1208	Index of Cancer-Associated Fibroblasts Is Superior to the Epithelial-Mesenchymal Transition Score in Prognosis Prediction. <i>Cancers</i> , 2020, 12, 1718.	1.7	18
1209	KLRG1+ Memory CD8 T Cells Combine Properties of Short-Lived Effectors and Long-Lived Memory. <i>Journal of Immunology</i> , 2020, 205, 1059-1069.	0.4	39
1210	Human neurogenesis. , 2020, , 751-767.		0
1211	Microglial Remodeling of the Extracellular Matrix Promotes Synapse Plasticity. <i>Cell</i> , 2020, 182, 388-403.e15.	13.5	337
1212	Flexible experimental designs for valid single-cell RNA-sequencing experiments allowing batch effects correction. <i>Nature Communications</i> , 2020, 11, 3274.	5.8	16

#	ARTICLE	IF	CITATIONS
1213	Single-cell analyses and machine learning define hematopoietic progenitor and HSC-like cells derived from human PSCs. <i>Blood</i> , 2020, 136, 2893-2904.	0.6	44
1214	Temporal Dynamics and Heterogeneity of Cell Populations during Skeletal Muscle Regeneration. <i>IScience</i> , 2020, 23, 100993.	1.9	151
1215	Single-Cell Transcriptomic Analyses of the Developing Meninges Reveal Meningeal Fibroblast Diversity and Function. <i>Developmental Cell</i> , 2020, 54, 43-59.e4.	3.1	122
1216	Loss of function of the mitochondrial peptidase PITRM1 induces proteotoxic stress and Alzheimer's disease-like pathology in human cerebral organoids. <i>Molecular Psychiatry</i> , 2021, 26, 5733-5750.	4.1	79
1217	Single-cell RNA sequencing for engineering and studying human islets. <i>Current Opinion in Biomedical Engineering</i> , 2020, 16, 27-33.	1.8	11
1218	Single-cell RNA-seq reveals that glioblastoma recapitulates a normal neurodevelopmental hierarchy. <i>Nature Communications</i> , 2020, 11, 3406.	5.8	300
1219	Absence of central tolerance in Aire-deficient mice synergizes with immune-checkpoint inhibition to enhance antitumor responses. <i>Communications Biology</i> , 2020, 3, 355.	2.0	5
1220	Characterization of Glycolysis-Associated Molecules in the Tumor Microenvironment Revealed by Pan-Cancer Tissues and Lung Cancer Single Cell Data. <i>Cancers</i> , 2020, 12, 1788.	1.7	53
1221	Cellular heterogeneity landscape in laryngeal squamous cell carcinoma. <i>International Journal of Cancer</i> , 2020, 147, 2879-2890.	2.3	43
1222	Single-cell deconstruction of post-sepsis skeletal muscle and adipose tissue microenvironments. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2020, 11, 1351-1363.	2.9	24
1223	Single cell sequencing revealed the underlying pathogenesis of the development of osteoarthritis. <i>Gene</i> , 2020, 757, 144939.	1.0	21
1224	Single-Cell RNA Sequencing for Precision Oncology: Current State-of-Art. <i>Journal of the Indian Institute of Science</i> , 2020, 100, 579-588.	0.9	9
1225	A dopamine-induced gene expression signature regulates neuronal function and cocaine response. <i>Science Advances</i> , 2020, 6, eaba4221.	4.7	114
1226	Evolution and transition of expression trajectory during human brain development. <i>BMC Evolutionary Biology</i> , 2020, 20, 72.	3.2	10
1227	Impact of Data Preprocessing on Integrative Matrix Factorization of Single Cell Data. <i>Frontiers in Oncology</i> , 2020, 10, 973.	1.3	10
1228	Cell Type-Specific Expression Analysis of the Inner Ear: A Technical Report. <i>Laryngoscope</i> , 2021, 131, S1-S16.	1.1	11
1229	Multimodal Analysis of Composition and Spatial Architecture in Human Squamous Cell Carcinoma. <i>Cell</i> , 2020, 182, 497-514.e22.	13.5	508
1230	Discovery of CD80 and CD86 as recent activation markers on regulatory T cells by protein-RNA single-cell analysis. <i>Genome Medicine</i> , 2020, 12, 55.	3.6	61

#	ARTICLE	IF	CITATIONS
1231	Variation of Human Neural Stem Cells Generating Organizer States In Vitro before Committing to Cortical Excitatory or Inhibitory Neuronal Fates. <i>Cell Reports</i> , 2020, 31, 107599.	2.9	20
1232	Beta-amyloid deposition around hepatic bile ducts is a novel pathobiological and diagnostic feature of biliary atresia. <i>Journal of Hepatology</i> , 2020, 73, 1391-1403.	1.8	31
1233	Molecular atlas of the adult mouse brain. <i>Science Advances</i> , 2020, 6, eabb3446.	4.7	183
1234	scICANs: single-cell RNA-seq imputation using generative adversarial networks. <i>Nucleic Acids Research</i> , 2020, 48, e85-e85.	6.5	93
1235	Tumour-reprogrammed stromal BCAT1 fuels branched-chain ketoacid dependency in stromal-rich PDAC tumours. <i>Nature Metabolism</i> , 2020, 2, 775-792.	5.1	110
1236	Immunophenotyping of COVID-19 and influenza highlights the role of type I interferons in development of severe COVID-19. <i>Science Immunology</i> , 2020, 5, .	5.6	689
1237	Genome-wide studies reveal the essential and opposite roles of ARID1A in controlling human cardiogenesis and neurogenesis from pluripotent stem cells. <i>Genome Biology</i> , 2020, 21, 169.	3.8	28
1238	PRMT1-p53 Pathway Controls Epicardial EMT and Invasion. <i>Cell Reports</i> , 2020, 31, 107739.	2.9	37
1239	Epigenetic regulation of neuronal cell specification inferred with single cell omics data. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 942-952.	1.9	6
1240	Transcriptional and clonal characterization of B cell plasmablast diversity following primary and secondary natural DENV infection. <i>EBioMedicine</i> , 2020, 54, 102733.	2.7	25
1241	Niche-Selective Inhibition of Pathogenic Th17 Cells by Targeting Metabolic Redundancy. <i>Cell</i> , 2020, 182, 641-654.e20.	13.5	77
1242	Spatio-molecular domains identified in the mouse subthalamic nucleus and neighboring glutamatergic and GABAergic brain structures. <i>Communications Biology</i> , 2020, 3, 338.	2.0	38
1243	NASQAR: a web-based platform for high-throughput sequencing data analysis and visualization. <i>BMC Bioinformatics</i> , 2020, 21, 267.	1.2	42
1244	Synovial cell cross-talk with cartilage plays a major role in the pathogenesis of osteoarthritis. <i>Scientific Reports</i> , 2020, 10, 10868.	1.6	161
1245	Multimodal single-cell analysis reveals distinct radioresistant stem-like and progenitor cell populations in murine glioma. <i>Glia</i> , 2020, 68, 2486-2502.	2.5	8
1246	Tissue substructure-specific deposition of the Î23-containing laminin-332 in the biliary epithelium of human and mouse livers. <i>Biochemical and Biophysical Research Communications</i> , 2020, 524, 465-471.	1.0	4
1247	Defining endogenous barcoding sites for CRISPR/Cas9-based cell lineage tracing in zebrafish. <i>Journal of Genetics and Genomics</i> , 2020, 47, 85-91.	1.7	8
1248	Cell Lineage Tracing Identifies Hormone-Regulated and Wnt-Responsive Vaginal Epithelial Stem Cells. <i>Cell Reports</i> , 2020, 30, 1463-1477.e7.	2.9	35

#	ARTICLE	IF	CITATIONS
1249	Identification of a Zeb1 expressing basal stem cell subpopulation in the prostate. <i>Nature Communications</i> , 2020, 11, 706.	5.8	42
1250	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020, 21, 31.	3.8	742
1251	Single-Cell RNA Sequencing in Human Retinal Degeneration Reveals Distinct Glial Cell Populations. <i>Cells</i> , 2020, 9, 438.	1.8	35
1252	The Molecular Anatomy of Mouse Skin during Hair Growth and Rest. <i>Cell Stem Cell</i> , 2020, 26, 441-457.e7.	5.2	198
1253	Restraining Lysosomal Activity Preserves Hematopoietic Stem Cell Quiescence and Potency. <i>Cell Stem Cell</i> , 2020, 26, 359-376.e7.	5.2	169
1254	Two waves of pro-inflammatory factors are released during the influenza A virus (IAV)-driven pulmonary immunopathogenesis. <i>PLoS Pathogens</i> , 2020, 16, e1008334.	2.1	35
1255	InÂVitro and InÂVivo Development of the Human Airway at Single-Cell Resolution. <i>Developmental Cell</i> , 2020, 53, 117-128.e6.	3.1	110
1256	Single-cell analysis of human ovarian cortex identifies distinct cell populations but no oogonial stem cells. <i>Nature Communications</i> , 2020, 11, 1147.	5.8	188
1257	TooManyCells identifies and visualizes relationships of single-cell clades. <i>Nature Methods</i> , 2020, 17, 405-413.	9.0	57
1258	Single-cell Transcriptome Mapping Identifies Common and Cell-type Specific Genes Affected by Acute Delta9-tetrahydrocannabinol in Humans. <i>Scientific Reports</i> , 2020, 10, 3450.	1.6	17
1259	Single-cell RNA-seq clustering: datasets, models, and algorithms. <i>RNA Biology</i> , 2020, 17, 765-783.	1.5	50
1260	Engineered immunogen binding to alum adjuvant enhances humoral immunity. <i>Nature Medicine</i> , 2020, 26, 430-440.	15.2	172
1261	Functionally distinct subgroups of oligodendrocyte precursor cells integrate neural activity and execute myelin formation. <i>Nature Neuroscience</i> , 2020, 23, 363-374.	7.1	154
1262	Single-cell analysis of olfactory neurogenesis and differentiation in adult humans. <i>Nature Neuroscience</i> , 2020, 23, 323-326.	7.1	165
1263	A Highly Conserved Circular RNA Is Required to Keep Neural Cells in a Progenitor State in the Mammalian Brain. <i>Cell Reports</i> , 2020, 30, 2170-2179.e5.	2.9	53
1264	Insulin-like Growth Factor 1 Supports a Pulmonary Niche that Promotes Type 3 Innate Lymphoid Cell Development in Newborn Lungs. <i>Immunity</i> , 2020, 52, 275-294.e9.	6.6	50
1265	ILC2s amplify PD-1 blockade by activating tissue-specific cancer immunity. <i>Nature</i> , 2020, 579, 130-135.	13.7	229
1266	STAT Signaling Modifies Ascl1 Chromatin Binding and Limits Neural Regeneration from Muller Glia in Adult Mouse Retina. <i>Cell Reports</i> , 2020, 30, 2195-2208.e5.	2.9	73

#	ARTICLE	IF	CITATIONS
1267	Cellular deconvolution of GTEx tissues powers discovery of disease and cell-type associated regulatory variants. <i>Nature Communications</i> , 2020, 11, 955.	5.8	96
1268	Tracing tumorigenesis in a solid tumor model at single-cell resolution. <i>Nature Communications</i> , 2020, 11, 991.	5.8	44
1269	Immunology in the Era of Single-Cell Technologies. <i>Annual Review of Immunology</i> , 2020, 38, 727-757.	9.5	57
1270	Exploring and analysing single cell multi-omics data with VDJView. <i>BMC Medical Genomics</i> , 2020, 13, 29.	0.7	15
1271	Prospective isolation of chondroprogenitors from human iPSCs based on cell surface markers identified using a CRISPR-Cas9-generated reporter. <i>Stem Cell Research and Therapy</i> , 2020, 11, 66.	2.4	46
1272	Frontline Science: Cxyc5 expression alters cell cycle and myeloid differentiation of mouse hematopoietic stem and progenitor cells. <i>Journal of Leukocyte Biology</i> , 2020, 108, 469-484.	1.5	6
1273	Defining the adult hippocampal neural stem cell secretome: In vivo versus in vitro transcriptomic differences and their correlation to secreted protein levels. <i>Brain Research</i> , 2020, 1735, 146717.	1.1	11
1274	Ascl2-Dependent Cell Dedifferentiation Drives Regeneration of Ablated Intestinal Stem Cells. <i>Cell Stem Cell</i> , 2020, 26, 377-390.e6.	5.2	152
1275	Distinct Mesenchymal Cell Populations Generate the Essential Intestinal BMP Signaling Gradient. <i>Cell Stem Cell</i> , 2020, 26, 391-402.e5.	5.2	211
1276	scTSSR: gene expression recovery for single-cell RNA sequencing using two-side sparse self-representation. <i>Bioinformatics</i> , 2020, 36, 3131-3138.	1.8	22
1277	Deconvolution of RNA-Seq Analysis of Hyperbaric Oxygen-Treated Mice Lungs Reveals Mesenchymal Cell Subtype Changes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1371.	1.8	9
1278	Cellular Heterogeneity and Lineage Restriction during Mouse Digit Tip Regeneration at Single-Cell Resolution. <i>Developmental Cell</i> , 2020, 52, 525-540.e5.	3.1	56
1279	Single-cell sperm transcriptomes and variants from fathers of children with and without autism spectrum disorder. <i>Npj Genomic Medicine</i> , 2020, 5, 14.	1.7	10
1280	Generation of human endothelium in pig embryos deficient in ETV2. <i>Nature Biotechnology</i> , 2020, 38, 297-302.	9.4	74
1281	Targeting the cytoskeleton to direct pancreatic differentiation of human pluripotent stem cells. <i>Nature Biotechnology</i> , 2020, 38, 460-470.	9.4	215
1282	Broad immune activation underlies shared set point signatures for vaccine responsiveness in healthy individuals and disease activity in patients with lupus. <i>Nature Medicine</i> , 2020, 26, 618-629.	15.2	144
1283	Investigating cone photoreceptor development using patient-derived NRL null retinal organoids. <i>Communications Biology</i> , 2020, 3, 82.	2.0	62
1284	Defining the emergence of myeloid-derived suppressor cells in breast cancer using single-cell transcriptomics. <i>Science Immunology</i> , 2020, 5, .	5.6	296

#	ARTICLE	IF	CITATIONS
1285	Lamina-Dependent Stretching and Unconventional Chromosome Compartments in Early <i>C.Âlegans</i> Embryos. <i>Molecular Cell</i> , 2020, 78, 96-111.e6.	4.5	43
1286	Single-Cell Determination of Cardiac Microtissue Structure and Function Using Light Sheet Microscopy. <i>Tissue Engineering - Part C: Methods</i> , 2020, 26, 207-215.	1.1	9
1287	Ensemble learning for classifying single-cell data and projection across reference atlases. <i>Bioinformatics</i> , 2020, 36, 3585-3587.	1.8	15
1288	Estimating the Allele-Specific Expression of SNVs From 10 ⁵ — Genomics Single-Cell RNA-Sequencing Data. <i>Genes</i> , 2020, 11, 240.	1.0	14
1289	Caloric Restriction Reprograms the Single-Cell Transcriptional Landscape of <i>Rattus Norvegicus</i> Aging. <i>Cell</i> , 2020, 180, 984-1001.e22.	13.5	206
1290	Single-cell transcriptomics of blood reveals a natural killer cell subset depletion in tuberculosis. <i>EBioMedicine</i> , 2020, 53, 102686.	2.7	94
1291	The Repertoire of Serous Ovarian Cancer Non-genetic Heterogeneity Revealed by Single-Cell Sequencing of Normal Fallopian Tube Epithelial Cells. <i>Cancer Cell</i> , 2020, 37, 226-242.e7.	7.7	117
1292	CLEAR: coverage-based limiting-cell experiment analysis for RNA-seq. <i>Journal of Translational Medicine</i> , 2020, 18, 63.	1.8	11
1293	Genetic Variation in Type 1 Diabetes Reconfigures the 3D Chromatin Organization of T Cells and Alters Gene Expression. <i>Immunity</i> , 2020, 52, 257-274.e11.	6.6	42
1294	CellTagging: combinatorial indexing to simultaneously map lineage and identity at single-cell resolution. <i>Nature Protocols</i> , 2020, 15, 750-772.	5.5	49
1295	Robustness and applicability of transcription factor and pathway analysis tools on single-cell RNA-seq data. <i>Genome Biology</i> , 2020, 21, 36.	3.8	216
1296	scCATCH: Automatic Annotation on Cell Types of Clusters from Single-Cell RNA Sequencing Data. <i>IScience</i> , 2020, 23, 100882.	1.9	178
1297	scID Uses Discriminant Analysis to Identify Transcriptionally Equivalent Cell Types across Single-Cell RNA-Seq Data with Batch Effect. <i>IScience</i> , 2020, 23, 100914.	1.9	47
1298	A general mathematical framework for understanding the behavior of heterogeneous stem cell regeneration. <i>Journal of Theoretical Biology</i> , 2020, 492, 110196.	0.8	10
1299	Single-Cell Genomic Characterization Reveals the Cellular Reprogramming of the Gastric Tumor Microenvironment. <i>Clinical Cancer Research</i> , 2020, 26, 2640-2653.	3.2	204
1300	Epithelial <i>Vegfa</i> Specifies a Distinct Endothelial Population in the Mouse Lung. <i>Developmental Cell</i> , 2020, 52, 617-630.e6.	3.1	142
1301	Treatment-Induced Tumor Dormancy through YAP-Mediated Transcriptional Reprogramming of the Apoptotic Pathway. <i>Cancer Cell</i> , 2020, 37, 104-122.e12.	7.7	267
1302	Human and mouse single-nucleus transcriptomics reveal TREM2-dependent and TREM2-independent cellular responses in Alzheimer's disease. <i>Nature Medicine</i> , 2020, 26, 131-142.	15.2	641

#	ARTICLE	IF	CITATIONS
1303	Uncovering axes of variation among single-cell cancer specimens. <i>Nature Methods</i> , 2020, 17, 302-310.	9.0	39
1304	The secret life of cells. <i>Nature Methods</i> , 2020, 17, 7-10.	9.0	10
1305	Deciphering the functional heterogeneity of skin fibroblasts using single-cell RNA sequencing. <i>FASEB Journal</i> , 2020, 34, 3677-3692.	0.2	102
1306	Intratumoral heterogeneity and clonal evolution in liver cancer. <i>Nature Communications</i> , 2020, 11, 291.	5.8	230
1307	A developmental landscape of 3D-cultured human pre-gastrulation embryos. <i>Nature</i> , 2020, 577, 537-542.	13.7	277
1308	Single-nucleus RNA sequencing reveals transcriptional changes of hippocampal neurons in APP23 mouse model of Alzheimer's disease. <i>Bioscience, Biotechnology and Biochemistry</i> , 2020, 84, 919-926.	0.6	10
1309	A benchmark of batch-effect correction methods for single-cell RNA sequencing data. <i>Genome Biology</i> , 2020, 21, 12.	3.8	586
1310	DENDRO: genetic heterogeneity profiling and subclone detection by single-cell RNA sequencing. <i>Genome Biology</i> , 2020, 21, 10.	3.8	35
1311	Global Gene Expression Analysis Identifies Age-Related Differences in Knee Joint Transcriptome during the Development of Post-Traumatic Osteoarthritis in Mice. <i>International Journal of Molecular Sciences</i> , 2020, 21, 364.	1.8	30
1312	Identification of a Master Regulator of Differentiation in <i>Toxoplasma</i> . <i>Cell</i> , 2020, 180, 359-372.e16.	13.5	170
1313	Transcriptional Programming of Human Mechanosensory Neuron Subtypes from Pluripotent Stem Cells. <i>Cell Reports</i> , 2020, 30, 932-946.e7.	2.9	57
1314	Silencing Trisomy 21 with XIST in Neural Stem Cells Promotes Neuronal Differentiation. <i>Developmental Cell</i> , 2020, 52, 294-308.e3.	3.1	41
1315	Snake Venom Gland Organoids. <i>Cell</i> , 2020, 180, 233-247.e21.	13.5	77
1316	Single-cell analysis reveals new evolutionary complexity in uveal melanoma. <i>Nature Communications</i> , 2020, 11, 496.	5.8	268
1317	Single-cell RNAseq analysis of testicular germ and somatic cell development during the perinatal period. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	61
1318	Single-cell transcriptional profiles in human skeletal muscle. <i>Scientific Reports</i> , 2020, 10, 229.	1.6	188
1319	VISTA is a checkpoint regulator for naïve T cell quiescence and peripheral tolerance. <i>Science</i> , 2020, 367, .	6.0	156
1320	Maximizing the ovarian reserve in mice by evading LINE-1 genotoxicity. <i>Nature Communications</i> , 2020, 11, 330.	5.8	41

#	ARTICLE	IF	CITATIONS
1321	Distinct Airway Epithelial Stem Cells Hide among Club Cells but Mobilize to Promote Alveolar Regeneration. <i>Cell Stem Cell</i> , 2020, 26, 346-358.e4.	5.2	151
1322	Elevated circulating Th2 but not group 2 innate lymphoid cell responses characterize canine atopic dermatitis. <i>Veterinary Immunology and Immunopathology</i> , 2020, 221, 110015.	0.5	6
1323	scMAGeCK links genotypes with multiple phenotypes in single-cell CRISPR screens. <i>Genome Biology</i> , 2020, 21, 19.	3.8	46
1324	Pro-efferocytic nanoparticles are specifically taken up by lesional macrophages and prevent atherosclerosis. <i>Nature Nanotechnology</i> , 2020, 15, 154-161.	15.6	173
1325	Cell stress in cortical organoids impairs molecular subtype specification. <i>Nature</i> , 2020, 578, 142-148.	13.7	387
1326	SHARP: hyperfast and accurate processing of single-cell RNA-seq data via ensemble random projection. <i>Genome Research</i> , 2020, 30, 205-213.	2.4	59
1327	Integration of eQTL and a Single-Cell Atlas in the Human Eye Identifies Causal Genes for Age-Related Macular Degeneration. <i>Cell Reports</i> , 2020, 30, 1246-1259.e6.	2.9	151
1328	Novel Alzheimer risk genes determine the microglia response to amyloid β but not to TAU pathology. <i>EMBO Molecular Medicine</i> , 2020, 12, e10606.	3.3	182
1330	A Wnt-mediated transformation of the bone marrow stromal cell identity orchestrates skeletal regeneration. <i>Nature Communications</i> , 2020, 11, 332.	5.8	184
1331	Transcriptomic and epigenetic mechanisms underlying myeloid diversity in the lung. <i>Nature Immunology</i> , 2020, 21, 221-231.	7.0	52
1332	Targeted therapy guided by single-cell transcriptomic analysis in drug-induced hypersensitivity syndrome: a case report. <i>Nature Medicine</i> , 2020, 26, 236-243.	15.2	107
1333	Multiplexed Single Cell mRNA Sequencing Analysis of Mouse Embryonic Cells. <i>Journal of Visualized Experiments</i> , 2020, , .	0.2	3
1334	Select autophagy genes maintain quiescence of tissue-resident macrophages and increase susceptibility to <i>Listeria monocytogenes</i> . <i>Nature Microbiology</i> , 2020, 5, 272-281.	5.9	36
1335	Ketogenesis activates metabolically protective $\gamma\delta$ T cells in visceral adipose tissue. <i>Nature Metabolism</i> , 2020, 2, 50-61.	5.1	107
1336	Benchmarking principal component analysis for large-scale single-cell RNA-sequencing. <i>Genome Biology</i> , 2020, 21, 9.	3.8	71
1337	T-Cell Receptor Signaling. <i>Methods in Molecular Biology</i> , 2020, , .	0.4	3
1338	netNMF-sc: leveraging gene-gene interactions for imputation and dimensionality reduction in single-cell expression analysis. <i>Genome Research</i> , 2020, 30, 195-204.	2.4	61
1339	Systematic Comparison of High-throughput Single-Cell and Single-Nucleus Transcriptomes during Cardiomyocyte Differentiation. <i>Scientific Reports</i> , 2020, 10, 1535.	1.6	74

#	ARTICLE	IF	CITATIONS
1340	Regulation of heterotopic ossification by monocytes in a mouse model of aberrant wound healing. <i>Nature Communications</i> , 2020, 11, 722.	5.8	104
1341	Evolving Transcriptomic Profiles from Single-cell RNA-seq Data using Nature-Inspired Multiobjective Optimization. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 18, 1-1.	1.9	1
1342	Single-Cell Transcriptomic Comparison of Human Fetal Retina, hPSC-Derived Retinal Organoids, and Long-Term Retinal Cultures. <i>Cell Reports</i> , 2020, 30, 1644-1659.e4.	2.9	188
1343	Replicational Dilution of H3K27me3 in Mammalian Cells and the Role of Poised Promoters. <i>Molecular Cell</i> , 2020, 78, 141-151.e5.	4.5	52
1344	A single-cell atlas of adult <i>Drosophila</i> ovary identifies transcriptional programs and somatic cell lineage regulating oogenesis. <i>PLoS Biology</i> , 2020, 18, e3000538.	2.6	85
1345	Single-cell transcriptomics combined with interstitial fluid proteomics defines cell type-specific immune regulation in atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 146, 1056-1069.	1.5	114
1346	Inferring spatial and signaling relationships between cells from single cell transcriptomic data. <i>Nature Communications</i> , 2020, 11, 2084.	5.8	184
1347	Runx1 promotes scar deposition and inhibits myocardial proliferation and survival during zebrafish heart regeneration. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	45
1348	Applications of single-cell sequencing for the field of otolaryngology: A contemporary review. <i>Laryngoscope Investigative Otolaryngology</i> , 2020, 5, 404-431.	0.6	6
1349	Integrative analysis of in vivo recording with single-cell RNA-seq data reveals molecular properties of light-sensitive neurons in mouse V1. <i>Protein and Cell</i> , 2020, 11, 417-432.	4.8	13
1350	Single-cell omics in ageing: a young and growing field. <i>Nature Metabolism</i> , 2020, 2, 293-302.	5.1	67
1351	Functional Genomics of the Pediatric Obese Asthma Phenotype Reveal Enrichment of Rho-GTPase Pathways. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 202, 259-274.	2.5	17
1352	Single-Cell Multi-Omics and Its Prospective Application in Cancer Biology. <i>Proteomics</i> , 2020, 20, 1900271.	1.3	28
1353	Single-cell RNA sequencing identifies senescent cerebrovascular endothelial cells in the aged mouse brain. <i>GeroScience</i> , 2020, 42, 429-444.	2.1	102
1354	An Airway Protection Program Revealed by Sweeping Genetic Control of Vagal Afferents. <i>Cell</i> , 2020, 181, 574-589.e14.	13.5	114
1355	Defining the Design Principles of Skin Epidermis Postnatal Growth. <i>Cell</i> , 2020, 181, 604-620.e22.	13.5	65
1356	A Targeted Multi-omic Analysis Approach Measures Protein Expression and Low-Abundance Transcripts on the Single-Cell Level. <i>Cell Reports</i> , 2020, 31, 107499.	2.9	80
1357	Transcriptional and Spatial Resolution of Cell Types in the Mammalian Habenula. <i>Neuron</i> , 2020, 106, 743-758.e5.	3.8	99

#	ARTICLE	IF	CITATIONS
1358	Identification of cell surface markers and establishment of monolayer differentiation to retinal pigment epithelial cells. <i>Nature Communications</i> , 2020, 11, 1609.	5.8	26
1359	Systematic comparison of single-cell and single-nucleus RNA-sequencing methods. <i>Nature Biotechnology</i> , 2020, 38, 737-746.	9.4	527
1360	Sci-fate characterizes the dynamics of gene expression in single cells. <i>Nature Biotechnology</i> , 2020, 38, 980-988.	9.4	89
1361	Transcriptional profiling and therapeutic targeting of oxidative stress in neuroinflammation. <i>Nature Immunology</i> , 2020, 21, 513-524.	7.0	118
1362	Mapping the cis-regulatory architecture of the human retina reveals noncoding genetic variation in disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9001-9012.	3.3	72
1363	Phagocytosis of Wnt inhibitor SFRP4 by late wound macrophages drives chronic Wnt activity for fibrotic skin healing. <i>Science Advances</i> , 2020, 6, eaay3704.	4.7	58
1364	JunB Controls Intestinal Effector Programs in Regulatory T Cells. <i>Frontiers in Immunology</i> , 2020, 11, 444.	2.2	9
1365	Preclinical safety studies of human embryonic stem cell-derived retinal pigment epithelial cells for the treatment of age-related macular degeneration. <i>Stem Cells Translational Medicine</i> , 2020, 9, 936-953.	1.6	14
1366	C/EBP β and GATA-2 Mutations Induce Bilineage Acute Erythroid Leukemia through Transformation of a Neomorphic Neutrophil-Erythroid Progenitor. <i>Cancer Cell</i> , 2020, 37, 690-704.e8.	7.7	16
1367	alona: a web server for single-cell RNA-seq analysis. <i>Bioinformatics</i> , 2020, 36, 3910-3912.	1.8	33
1368	Single-cell multiomic analysis of in vivo and in vitro matured human oocytes. <i>Human Reproduction</i> , 2020, 35, 886-900.	0.4	20
1369	Single Cell RNA Sequencing in Atherosclerosis Research. <i>Circulation Research</i> , 2020, 126, 1112-1126.	2.0	84
1370	Lgr5+Âtelocytes are a signaling source at the intestinal villus tip. <i>Nature Communications</i> , 2020, 11, 1936.	5.8	105
1371	Single-cell analysis of a mutant library generated using CRISPR-guided deaminase in human melanoma cells. <i>Communications Biology</i> , 2020, 3, 154.	2.0	25
1372	Prediction of condition-specific regulatory genes using machine learning. <i>Nucleic Acids Research</i> , 2020, 48, e62-e62.	6.5	37
1373	Improved Prognostic Prediction of Glioblastoma using a PAS Detected from Single-cell RNA-seq. <i>Journal of Cancer</i> , 2020, 11, 3751-3761.	1.2	1
1374	Accurate estimation of cell composition in bulk expression through robust integration of single-cell information. <i>Nature Communications</i> , 2020, 11, 1971.	5.8	200
1375	Cathepsin S Regulates Antigen Processing and T Cell Activity in Non-Hodgkin Lymphoma. <i>Cancer Cell</i> , 2020, 37, 674-689.e12.	7.7	55

#	ARTICLE	IF	CITATIONS
1376	SARS-CoV-2 Receptor ACE2 Is an Interferon-Stimulated Gene in Human Airway Epithelial Cells and Is Detected in Specific Cell Subsets across Tissues. <i>Cell</i> , 2020, 181, 1016-1035.e19.	13.5	1,956
1377	Single-nucleus transcriptomics of the prefrontal cortex in major depressive disorder implicates oligodendrocyte precursor cells and excitatory neurons. <i>Nature Neuroscience</i> , 2020, 23, 771-781.	7.1	258
1378	Disease-associated astrocytes in Alzheimer's disease and aging. <i>Nature Neuroscience</i> , 2020, 23, 701-706.	7.1	525
1379	Gene-edited human stem cell-derived β^2 cells from a patient with monogenic diabetes reverse preexisting diabetes in mice. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	123
1380	GiniClust3: a fast and memory-efficient tool for rare cell type identification. <i>BMC Bioinformatics</i> , 2020, 21, 158.	1.2	28
1381	Scedar: A scalable Python package for single-cell RNA-seq exploratory data analysis. <i>PLoS Computational Biology</i> , 2020, 16, e1007794.	1.5	9
1382	A single cell transcriptome atlas of the developing zebrafish hindbrain. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	39
1383	Collagen-producing lung cell atlas identifies multiple subsets with distinct localization and relevance to fibrosis. <i>Nature Communications</i> , 2020, 11, 1920.	5.8	346
1384	Pooled Knockin Targeting for Genome Engineering of Cellular Immunotherapies. <i>Cell</i> , 2020, 181, 728-744.e21.	13.5	131
1385	Single-Cell Analyses Inform Mechanisms of Myeloid-Targeted Therapies in Colon Cancer. <i>Cell</i> , 2020, 181, 442-459.e29.	13.5	741
1386	Computational Oncology in the Multi-Omics Era: State of the Art. <i>Frontiers in Oncology</i> , 2020, 10, 423.	1.3	59
1387	Advances and challenges in epigenomic single-cell sequencing applications. <i>Current Opinion in Chemical Biology</i> , 2020, 57, 17-26.	2.8	13
1388	IL-33-PU.1 Transcriptome Reprogramming Drives Functional State Transition and Clearance Activity of Microglia in Alzheimer's Disease. <i>Cell Reports</i> , 2020, 31, 107530.	2.9	65
1389	Super-Enhancer Redistribution as a Mechanism of Broad Gene Dysregulation in Repeatedly Drug-Treated Cancer Cells. <i>Cell Reports</i> , 2020, 31, 107532.	2.9	29
1390	Integrated scRNA-Seq Identifies Human Postnatal Thymus Seeding Progenitors and Regulatory Dynamics of Differentiating Immature Thymocytes. <i>Immunity</i> , 2020, 52, 1088-1104.e6.	6.6	79
1391	PNOCARC Neurons Promote Hyperphagia and Obesity upon High-Fat-Diet Feeding. <i>Neuron</i> , 2020, 106, 1009-1025.e10.	3.8	64
1392	Dermal Adipocyte Lipolysis and Myofibroblast Conversion Are Required for Efficient Skin Repair. <i>Cell Stem Cell</i> , 2020, 26, 880-895.e6.	5.2	154
1393	C-KIT Expression Distinguishes Fetal from Postnatal Skeletal Progenitors. <i>Stem Cell Reports</i> , 2020, 14, 614-630.	2.3	6

#	ARTICLE	IF	CITATIONS
1394	Single-cell transcriptomics identifies an effectorness gradient shaping the response of CD4+ T cells to cytokines. <i>Nature Communications</i> , 2020, 11, 1801.	5.8	153
1395	Exploiting evolutionary steering to induce collateral drug sensitivity in cancer. <i>Nature Communications</i> , 2020, 11, 1923.	5.8	79
1396	Cxcl10+ monocytes define a pathogenic subset in the central nervous system during autoimmune neuroinflammation. <i>Nature Immunology</i> , 2020, 21, 525-534.	7.0	74
1397	Redefining the heterogeneity of peripheral nerve cells in health and autoimmunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9466-9476.	3.3	97
1398	Characterizing and inferring quantitative cell cycle phase in single-cell RNA-seq data analysis. <i>Genome Research</i> , 2020, 30, 611-621.	2.4	63
1399	Environmental Carcinogenesis at the Single-Cell Level. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1880-1886.	1.1	1
1400	Modern human changes in regulatory regions implicated in cortical development. <i>BMC Genomics</i> , 2020, 21, 304.	1.2	16
1401	Macrophage-Derived CXCL9 and CXCL10 Are Required for Antitumor Immune Responses Following Immune Checkpoint Blockade. <i>Clinical Cancer Research</i> , 2020, 26, 487-504.	3.2	355
1402	Nivolumab treatment of relapsed/refractory Epstein-Barr virus-associated hemophagocytic lymphohistiocytosis in adults. <i>Blood</i> , 2020, 135, 826-833.	0.6	74
1403	Diversity of peripheral blood human NK cells identified by single-cell RNA sequencing. <i>Blood Advances</i> , 2020, 4, 1388-1406.	2.5	125
1404	Single-cell RNA-seq highlights heterogeneity in human primary Wharton's jelly mesenchymal stem/stromal cells cultured in vitro. <i>Stem Cell Research and Therapy</i> , 2020, 11, 149.	2.4	60
1405	Integrating GWAS with bulk and single-cell RNA-sequencing reveals a role for LY86 in the anti-Candida host response. <i>PLoS Pathogens</i> , 2020, 16, e1008408.	2.1	18
1406	Evaluation of STAR and Kallisto on Single Cell RNA-Seq Data Alignment. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1775-1783.	0.8	34
1407	Single-Cell Analysis of Neuroinflammatory Responses Following Intracranial Injection of G-Deleted Rabies Viruses. <i>Frontiers in Cellular Neuroscience</i> , 2020, 14, 65.	1.8	35
1408	YAP1 mediates gastric adenocarcinoma peritoneal metastases that are attenuated by YAP1 inhibition. <i>Gut</i> , 2021, 70, 55-66.	6.1	53
1409	Dissecting the initiation of female meiosis in the mouse at single-cell resolution. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 695-713.	2.4	38
1410	Computational methods for the integrative analysis of single-cell data. <i>Briefings in Bioinformatics</i> , 2021, 22, 20-29.	3.2	43
1411	scCancer: a package for automated processing of single-cell RNA-seq data in cancer. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	35

#	ARTICLE	IF	CITATIONS
1412	SMNN: batch effect correction for single-cell RNA-seq data via supervised mutual nearest neighbor detection. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	17
1413	Cisplatin-induced peripheral neuropathy is associated with neuronal senescence-like response. <i>Neuro-Oncology</i> , 2021, 23, 88-99.	0.6	36
1414	High-dimensional single-cell analysis reveals the immune characteristics of COVID-19. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2021, 320, L84-L98.	1.3	22
1415	Neuronal diversity and convergence in a visual system developmental atlas. <i>Nature</i> , 2021, 589, 88-95.	13.7	152
1416	A Transcriptome-Based Drug Discovery Paradigm for Neurodevelopmental Disorders. <i>Annals of Neurology</i> , 2021, 89, 199-211.	2.8	14
1417	Single-Cell Transcriptomic Heterogeneity in Invasive Ductal and Lobular Breast Cancer Cells. <i>Cancer Research</i> , 2021, 81, 268-281.	0.4	28
1418	The Power of Single-Cell Analysis for the Study of Liver Pathobiology. <i>Hepatology</i> , 2021, 73, 437-448.	3.6	19
1419	Identifying adaptive alleles in the human genome: from selection mapping to functional validation. <i>Human Genetics</i> , 2021, 140, 241-276.	1.8	13
1420	Immune cell infiltration features and related marker genes in lung cancer based on single-cell RNA-seq. <i>Clinical and Translational Oncology</i> , 2021, 23, 405-417.	1.2	33
1421	Integrated analysis of single-cell RNA-seq and bulk RNA-seq unravels tumour heterogeneity plus M2-like tumour-associated macrophage infiltration and aggressiveness in TNBC. <i>Cancer Immunology, Immunotherapy</i> , 2021, 70, 189-202.	2.0	82
1422	Combinatorial Transcriptional Profiling of Mouse and Human Enteric Neurons Identifies Shared and Disparate Subtypes In Situ. <i>Gastroenterology</i> , 2021, 160, 755-770.e26.	0.6	67
1423	Excessive deubiquitination of NLRP3-R779C variant contributes to very-early-onset inflammatory bowel disease development. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 267-279.	1.5	38
1424	MYC Promotes Bone Marrow Stem Cell Dysfunction in Fanconi Anemia. <i>Cell Stem Cell</i> , 2021, 28, 33-47.e8.	5.2	31
1425	Sympathetic Input to Multiple Cell Types in Mouse and Human Colon Produces Region-Specific Responses. <i>Gastroenterology</i> , 2021, 160, 1208-1223.e4.	0.6	23
1426	Single-Cell Study of Two Rat Models of Pulmonary Arterial Hypertension Reveals Connections to Human Pathobiology and Drug Repositioning. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2021, 203, 1006-1022.	2.5	36
1427	Fructose Promotes Cytoprotection in Melanoma Tumors and Resistance to Immunotherapy. <i>Cancer Immunology Research</i> , 2021, 9, 227-238.	1.6	17
1428	Airspace Macrophages and Monocytes Exist in Transcriptionally Distinct Subsets in Healthy Adults. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2021, 203, 946-956.	2.5	63
1429	Derivation of Airway Basal Stem Cells from Human Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2021, 28, 79-95.e8.	5.2	119

#	ARTICLE	IF	CITATIONS
1430	mTORC1 hyperactivation in lymphangiomyomatosis leads to ACE2 upregulation in type II pneumocytes: implications for COVID-19. <i>European Respiratory Journal</i> , 2021, 57, 2002737.	3.1	11
1431	Ensemble learning models that predict surface protein abundance from single-cell multimodal omics data. <i>Methods</i> , 2021, 189, 65-73.	1.9	13
1432	Aggressive PDACs Show Hypomethylation of Repetitive Elements and the Execution of an Intrinsic IFN Program Linked to a Ductal Cell of Origin. <i>Cancer Discovery</i> , 2021, 11, 638-659.	7.7	65
1433	Single-cell RNA-seq reveals developmental plasticity with coexisting oncogenic states and immune evasion programs in ETP-ALL. <i>Blood</i> , 2021, 137, 2463-2480.	0.6	35
1434	Transcriptional dynamics of induced pluripotent stem cell differentiation into \hat{I}^2 cells reveals full endodermal commitment and homology with human islets. <i>Cytotherapy</i> , 2021, 23, 311-319.	0.3	9
1435	lLoReg: a tool for high-resolution cell population identification from single-cell RNA-seq data. <i>Bioinformatics</i> , 2021, 37, 1107-1114.	1.8	5
1436	Capture of Mouse and Human Stem Cells with Features of Formative Pluripotency. <i>Cell Stem Cell</i> , 2021, 28, 453-471.e8.	5.2	151
1437	Cyclophosphamide and Vinorelbine Activate Stem-Like CD8+ T Cells and Improve Anti-PD-1 Efficacy in Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2021, 81, 685-697.	0.4	31
1438	Comprehensive Profiling of an Aging Immune System Reveals Clonal GZMK+ CD8+ T Cells as Conserved Hallmark of Inflammaging. <i>Immunity</i> , 2021, 54, 99-115.e12.	6.6	258
1439	Area Postrema Cell Types that Mediate Nausea-Associated Behaviors. <i>Neuron</i> , 2021, 109, 461-472.e5.	3.8	106
1440	Analysis of canine myeloid-derived suppressor cells (MDSCs) utilizing fluorescence-activated cell sorting, RNA protection mediums to yield quality RNA for single-cell RNA sequencing. <i>Veterinary Immunology and Immunopathology</i> , 2021, 231, 110144.	0.5	10
1441	Stromal SOX2 Upregulation Promotes Tumorigenesis through the Generation of a SFRP1/2-Expressing Cancer-Associated Fibroblast Population. <i>Developmental Cell</i> , 2021, 56, 95-110.e10.	3.1	50
1442	Deletion of the Brain-Specific \hat{I}^{\pm} and \hat{I}^{\uparrow} Isoforms of Adapter Protein SH2B1 Protects Mice From Obesity. <i>Diabetes</i> , 2021, 70, 400-414.	0.3	4
1443	The Power of Plasticity—Metabolic Regulation of Hepatic Stellate Cells. <i>Cell Metabolism</i> , 2021, 33, 242-257.	7.2	173
1444	VEGF-B Promotes Endocardium-Derived Coronary Vessel Development and Cardiac Regeneration. <i>Circulation</i> , 2021, 143, 65-77.	1.6	57
1445	A Single-Cell Transcriptomic Atlas of Human Skin Aging. <i>Developmental Cell</i> , 2021, 56, 383-397.e8.	3.1	145
1446	A replicating stem-like cell that contributes to bone morphogenetic protein 2-induced heterotopic bone formation. <i>Stem Cells Translational Medicine</i> , 2021, 10, 623-635.	1.6	6
1447	Single-cell RNA sequencing and lipidomics reveal cell and lipid dynamics of fat infiltration in skeletal muscle. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2021, 12, 109-129.	2.9	46

#	ARTICLE	IF	CITATIONS
1448	Macrophage expression and prognostic significance of the long pentraxin PTX3 in COVID-19. <i>Nature Immunology</i> , 2021, 22, 19-24.	7.0	101
1449	Looking at the developing lung in single-cell resolution. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2021, 320, L680-L687.	1.3	7
1450	Molecular detection of maturation stages in the developing kidney. <i>Developmental Biology</i> , 2021, 470, 62-73.	0.9	14
1451	Reshaping the Immune Microenvironment by Oncolytic Herpes Simplex Virus in Murine Pancreatic Ductal Adenocarcinoma. <i>Molecular Therapy</i> , 2021, 29, 744-761.	3.7	24
1452	TISCH: a comprehensive web resource enabling interactive single-cell transcriptome visualization of tumor microenvironment. <i>Nucleic Acids Research</i> , 2021, 49, D1420-D1430.	6.5	481
1453	Uncovering cellular networks in branching morphogenesis using single-cell transcriptomics. <i>Current Topics in Developmental Biology</i> , 2021, 143, 239-280.	1.0	6
1454	An extracellular vesicle-related gene expression signature identifies high-risk patients in medulloblastoma. <i>Neuro-Oncology</i> , 2021, 23, 586-598.	0.6	8
1455	Gene Regulatory Network Analysis and Engineering Directs Development and Vascularization of Multilineage Human Liver Organoids. <i>Cell Systems</i> , 2021, 12, 41-55.e11.	2.9	59
1456	Heterogeneous bone-marrow stromal progenitors drive myelofibrosis via a druggable alarmin axis. <i>Cell Stem Cell</i> , 2021, 28, 637-652.e8.	5.2	92
1457	Diversification of molecularly defined myenteric neuron classes revealed by single-cell RNA sequencing. <i>Nature Neuroscience</i> , 2021, 24, 34-46.	7.1	151
1458	Tutorial: guidelines for the computational analysis of single-cell RNA sequencing data. <i>Nature Protocols</i> , 2021, 16, 1-9.	5.5	169
1459	Single-cell analyses reveal YAP/TAZ as regulators of stemness and cell plasticity in glioblastoma. <i>Nature Cancer</i> , 2021, 2, 174-188.	5.7	83
1460	A microfluidics-based stem cell model of early post-implantation human development. <i>Nature Protocols</i> , 2021, 16, 309-326.	5.5	16
1461	Modeling Human TBX5 Haploinsufficiency Predicts Regulatory Networks for Congenital Heart Disease. <i>Developmental Cell</i> , 2021, 56, 292-309.e9.	3.1	63
1462	Panoramic transcriptome analysis and functional screening of long noncoding RNAs in mouse spermatogenesis. <i>Genome Research</i> , 2021, 31, 13-26.	2.4	23
1463	Decoding Human Megakaryocyte Development. <i>Cell Stem Cell</i> , 2021, 28, 535-549.e8.	5.2	79
1464	Integrative single-cell transcriptome analysis reveals a subpopulation of fibroblasts associated with favorable prognosis of liver cancer patients. <i>Translational Oncology</i> , 2021, 14, 100981.	1.7	12
1465	CCAAT/enhancer-binding protein beta promotes muscle stem cell quiescence through regulation of quiescence-associated genes. <i>Stem Cells</i> , 2021, 39, 345-357.	1.4	6

#	ARTICLE	IF	CITATIONS
1466	Benchmarking Computational Doublet-Detection Methods for Single-Cell RNA Sequencing Data. <i>Cell Systems</i> , 2021, 12, 176-194.e6.	2.9	99
1467	Transcriptional landscape of rice roots at the single-cell resolution. <i>Molecular Plant</i> , 2021, 14, 384-394.	3.9	131
1468	Microglia facilitate repair of demyelinated lesions via post-squalene sterol synthesis. <i>Nature Neuroscience</i> , 2021, 24, 47-60.	7.1	134
1469	Integrative Single-Cell RNA-Seq and ATAC-Seq Analysis of Human Developmental Hematopoiesis. <i>Cell Stem Cell</i> , 2021, 28, 472-487.e7.	5.2	184
1470	dittoSeq: universal user-friendly single-cell and bulk RNA sequencing visualization toolkit. <i>Bioinformatics</i> , 2021, 36, 5535-5536.	1.8	85
1471	Durable Suppression of Acquired MEK Inhibitor Resistance in Cancer by Sequestering MEK from ERK and Promoting Antitumor T-cell Immunity. <i>Cancer Discovery</i> , 2021, 11, 714-735.	7.7	45
1472	Replication and meta-analyses nominate numerous eosinophilic esophagitis risk genes. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 255-266.	1.5	25
1473	A reliable strategy for single-cell RNA sequencing analysis using cryoconserved primary cortical cells. <i>Journal of Neuroscience Methods</i> , 2021, 347, 108960.	1.3	6
1474	Lymph nodes are innervated by a unique population of sensory neurons with immunomodulatory potential. <i>Cell</i> , 2021, 184, 441-459.e25.	13.5	101
1475	Differential encoding in prefrontal cortex projection neuron classes across cognitive tasks. <i>Cell</i> , 2021, 184, 489-506.e26.	13.5	58
1476	Merkel cell carcinoma-derived exosome-shuttle miR-375 induces fibroblast polarization by inhibition of RBPJ and p53. <i>Oncogene</i> , 2021, 40, 980-996.	2.6	32
1477	Lineage-specific regulation of inducible and constitutive mast cells in allergic airway inflammation. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	42
1478	FGF9 promotes mouse spermatogonial stem cell proliferation mediated by p38 MAPK signalling. <i>Cell Proliferation</i> , 2021, 54, e12933.	2.4	36
1479	In silico analysis of inner ear development using public whole embryonic body single-cell RNA-sequencing data. <i>Developmental Biology</i> , 2021, 469, 160-171.	0.9	10
1480	Single-cell patterning and axis characterization in the murine and human definitive endoderm. <i>Cell Research</i> , 2021, 31, 326-344.	5.7	13
1481	Single-Cell Transcriptome Analysis in Plants: Advances and Challenges. <i>Molecular Plant</i> , 2021, 14, 115-126.	3.9	127
1482	BMP10 Signaling Promotes the Development of Endocardial Cells from Human Pluripotent Stem Cell-Derived Cardiovascular Progenitors. <i>Cell Stem Cell</i> , 2021, 28, 96-111.e7.	5.2	43
1483	Intravenous nanoparticle vaccination generates stem-like TCF1+ neoantigen-specific CD8+ T cells. <i>Nature Immunology</i> , 2021, 22, 41-52.	7.0	110

#	ARTICLE	IF	CITATIONS
1484	Single nucleus transcriptomics data integration recapitulates the major cell types in human liver. <i>Hepatology Research</i> , 2021, 51, 233-238.	1.8	7
1485	Early development and functional properties of tryptase/chymase double-positive mast cells from human pluripotent stem cells. <i>Journal of Molecular Cell Biology</i> , 2021, 13, 104-115.	1.5	5
1486	Serial single-cell profiling analysis of metastatic TNBC during Nab-paclitaxel and pembrolizumab treatment. <i>Breast Cancer Research and Treatment</i> , 2021, 185, 85-94.	1.1	15
1487	The Gustatory Sensory G-Protein GNAT3 Suppresses Pancreatic Cancer Progression in Mice. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021, 11, 349-369.	2.3	25
1488	Single-Nuclei RNA Sequencing Assessment of the Hepatic Effects of 2,3,7,8-Tetrachlorodibenzo-p-dioxin. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021, 11, 147-159.	2.3	42
1489	Human kidney organoids produce functional renin. <i>Kidney International</i> , 2021, 99, 134-147.	2.6	36
1490	Single-cell transcriptomic atlas of primate cardiopulmonary aging. <i>Cell Research</i> , 2021, 31, 415-432.	5.7	88
1491	Next-generation humanized patient-derived xenograft mouse model for pre-clinical antibody studies in neuroblastoma. <i>Cancer Immunology, Immunotherapy</i> , 2021, 70, 721-732.	2.0	17
1493	Investigating Inter- and Intrasample Diversity of Single-Cell RNA Sequencing Datasets. <i>Methods in Molecular Biology</i> , 2021, 2194, 177-186.	0.4	4
1494	Intestinal Receptor of SARS-CoV-2 in Inflamed IBD Tissue Seems Downregulated by HNF4A in Ileum and Upregulated by Interferon Regulating Factors in Colon. <i>Journal of Crohn's and Colitis</i> , 2021, 15, 485-498.	0.6	34
1495	Single-cell RNA expression profiling of SARS-CoV-2-related ACE2 and TMPRSS2 in human trophoblast and placenta. <i>Ultrasound in Obstetrics and Gynecology</i> , 2021, 57, 248-256.	0.9	54
1496	SCDC: bulk gene expression deconvolution by multiple single-cell RNA sequencing references. <i>Briefings in Bioinformatics</i> , 2021, 22, 416-427.	3.2	156
1497	HBsAg-specific CD8+ T cells as an indispensable trigger to induce murine hepatocellular carcinoma. <i>Cellular and Molecular Immunology</i> , 2021, 18, 128-137.	4.8	21
1498	AP-2 β Is Required for Maintenance of Multipotent Mammary Stem Cells. <i>Stem Cell Reports</i> , 2021, 16, 106-119.	2.3	4
1507	An in vivo screen of noncoding loci reveals that <i>Daedalus</i> is a gatekeeper of an Ikaros-dependent checkpoint during haematopoiesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	2
1508	Temporally integrated single cell RNA sequencing analysis of PBMC from experimental and natural primary human DENV-1 infections. <i>PLoS Pathogens</i> , 2021, 17, e1009240.	2.1	23
1509	Spermatogonia Loss Correlates with LAMA 1 Expression in Human Prepubertal Testes Stored for Fertility Preservation. <i>Cells</i> , 2021, 10, 241.	1.8	14
1510	A transcriptomic taxonomy of <i>Drosophila</i> circadian neurons around the clock. <i>ELife</i> , 2021, 10, .	2.8	72

#	ARTICLE	IF	CITATIONS
1511	Phased differentiation of $\hat{I}^3\hat{I}^7$ T and T CD8 tumor-infiltrating lymphocytes revealed by single-cell transcriptomics of human cancers. <i>Oncolmmunology</i> , 2021, 10, 1939518.	2.1	11
1512	QKI is a critical pre-mRNA alternative splicing regulator of cardiac myofibrillogenesis and contractile function. <i>Nature Communications</i> , 2021, 12, 89.	5.8	47
1513	A road map from single-cell transcriptome to patient classification for the immune response to trauma. <i>JCI Insight</i> , 2021, 6, .	2.3	29
1514	The orchestrated cellular and molecular responses of the kidney to endotoxin define a precise sepsis timeline. <i>ELife</i> , 2021, 10, .	2.8	78
1515	tidybulk: an R tidy framework for modular transcriptomic data analysis. <i>Genome Biology</i> , 2021, 22, 42.	3.8	25
1516	Identification of Novel Population-Specific Cell Subsets in Chinese Ulcerative Colitis Patients Using Single-Cell RNA Sequencing. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021, 12, 99-117.	2.3	15
1517	Flow Cytometry-Based Analysis of the Mouse Bone Marrow Stromal and Perivascular Compartment. <i>Methods in Molecular Biology</i> , 2021, 2308, 83-94.	0.4	9
1519	Susceptibility Factors of Stomach for SARS-CoV-2 and Treatment Implication of Mucosal Protective Agent in COVID-19. <i>Frontiers in Medicine</i> , 2020, 7, 597967.	1.2	13
1520	Loss of PRC2 Enforces a Mesenchymal Neural Crest Stem Cell Phenotype in NF1-Deficient Cancer Through Activation of Core Transcription Factors. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1521	Opposing immune and genetic mechanisms shape oncogenic programs in synovial sarcoma. <i>Nature Medicine</i> , 2021, 27, 289-300.	15.2	64
1522	Induced organoids derived from patients with ulcerative colitis recapitulate colitic reactivity. <i>Nature Communications</i> , 2021, 12, 262.	5.8	51
1523	Single cell sequencing reveals endothelial plasticity with transient mesenchymal activation after myocardial infarction. <i>Nature Communications</i> , 2021, 12, 681.	5.8	158
1524	Ethanol exposure drives colon location specific cell composition changes in a normal colon crypt 3D organoid model. <i>Scientific Reports</i> , 2021, 11, 432.	1.6	14
1525	Patch-seq: Past, Present, and Future. <i>Journal of Neuroscience</i> , 2021, 41, 937-946.	1.7	60
1526	Inhibitory signaling sustains a distinct early memory CD8 ⁺ T cell precursor that is resistant to DNA damage. <i>Science Immunology</i> , 2021, 6, .	5.6	52
1527	Multi-domain translation between single-cell imaging and sequencing data using autoencoders. <i>Nature Communications</i> , 2021, 12, 31.	5.8	71
1528	CREBBP/EP300 mutations promoted tumor progression in diffuse large B-cell lymphoma through altering tumor-associated macrophage polarization via FBXW7-NOTCH-CCL2/CSF1 axis. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 10.	7.1	93
1529	Recent Advances in Variational Autoencoders With Representation Learning for Biomedical Informatics: A Survey. <i>IEEE Access</i> , 2021, 9, 4939-4956.	2.6	35

#	ARTICLE	IF	CITATIONS
1530	Single cell resolution of SARS-CoV-2 tropism, antiviral responses, and susceptibility to therapies in primary human airway epithelium. <i>PLoS Pathogens</i> , 2021, 17, e1009292.	2.1	76
1531	Lung megakaryocytes are immune modulatory cells. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	96
1532	Gradient of Developmental and Injury Response transcriptional states defines functional vulnerabilities underpinning glioblastoma heterogeneity. <i>Nature Cancer</i> , 2021, 2, 157-173.	5.7	147
1533	Expansion sequencing: Spatially precise in situ transcriptomics in intact biological systems. <i>Science</i> , 2021, 371, .	6.0	197
1534	Human intestinal tissue-resident memory T cells comprise transcriptionally and functionally distinct subsets. <i>Cell Reports</i> , 2021, 34, 108661.	2.9	56
1535	DRscDB: A single-cell RNA-seq resource for data mining and data comparison across species. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2018-2026.	1.9	17
1536	Genetic mapping of developmental trajectories for complex traits and diseases. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3458-3469.	1.9	1
1537	Benchmarking joint multi-omics dimensionality reduction approaches for the study of cancer. <i>Nature Communications</i> , 2021, 12, 124.	5.8	89
1538	Kinomic profile in patient-derived glioma cells during hypoxia reveals c-MET-PI3K dependency for adaptation. <i>Theranostics</i> , 2021, 11, 5127-5142.	4.6	7
1539	Mitochondrial gene expression in single cells shape pancreatic beta cells' sub-populations and explain variation in insulin pathway. <i>Scientific Reports</i> , 2021, 11, 466.	1.6	9
1543	Targeting Lymphotoxin Beta and Paired Box 5: a potential therapeutic strategy for soft tissue sarcoma metastasis. <i>Cancer Cell International</i> , 2021, 21, 3.	1.8	0
1544	Novel Targets of SARS-CoV-2 Spike Protein in Human Fetal Brain Development Suggest Early Pregnancy Vulnerability. <i>Frontiers in Neuroscience</i> , 2020, 14, 614680.	1.4	15
1549	Toward a humanized mouse model of <i>Pneumocystis pneumonia</i> . <i>JCI Insight</i> , 2021, 6, .	2.3	4
1550	Resolving Transcriptional States and Predicting Lineages in the Annelid <i>Capitella teleta</i> Using Single-Cell RNAseq. <i>Frontiers in Ecology and Evolution</i> , 2021, 8, .	1.1	6
1552	Single-Cell Transcriptome Profiling. <i>Methods in Molecular Biology</i> , 2021, 2243, 311-325.	0.4	3
1553	Single-cell RNA sequencing in cardiovascular science. , 2021, , 377-394.		0
1554	Single-cell mapper (scMappR): using scRNA-seq to infer the cell-type specificities of differentially expressed genes. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab011.	1.5	23
1555	Complement Activation Induces Excessive T Cell Cytotoxicity in Severe COVID-19. <i>SSRN Electronic Journal</i> , 0, , .	0.4	2

#	ARTICLE	IF	CITATIONS
1556	Neuromesodermal Progenitor Origin of Trunk Neural Crest &in vivo&. SSRN Electronic Journal, 0, , .	0.4	1
1558	Single-cell analysis reveals transcriptomic remodellings in distinct cell types that contribute to human prostate cancer progression. Nature Cell Biology, 2021, 23, 87-98.	4.6	209
1560	Single Cell Clonal Analysis Identifies an AID-Dependent Pathway of Plasma Cell Differentiation. SSRN Electronic Journal, 0, , .	0.4	0
1561	scDA: Single cell discriminant analysis for single-cell RNA sequencing data. Computational and Structural Biotechnology Journal, 2021, 19, 3234-3244.	1.9	3
1565	Single-Cell Gene Network Analysis and Transcriptional Landscape of MYCN-Amplified Neuroblastoma Cell Lines. Biomolecules, 2021, 11, 177.	1.8	10
1566	The T-box transcription factor Eomesodermin governs haemogenic competence of yolk sac mesodermal progenitors. Nature Cell Biology, 2021, 23, 61-74.	4.6	10
1567	JOINT for large-scale single-cell RNA-sequencing analysis via soft-clustering and parallel computing. BMC Genomics, 2021, 22, 47.	1.2	3
1570	Genetic analysis of amyotrophic lateral sclerosis identifies contributing pathways and cell types. Science Advances, 2021, 7, .	4.7	59
1571	Single-Cell Sequencing of Brain Cell Transcriptomes and Epigenomes. Neuron, 2021, 109, 11-26.	3.8	135
1572	Distinct identities of leaf phloem cells revealed by single cell transcriptomics. Plant Cell, 2021, 33, 511-530.	3.1	162
1573	Persistence of mature dendritic cells, T _H 2A, and Tc2 cells characterize clinically resolved atopic dermatitis under IL-4R α blockade. Science Immunology, 2021, 6, .	5.6	76
1574	Evaluating totipotency using criteria of increasing stringency. Nature Cell Biology, 2021, 23, 49-60.	4.6	121
1576	Computational Analysis of Single-Cell RNA-Seq Data. Methods in Molecular Biology, 2021, 2284, 289-301.	0.4	0
1579	Integration of single-cell and bulk RNA sequencing data reveals key cell types and regulators in traumatic brain injury. Mathematical Biosciences and Engineering, 2021, 18, 1201-1214.	1.0	3
1580	DiscBio: A User-Friendly Pipeline for Biomarker Discovery in Single-Cell Transcriptomics. International Journal of Molecular Sciences, 2021, 22, 1399.	1.8	6
1581	Construction of Bone Metastasis-Specific Regulation Network Based on Prognostic Stemness-Related Signatures in Breast Invasive Carcinoma. Frontiers in Oncology, 2020, 10, 613333.	1.3	2
1583	Transcriptomic alterations underline aging of osteogenic bone marrow stromal cells. World Journal of Stem Cells, 2021, 13, 128-138.	1.3	1
1585	Vitamin D sufficiency enhances differentiation of patient-derived prostate epithelial organoids. IScience, 2021, 24, 101974.	1.9	18

#	ARTICLE	IF	CITATIONS
1587	No detectable alloreactive transcriptional responses under standard sample preparation conditions during donor-multiplexed single-cell RNA sequencing of peripheral blood mononuclear cells. <i>BMC Biology</i> , 2021, 19, 10.	1.7	9
1588	Exome-wide evaluation of rare coding variants using electronic health records identifies new gene–phenotype associations. <i>Nature Medicine</i> , 2021, 27, 66-72.	15.2	44
1589	Decoding the multicellular ecosystem of lung adenocarcinoma manifested as pulmonary subsolid nodules by single-cell RNA sequencing. <i>Science Advances</i> , 2021, 7, .	4.7	88
1590	Age-related injury responses of human oligodendrocytes to metabolic insults: link to BCL-2 and autophagy pathways. <i>Communications Biology</i> , 2021, 4, 20.	2.0	17
1591	SARS-CoV-2 Infection of Circulating Immune Cells is Not Responsible for Virus Dissemination in Severe COVID-19 Patients. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
1592	Longitudinal single-cell RNA-seq of hESCs-derived retinal organoids. <i>Science China Life Sciences</i> , 2021, 64, 1661-1676.	2.3	8
1593	<i>DDX58</i> (RIG-I)-related disease is associated with tissue-specific interferon pathway activation. <i>Journal of Medical Genetics</i> , 2022, 59, 294-304.	1.5	16
1594	Fibroblast and Myofibroblast Subtypes: Single Cell Sequencing. <i>Methods in Molecular Biology</i> , 2021, 2299, 49-84.	0.4	7
1595	Sequential fate-switches in stem-like cells drive the tumorigenic trajectory from human neural stem cells to malignant glioma. <i>Cell Research</i> , 2021, 31, 684-702.	5.7	41
1596	MUC1-C integrates activation of the IFN- β pathway with suppression of the tumor immune microenvironment in triple-negative breast cancer. , 2021, 9, e002115.		41
1597	Single-Cell RNA Sequencing of Tocilizumab-Treated Peripheral Blood Mononuclear Cells as an in vitro Model of Inflammation. <i>Frontiers in Genetics</i> , 2020, 11, 610682.	1.1	6
1598	A Streamlined scRNA-Seq Data Analysis Framework Based on Improved Sparse Subspace Clustering. <i>IEEE Access</i> , 2021, 9, 9719-9727.	2.6	18
1599	Imaging dynamic mTORC1 pathway activity in vivo reveals marked shifts that support time-specific inhibitor therapy in AML. <i>Nature Communications</i> , 2021, 12, 245.	5.8	18
1600	Gut Microbe-Derived Metabolite Trimethylamine N-Oxide Activates PERK to Drive Mesenchymal Differentiation and Fibrosis. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1601	Differential transcript usage unravels gene expression alterations in Alzheimer’s disease human brains. <i>Npj Aging and Mechanisms of Disease</i> , 2021, 7, 2.	4.5	49
1602	Transcriptome features of striated muscle aging and predictability of protein level changes. <i>Molecular Omics</i> , 2021, 17, 796-808.	1.4	9
1603	Single-Cell Multiomics Analysis Reveals Heterogeneous Cell States Linked to Metastatic Potential in Liver Cancer Cell Lines. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1604	Immunosuppressive Myeloid Cells Induce Nitric Oxide–Dependent DNA Damage and p53 Pathway Activation in CD8+ T Cells. <i>Cancer Immunology Research</i> , 2021, 9, 470-485.	1.6	17

#	ARTICLE	IF	CITATIONS
1605	Potentiality of multiple modalities for single-cell analyses to evaluate the tumor microenvironment in clinical specimens. <i>Scientific Reports</i> , 2021, 11, 341.	1.6	17
1606	Single-cell RNA-seq reveals invasive trajectory and determines cancer stem cell-related prognostic genes in pancreatic cancer. <i>Bioengineered</i> , 2021, 12, 5056-5068.	1.4	11
1607	Single-Cell RNA Sequencing Technologies. , 2021, , 555-584.		0
1608	Subcellular sequencing of single neurons reveals the dendritic transcriptome of GABAergic interneurons. <i>ELife</i> , 2021, 10, .	2.8	48
1609	Automated methods for cell type annotation on scRNA-seq data. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 961-969.	1.9	122
1610	Comprehensive annotation of the Chinese tree shrew genome by large-scale RNA sequencing and long-read isoform sequencing. <i>Zoological Research</i> , 2021, 42, 692-709.	0.9	18
1611	Gut CD4+ T cell phenotypes are a continuum molded by microbes, not by TH archetypes. <i>Nature Immunology</i> , 2021, 22, 216-228.	7.0	116
1612	A noninflammatory mRNA vaccine for treatment of experimental autoimmune encephalomyelitis. <i>Science</i> , 2021, 371, 145-153.	6.0	253
1614	Defining human mesenchymal and epithelial heterogeneity in response to oral inflammatory disease. <i>ELife</i> , 2021, 10, .	2.8	52
1615	Single-cell atlas of developing murine adrenal gland reveals relation of Schwann cell precursor signature to neuroblastoma phenotype. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	47
1617	Sparsely-connected autoencoder (SCA) for single cell RNAseq data mining. <i>Npj Systems Biology and Applications</i> , 2021, 7, 1.	1.4	53
1618	Optimal Transport With Relaxed Marginal Constraints. <i>IEEE Access</i> , 2021, 9, 58142-58160.	2.6	1
1622	Loss of Adam10 Disrupts Ion Transport in Immortalized Kidney Collecting Duct Cells. <i>Function</i> , 2021, 2, zqab024.	1.1	1
1625	HieRFIT: a hierarchical cell type classification tool for projections from complex single-cell atlas datasets. <i>Bioinformatics</i> , 2021, 37, 4431-4436.	1.8	2
1627	Cellular Tropism of SARS-CoV-2 across Human Tissues and Age-related Expression of ACE2 and TMPRSS2 in Immune-inflammatory Stromal Cells. , 2021, 12, 718.		7
1628	SCA-1 micro-heterogeneity in the fate decision of dystrophic fibro/adipogenic progenitors. <i>Cell Death and Disease</i> , 2021, 12, 122.	2.7	21
1629	Haematopoietic ageing through the lens of single-cell technologies. <i>DMM Disease Models and Mechanisms</i> , 2021, 14, .	1.2	6
1630	Bioinformatics Tools for Gene and Genome Annotation Analysis of Microbes for Synthetic Biology and Cancer Biology Applications. , 2021, , 317-332.		0

#	ARTICLE	IF	CITATIONS
1631	An integrative microenvironment approach for laryngeal carcinoma: the role of immune/methylation/autophagy signatures on disease clinical prognosis and single-cell genotypes. <i>Journal of Cancer</i> , 2021, 12, 4148-4171.	1.2	19
1632	A Novel Method for Constructing EEG Large-Scale Cortical Dynamical Functional Network Connectivity (dFNC): WTCS. <i>IEEE Transactions on Cybernetics</i> , 2022, 52, 12869-12881.	6.2	20
1633	Bcl9 Depletion Modulates Endothelial Cell in Tumor Immune Microenvironment in Colorectal Cancer Tumor. <i>Frontiers in Oncology</i> , 2020, 10, 603702.	1.3	3
1634	Phagocyte-mediated synapse removal in cortical neuroinflammation is promoted by local calcium accumulation. <i>Nature Neuroscience</i> , 2021, 24, 355-367.	7.1	49
1635	Congenital heart disease risk loci identified by genome-wide association study in European patients. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	47
1636	Single-cell Immune Landscape of Human Recurrent Miscarriage. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 208-222.	3.0	66
1637	A spatially resolved brain region- and cell type-specific isoform atlas of the postnatal mouse brain. <i>Nature Communications</i> , 2021, 12, 463.	5.8	109
1638	Dissecting human embryonic skeletal stem cell ontogeny by single-cell transcriptomic and functional analyses. <i>Cell Research</i> , 2021, 31, 742-757.	5.7	49
1639	Single cell transcriptomic analysis of human pluripotent stem cell chondrogenesis. <i>Nature Communications</i> , 2021, 12, 362.	5.8	98
1641	Chromatin regulatory dynamics of early human small intestinal development using a directed differentiation model. <i>Nucleic Acids Research</i> , 2021, 49, 726-744.	6.5	14
1642	Tissue-resident CD4 ⁺ T helper cells assist the development of protective respiratory B and CD8 ⁺ T cell memory responses. <i>Science Immunology</i> , 2021, 6, .	5.6	116
1643	Mapping the immune environment in clear cell renal carcinoma by single-cell genomics. <i>Communications Biology</i> , 2021, 4, 122.	2.0	139
1644	Protective Immune Trajectories in Early Viral Containment of Non-Pneumonic SARS-CoV-2 Infection. <i>SSRN Electronic Journal</i> , 0, , .	0.4	3
1645	Gene Expression Analysis of T-Cells by Single-Cell RNA-Seq. <i>Methods in Molecular Biology</i> , 2021, 2285, 277-296.	0.4	1
1646	Single-Cell RNA Sequencing Analysis: A Step-by-Step Overview. <i>Methods in Molecular Biology</i> , 2021, 2284, 343-365.	0.4	65
1647	Tool recommender system in Galaxy using deep learning. <i>GigaScience</i> , 2021, 10, .	3.3	9
1648	Glycolytic metabolism of pathogenic T cells enables early detection of GVHD by 13C-MRI. <i>Blood</i> , 2021, 137, 126-137.	0.6	29
1649	Single-cell profiling of the human decidual immune microenvironment in patients with recurrent pregnancy loss. <i>Cell Discovery</i> , 2021, 7, 1.	3.1	152

#	ARTICLE	IF	CITATIONS
1650	An Integrated Transcriptome Analysis Reveals IGFBP7 Upregulation in Vasculature in Traumatic Brain Injury. <i>Frontiers in Genetics</i> , 2020, 11, 599834.	1.1	4
1651	Transcriptional profiling of pediatric cholestatic livers identifies three distinct macrophage populations. <i>PLoS ONE</i> , 2021, 16, e0244743.	1.1	20
1653	scSorter: assigning cells to known cell types according to marker genes. <i>Genome Biology</i> , 2021, 22, 69.	3.8	57
1657	Single Cell RNA-Seq and Machine Learning Reveal Novel Subpopulations in Low-Grade Inflammatory Monocytes With Unique Regulatory Circuits. <i>Frontiers in Immunology</i> , 2021, 12, 627036.	2.2	12
1659	Using Galaxy to Perform Large-Scale Interactive Data Analyses—An Update. <i>Current Protocols</i> , 2021, 1, e31.	1.3	4
1661	Th17 T cells play a vital role in fetal human skin development and immunity. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	17
1662	Cross-Comparison of Human iPSC Motor Neuron Models of Familial and Sporadic ALS Reveals Early and Convergent Transcriptomic Disease Signatures. <i>Cell Systems</i> , 2021, 12, 159-175.e9.	2.9	33
1664	Plant virus evolution under strong drought conditions results in a transition from parasitism to mutualism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	58
1665	Diversified transcriptional responses of myeloid and glial cells in spinal cord injury shaped by HDAC3 activity. <i>Science Advances</i> , 2021, 7, .	4.7	35
1666	Single-cell profiling identifies pre-existing CD19-negative subclones in a B-ALL patient with CD19-negative relapse after CAR-T therapy. <i>Nature Communications</i> , 2021, 12, 865.	5.8	81
1667	Natural genetic variation determines microglia heterogeneity in wild-derived mouse models of Alzheimer's disease. <i>Cell Reports</i> , 2021, 34, 108739.	2.9	49
1668	Reactivation of the pluripotency program precedes formation of the cranial neural crest. <i>Science</i> , 2021, 371, .	6.0	84
1669	Leveraging systems biology for predicting modulators of inflammation in patients with COVID-19. <i>Science Advances</i> , 2021, 7, .	4.7	18
1670	An atlas of neural crest lineages along the posterior developing zebrafish at single-cell resolution. <i>ELife</i> , 2021, 10, .	2.8	43
1671	Macrophages provide a transient muscle stem cell niche via NAMPT secretion. <i>Nature</i> , 2021, 591, 281-287.	13.7	111
1672	Single-cell RNA sequencing reveals functional heterogeneity of glioma-associated brain macrophages. <i>Nature Communications</i> , 2021, 12, 1151.	5.8	187
1673	Cholangiocyte organoids can repair bile ducts after transplantation in the human liver. <i>Science</i> , 2021, 371, 839-846.	6.0	170
1674	Molecular Signatures of Inflammatory Profile and B-Cell Function in Patients with Severe Fever with Thrombocytopenia Syndrome. <i>MBio</i> , 2021, 12, .	1.8	25

#	ARTICLE	IF	CITATIONS
1675	Single Cell Omics for Musculoskeletal Research. <i>Current Osteoporosis Reports</i> , 2021, 19, 131-140.	1.5	10
1676	IRIS-FGM: an integrative single-cell RNA-Seq interpretation system for functional gene module analysis. <i>Bioinformatics</i> , 2021, 37, 3045-3047.	1.8	3
1679	Independent component analysis based gene co-expression network inference (ICAnet) to decipher functional modules for better single-cell clustering and batch integration. <i>Nucleic Acids Research</i> , 2021, 49, e54-e54.	6.5	20
1680	redPATH: Reconstructing the Pseudo Development Time of Cell Lineages in Single-cell RNA-seq Data and Applications in Cancer. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 292-305.	3.0	2
1683	A single-cell atlas of mouse olfactory bulb chromatin accessibility. <i>Journal of Genetics and Genomics</i> , 2021, 48, 147-162.	1.7	3
1684	Single-cell immune repertoire and transcriptome sequencing reveals that clonally expanded and transcriptionally distinct lymphocytes populate the aged central nervous system in mice. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20202793.	1.2	14
1685	EKLF/KLF1 expression defines a unique macrophage subset during mouse erythropoiesis. <i>ELife</i> , 2021, 10, .	2.8	21
1686	Distinct subtypes of proprioceptive dorsal root ganglion neurons regulate adaptive proprioception in mice. <i>Nature Communications</i> , 2021, 12, 1026.	5.8	54
1687	A Progressive Somatic Cell Niche Regulates Germline Cyst Differentiation in the Drosophila Ovary. <i>Current Biology</i> , 2021, 31, 840-852.e5.	1.8	27
1688	Profiling Chromatin Accessibility at Single-cell Resolution. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 172-190.	3.0	18
1691	Sex-Stratified Gene Regulatory Networks Reveal Female Key Driver Genes of Atherosclerosis Involved in Smooth Muscle Cell Phenotype Switching. <i>Circulation</i> , 2021, 143, 713-726.	1.6	61
1692	Adult trkB Signaling in Parvalbumin Interneurons is Essential to Prefrontal Network Dynamics. <i>Journal of Neuroscience</i> , 2021, 41, 3120-3141.	1.7	16
1693	Dynamic sex chromosome expression in Drosophila male germ cells. <i>Nature Communications</i> , 2021, 12, 892.	5.8	53
1694	Single-Cell Analysis of Blood-Brain Barrier Response to Pericyte Loss. <i>Circulation Research</i> , 2021, 128, e46-e62.	2.0	98
1695	Homozygous BCMA gene deletion in response to anti-BCMA CAR T cells in a patient with multiple myeloma. <i>Nature Medicine</i> , 2021, 27, 616-619.	15.2	140
1698	Antigen Nonspecific Induction of Distinct Regulatory T Cell States in Oncogene-Driven Hyperproliferative Skin. <i>ImmunoHorizons</i> , 2021, 5, 102-116.	0.8	3
1699	Single-Cell Transcriptomic Reveals Dual and Multi-Transmitter Use in Neurons Across Metazoans. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 623148.	1.4	16
1702	Targeting PIM1-Mediated Metabolism in Myeloid Suppressor Cells to Treat Cancer. <i>Cancer Immunology Research</i> , 2021, 9, 454-469.	1.6	23

#	ARTICLE	IF	CITATIONS
1704	Single-cell RNA sequencing reveals developmental heterogeneity among Plasmodium berghei sporozoites. Scientific Reports, 2021, 11, 4127.	1.6	21
1710	Non-coding deletions identify Maenli lncRNA as a limb-specific En1 regulator. Nature, 2021, 592, 93-98.	13.7	53
1711	Variability within rare cell states enables multiple paths toward drug resistance. Nature Biotechnology, 2021, 39, 865-876.	9.4	94
1712	Increased <i>APOE</i> ϵ 4 expression is associated with the difference in Alzheimer's disease risk from diverse ancestral backgrounds. Alzheimer's and Dementia, 2021, 17, 1179-1188.	0.4	33
1713	Tumor to normal single-cell mRNA comparisons reveal a pan-neuroblastoma cancer cell. Science Advances, 2021, 7, .	4.7	78
1714	FK506-Binding Protein 13 Expression Is Upregulated in Interstitial Lung Disease and Correlated with Clinical Severity. A Potentially Protective Role. American Journal of Respiratory Cell and Molecular Biology, 2021, 64, 235-246.	1.4	10
1715	DeePaN: deep patient graph convolutional network integrating clinico-genomic evidence to stratify lung cancers for immunotherapy. Npj Digital Medicine, 2021, 4, 14.	5.7	23
1716	Single-cell analysis of human B cell maturation predicts how antibody class switching shapes selection dynamics. Science Immunology, 2021, 6, .	5.6	149
1718	SSRE: Cell Type Detection Based on Sparse Subspace Representation and Similarity Enhancement. Genomics, Proteomics and Bioinformatics, 2021, 19, 282-291.	3.0	21
1719	Time-Resolved scRNA-Seq Tracks the Adaptation of a Sensitive MCL Cell Line to Ibrutinib Treatment. International Journal of Molecular Sciences, 2021, 22, 2276.	1.8	4
1720	Single-Cell Transcriptomics Reveals a Heterogeneous Cellular Response to BK Virus Infection. Journal of Virology, 2021, 95, .	1.5	11
1722	Characteristics of B lymphocyte infiltration in HPV ⁺ head and neck squamous cell carcinoma. Cancer Science, 2021, 112, 1402-1416.	1.7	22
1725	Potential applications of deep learning in single-cell RNA sequencing analysis for cell therapy and regenerative medicine. Stem Cells, 2021, 39, 511-521.	1.4	16
1726	Novel risk factors for craniofacial microsomia and assessment of their utility in clinic diagnosis. Human Molecular Genetics, 2021, 30, 1045-1056.	1.4	3
1727	Progastrin production transitions from Bmi1 ⁺ /Prox1 ⁺ to Lgr5 ^{high} cells during early intestinal tumorigenesis. Translational Oncology, 2021, 14, 101001.	1.7	1
1728	Radiation Impacts Early Atherosclerosis by Suppressing Intimal LDL Accumulation. Circulation Research, 2021, 128, 530-543.	2.0	12
1729	Maternal schistosomiasis impairs offspring Interleukin-4 production and B cell expansion. PLoS Pathogens, 2021, 17, e1009260.	2.1	6
1731	Non-CG methylation and multiple histone profiles associate child abuse with immune and small GTPase dysregulation. Nature Communications, 2021, 12, 1132.	5.8	24

#	ARTICLE	IF	CITATIONS
1732	Molecular Features of Cancer-associated Fibroblast Subtypes and their Implication on Cancer Pathogenesis, Prognosis, and Immunotherapy Resistance. <i>Clinical Cancer Research</i> , 2021, 27, 2636-2647.	3.2	140
1734	Space: the final frontier – achieving single-cell, spatially resolved transcriptomics in plants. <i>Emerging Topics in Life Sciences</i> , 2021, 5, 179-188.	1.1	13
1735	Human marginal zone B cell development from early T2 progenitors. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	49
1737	Oxidized phosphatidylcholines found in multiple sclerosis lesions mediate neurodegeneration and are neutralized by microglia. <i>Nature Neuroscience</i> , 2021, 24, 489-503.	7.1	85
1738	Atypical B cells are part of an alternative lineage of B cells that participates in responses to vaccination and infection in humans. <i>Cell Reports</i> , 2021, 34, 108684.	2.9	134
1739	Affinity-coupled CCL22 promotes positive selection in germinal centres. <i>Nature</i> , 2021, 592, 133-137.	13.7	38
1740	Nitric oxide prevents aortic valve calcification by S-nitrosylation of USP9X to activate NOTCH signaling. <i>Science Advances</i> , 2021, 7, .	4.7	43
1741	Lipid signalling enforces functional specialization of Treg cells in tumours. <i>Nature</i> , 2021, 591, 306-311.	13.7	187
1742	Single-cell mapping of focused ultrasound-transfected brain. <i>Gene Therapy</i> , 2023, 30, 255-263.	2.3	14
1743	Development and Multi-Data Set Verification of an RNA Binding Protein Signature for Prognosis Prediction in Glioma. <i>Frontiers in Medicine</i> , 2021, 8, 637803.	1.2	2
1751	Assembly and Exploration of a Single Cell Atlas of the Drosophila Larval Ventral Cord. Identification of Rare Cell Types. <i>Current Protocols</i> , 2021, 1, e37.	1.3	13
1752	Enabling single-cell trajectory network enrichment. <i>Nature Computational Science</i> , 2021, 1, 153-163.	3.8	5
1753	Assigning immunoglobulin class from single-cell transcriptomes in IgA1-secreting versus membrane subpopulations. <i>BioTechniques</i> , 2021, 70, 89-99.	0.8	1
1754	Single-cell RNA sequencing reveals species-specific time spans of cell cycle transitions in early oogenesis. <i>Human Molecular Genetics</i> , 2021, 30, 525-535.	1.4	1
1755	Sinoatrial node pacemaker cells share dominant biological properties with glutamatergic neurons. <i>Protein and Cell</i> , 2021, 12, 545-556.	4.8	12
1756	Linear-time cluster ensembles of large-scale single-cell RNA-seq and multimodal data. <i>Genome Research</i> , 2021, 31, 677-688.	2.4	13
1757	Single-cell transcriptomic profiling and characterization of endothelial progenitor cells: new approach for finding novel markers. <i>Stem Cell Research and Therapy</i> , 2021, 12, 145.	2.4	17
1758	Innate immune evasion revealed in a colorectal zebrafish xenograft model. <i>Nature Communications</i> , 2021, 12, 1156.	5.8	41

#	ARTICLE	IF	CITATIONS
1759	Single-cell RNA sequencing identifies macrophage transcriptional heterogeneities in granulomatous diseases. <i>European Respiratory Journal</i> , 2021, 57, 2003794.	3.1	13
1760	eHSCPr discriminating the cell identity involved in endothelial to hematopoietic transition. <i>Bioinformatics</i> , 2021, 37, 2157-2164.	1.8	19
1761	Pitfalls of Applying Mouse Markers to Human Adrenal Medullary Cells. <i>Cancer Cell</i> , 2021, 39, 132-133.	7.7	12
1762	Hippocampal neurons respond to brain activity with functional hypoxia. <i>Molecular Psychiatry</i> , 2021, 26, 1790-1807.	4.1	28
1763	Biomarkers of inflammation and repair in kidney disease progression. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	95
1764	Spatiotemporal analysis of human intestinal development at single-cell resolution. <i>Cell</i> , 2021, 184, 810-826.e23.	13.5	263
1765	Activity-dependent regulome of human GABAergic neurons reveals new patterns of gene regulation and neurological disease heritability. <i>Nature Neuroscience</i> , 2021, 24, 437-448.	7.1	33
1766	Midkine is neuroprotective and influences glial reactivity and the formation of Müller glia-derived progenitor cells in chick and mouse retinas. <i>Glia</i> , 2021, 69, 1515-1539.	2.5	23
1767	Single-cell RNA sequencing reveals the induction of novel myeloid and myeloid-associated cell populations in visceral fat with long-term obesity. <i>FASEB Journal</i> , 2021, 35, e21417.	0.2	23
1768	Vasculature-driven stem cell population coordinates tissue scaling in dynamic organs. <i>Science Advances</i> , 2021, 7, .	4.7	11
1769	Guide Cells Support Muscle Regeneration and Affect Neuro-Muscular Junction Organization. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1939.	1.8	13
1770	Sialic acids in pancreatic cancer cells drive tumour-associated macrophage differentiation via the Siglec receptors Siglec-7 and Siglec-9. <i>Nature Communications</i> , 2021, 12, 1270.	5.8	111
1771	Lymphoma Heterogeneity Unraveled by Single-Cell Transcriptomics. <i>Frontiers in Immunology</i> , 2021, 12, 597651.	2.2	9
1774	Identifying Differentially Expressed Genes of Zero Inflated Single Cell RNA Sequencing Data Using Mixed Model Score Tests. <i>Frontiers in Genetics</i> , 2021, 12, 616686.	1.1	3
1778	Tissue-resident macrophages regulate lymphatic vessel growth and patterning in the developing heart. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	55
1779	Spontaneously Resolved Atopic Dermatitis Shows Melanocyte and Immune Cell Activation Distinct From Healthy Control Skin. <i>Frontiers in Immunology</i> , 2021, 12, 630892.	2.2	21
1780	Urinary Single-Cell Profiling Captures the Cellular Diversity of the Kidney. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 614-627.	3.0	64
1781	Tmem100- and Acta2-Lineage Cells Contribute to Implant Osseointegration in a Mouse Model. <i>Journal of Bone and Mineral Research</i> , 2020, 36, 1000-1011.	3.1	5

#	ARTICLE	IF	CITATIONS
1783	Selecting single cell clustering parameter values using subsampling-based robustness metrics. BMC Bioinformatics, 2021, 22, 39.	1.2	45
1784	Functional characterization of the dural sinuses as a neuroimmune interface. Cell, 2021, 184, 1000-1016.e27.	13.5	299
1786	Leukemia vaccine overcomes limitations of checkpoint blockade by evoking clonal T cell responses in a murine acute myeloid leukemia model. Haematologica, 2021, 106, 1330-1342.	1.7	19
1787	A multi-center cross-platform single-cell RNA sequencing reference dataset. Scientific Data, 2021, 8, 39.	2.4	14
1788	The transcriptional landscape of Venezuelan equine encephalitis virus (TC-83) infection. PLoS Neglected Tropical Diseases, 2021, 15, e0009306.	1.3	5
1790	Taking Data Science to Heart: Next Scale of Gene Regulation. Current Cardiology Reports, 2021, 23, 46.	1.3	2
1791	Lung gene expression and single cell analyses reveal two subsets of idiopathic pulmonary fibrosis (IPF) patients associated with different pathogenic mechanisms. PLoS ONE, 2021, 16, e0248889.	1.1	10
1792	Knowledge-based classification of fine-grained immune cell types in single-cell RNA-Seq data. Briefings in Bioinformatics, 2021, 22, .	3.2	11
1793	Brain proteomic changes by histone deacetylase inhibition after traumatic brain injury. Trauma Surgery and Acute Care Open, 2021, 6, e000682.	0.8	2
1794	simATAC: a single-cell ATAC-seq simulation framework. Genome Biology, 2021, 22, 74.	3.8	14
1797	Altered Monocyte Subsets in Kawasaki Disease Revealed by Single-cell RNA-Sequencing. Journal of Inflammation Research, 2021, Volume 14, 885-896.	1.6	21
1798	Prognostic Implication of the Expression Level of PECAM-1 in Non-small Cell Lung Cancer. Frontiers in Oncology, 2021, 11, 587744.	1.3	3
1799	CRISPR/Cas9-mediated gene editing in R66.1 Rag1 ^{fl/fl} Minipigs as a Model to Evaluate Longevity, Functionality, and Memory of Immune Response Induced by Pertussis Vaccines. Frontiers in Immunology, 2021, 12, 613810.	2.2	4
1800	Multiplexed Analysis of Retinal Gene Expression and Chromatin Accessibility Using scRNA-Seq and scATAC-Seq. Journal of Visualized Experiments, 2021, , .	0.2	2
1802	Inhibition of macrophage histone demethylase JMJD3 protects against abdominal aortic aneurysms. Journal of Experimental Medicine, 2021, 218, .	4.2	63
1803	Single-cell transcriptomic analyses provide insights into the developmental origins of neuroblastoma. Nature Genetics, 2021, 53, 683-693.	9.4	128
1804	Identifying CNS-colonizing T cells as potential therapeutic targets to prevent progression of multiple sclerosis. Med, 2021, 2, 296-312.e8.	2.2	43
1806	Robust integration of multiple single-cell RNA sequencing datasets using a single reference space. Nature Biotechnology, 2021, 39, 877-884.	9.4	26

#	ARTICLE	IF	CITATIONS
1807	Tracing production instability in a clonally derived CHO cell line using single-cell transcriptomics. <i>Biotechnology and Bioengineering</i> , 2021, 118, 2016-2030.	1.7	11
1808	Pluripotent stem cell-derived models of neurological diseases reveal early transcriptional heterogeneity. <i>Genome Biology</i> , 2021, 22, 73.	3.8	6
1810	CARM1 Inhibition Enables Immunotherapy of Resistant Tumors by Dual Action on Tumor Cells and T Cells. <i>Cancer Discovery</i> , 2021, 11, 2050-2071.	7.7	43
1812	Obesity-Dependent Adipokine Chemerin Suppresses Fatty Acid Oxidation to Confer Ferroptosis Resistance. <i>Cancer Discovery</i> , 2021, 11, 2072-2093.	7.7	43
1813	Hyperbolic geometry of gene expression. <i>IScience</i> , 2021, 24, 102225.	1.9	15
1814	Single cell transcriptomic analysis of murine lung development on hyperoxia-induced damage. <i>Nature Communications</i> , 2021, 12, 1565.	5.8	89
1816	Resident and circulating memory T cells persist for years in melanoma patients with durable responses to immunotherapy. <i>Nature Cancer</i> , 2021, 2, 300-311.	5.7	70
1817	Single-Cell Transcriptomics and In Situ Morphological Analyses Reveal Microglia Heterogeneity Across the Nigrostriatal Pathway. <i>Frontiers in Immunology</i> , 2021, 12, 639613.	2.2	30
1818	Single-Cell Transcriptomics Reveals Compartment-Specific Differences in Immune Responses and Contributions for Complement Factor 3 in Hemorrhagic Shock Plus Tissue Trauma. <i>Shock</i> , 2021, 56, 994-1008.	1.0	2
1819	Single-Cell Transcriptomic Analyses Define Distinct Peripheral B Cell Subsets and Discrete Development Pathways. <i>Frontiers in Immunology</i> , 2021, 12, 602539.	2.2	83
1820	Targeting a Braf/Mapk pathway rescues podocyte lipid peroxidation in CoQ-deficiency kidney disease. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	25
1821	MAP3K2-regulated intestinal stromal cells define a distinct stem cell niche. <i>Nature</i> , 2021, 592, 606-610.	13.7	53
1822	CytoTree: an R/Bioconductor package for analysis and visualization of flow and mass cytometry data. <i>BMC Bioinformatics</i> , 2021, 22, 138.	1.2	18
1823	Exponential-Family Embedding With Application to Cell Developmental Trajectories for Single-Cell RNA-Seq Data. <i>Journal of the American Statistical Association</i> , 2021, 116, 457-470.	1.8	7
1827	Detection of gene cis-regulatory element perturbations in single-cell transcriptomes. <i>PLoS Computational Biology</i> , 2021, 17, e1008789.	1.5	0
1830	Functional annotation of lung cancer-associated genetic variants by cell type-specific epigenome and long-range chromatin interactome. <i>Genomics and Informatics</i> , 2021, 19, e3.	0.4	0
1831	A single-cell survey of the human glomerulonephritis. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 4684-4695.	1.6	25
1833	An Integrative Single-cell Transcriptomic Atlas of the Post-natal Mouse Mammary Gland Allows Discovery of New Developmental Trajectories in the Luminal Compartment. <i>Journal of Mammary Gland Biology and Neoplasia</i> , 2021, 26, 29-42.	1.0	7

#	ARTICLE	IF	CITATIONS
1834	Targeted Therapy Given after Anti-PD-1 Leads to Prolonged Responses in Mouse Melanoma Models through Sustained Antitumor Immunity. <i>Cancer Immunology Research</i> , 2021, 9, 554-567.	1.6	15
1835	The AIM2 inflammasome exacerbates atherosclerosis in clonal haematopoiesis. <i>Nature</i> , 2021, 592, 296-301.	13.7	236
1836	Single-Cell RNA Sequencing Procedures and Data Analysis. , 0, , 19-35.		10
1837	Modeling expression ranks for noise-tolerant differential expression analysis of scRNA-seq data. <i>Genome Research</i> , 2021, 31, 689-697.	2.4	6
1838	Connecting the Dots: Resolving the Bone Marrow Niche Heterogeneity. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 622519.	1.8	51
1839	Ndufs1 Deficiency Aggravates the Mitochondrial Membrane Potential Dysfunction in Pressure Overload-Induced Myocardial Hypertrophy. <i>Oxidative Medicine and Cellular Longevity</i> , 2021, 2021, 1-21.	1.9	18
1840	Patients With Short PFS to EGFR-TKIs Predicted Better Response to Subsequent Anti-PD-1/PD-L1 Based Immunotherapy in EGFR Common Mutation NSCLC. <i>Frontiers in Oncology</i> , 2021, 11, 639947.	1.3	24
1841	Single-cell transcriptomic analysis of eutopic endometrium and ectopic lesions of adenomyosis. <i>Cell and Bioscience</i> , 2021, 11, 51.	2.1	25
1842	Single-cell transcriptomic analysis of somatosensory neurons uncovers temporal development of neuropathic pain. <i>Cell Research</i> , 2021, 31, 904-918.	5.7	79
1844	Prosaposin mediates inflammation in atherosclerosis. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	42
1845	Progenitor cell diversity in the developing mouse neocortex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	33
1846	Mitochondrial metabolism is essential for invariant natural killer T cell development and function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	20
1847	Multiple sclerosis risk gene <i>Mertk</i> is required for microglial activation and subsequent remyelination. <i>Cell Reports</i> , 2021, 34, 108835.	2.9	61
1848	Abnormal upregulation of cardiovascular disease biomarker PLA2G7 induced by proinflammatory macrophages in COVID-19 patients. <i>Scientific Reports</i> , 2021, 11, 6811.	1.6	19
1849	Differences in Tumor Immune Microenvironment in Metastatic Sites of Breast Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 649004.	1.3	19
1850	Spatiotemporal single-cell RNA sequencing of developing chicken hearts identifies interplay between cellular differentiation and morphogenesis. <i>Nature Communications</i> , 2021, 12, 1771.	5.8	109
1852	DEEPsc: A Deep Learning-Based Map Connecting Single-Cell Transcriptomics and Spatial Imaging Data. <i>Frontiers in Genetics</i> , 2021, 12, 636743.	1.1	22
1853	Leveraging Single-Cell RNA-seq Data to Uncover the Association Between Cell Type and Chronic Liver Diseases. <i>Frontiers in Genetics</i> , 2021, 12, 637322.	1.1	4

#	ARTICLE	IF	CITATIONS
1857	Localized EMT reprograms glial progenitors to promote spinal cord repair. <i>Developmental Cell</i> , 2021, 56, 613-626.e7.	3.1	40
1861	Dual role of endothelial <i>Myct1</i> in tumor angiogenesis and tumor immunity. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	35
1862	Epithelial response to IFN γ promotes SARS-CoV-2 infection. <i>EMBO Molecular Medicine</i> , 2021, 13, e13191.	3.3	62
1863	Transcriptional mediators of treatment resistance in lethal prostate cancer. <i>Nature Medicine</i> , 2021, 27, 426-433.	15.2	90
1866	SARS-CoV-2 in severe COVID-19 induces a TGF β -dominated chronic immune response that does not target itself. <i>Nature Communications</i> , 2021, 12, 1961.	5.8	145
1867	ShinyCell: simple and sharable visualization of single-cell gene expression data. <i>Bioinformatics</i> , 2021, 37, 3374-3376.	1.8	83
1869	Transcriptional Profiling Reveals Kidney Neutrophil Heterogeneity in Both Healthy People and ccRCC Patients. <i>Journal of Immunology Research</i> , 2021, 2021, 1-17.	0.9	13
1870	Super-Enhancer-Associated Transcription Factors Maintain Transcriptional Regulation in Mature Podocytes. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 1323-1337.	3.0	4
1871	Intrinsic Immunogenicity of Small Cell Lung Carcinoma Revealed by Its Cellular Plasticity. <i>Cancer Discovery</i> , 2021, 11, 1952-1969.	7.7	87
1872	Single-cell transcriptomics dissects hematopoietic cell destruction and T-cell engagement in aplastic anemia. <i>Blood</i> , 2021, 138, 23-33.	0.6	33
1873	A RIPK1-regulated inflammatory microglial state in amyotrophic lateral sclerosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	36
1874	scGNN is a novel graph neural network framework for single-cell RNA-Seq analyses. <i>Nature Communications</i> , 2021, 12, 1882.	5.8	139
1875	A single-cell resolution developmental atlas of hematopoietic stem and progenitor cell expansion in zebrafish. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	34
1876	Epithelial miR-141 regulates IL-13-induced airway mucus production. <i>JCI Insight</i> , 2021, 6, .	2.3	29
1877	Integration and transfer learning of single-cell transcriptomes via cFIT. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	19
1878	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
1879	Noise regularization removes correlation artifacts in single-cell RNA-seq data preprocessing. <i>Patterns</i> , 2021, 2, 100211.	3.1	9
1880	In vivo CRISPR screening reveals nutrient signaling processes underpinning CD8+ T cell fate decisions. <i>Cell</i> , 2021, 184, 1245-1261.e21.	13.5	68

#	ARTICLE	IF	CITATIONS
1881	Auto-aggressive CXCR6+ CD8 T cells cause liver immune pathology in NASH. <i>Nature</i> , 2021, 592, 444-449.	13.7	233
1882	Single Cell Analysis of Blood Mononuclear Cells Stimulated Through Either LPS or Anti-CD3 and Anti-CD28. <i>Frontiers in Immunology</i> , 2021, 12, 636720.	2.2	32
1883	Oncolytic virotherapy-mediated anti-tumor response: a single-cell perspective. <i>Cancer Cell</i> , 2021, 39, 394-406.e4.	7.7	63
1884	Nutrient restriction synergizes with retinoic acid to induce mammalian meiotic initiation in vitro. <i>Nature Communications</i> , 2021, 12, 1758.	5.8	17
1886	A Novel Method to Identify the Differences Between Two Single Cell Groups at Single Gene, Gene Pair, and Gene Module Levels. <i>Frontiers in Genetics</i> , 2021, 12, 648898.	1.1	2
1887	Penalized Latent Dirichlet Allocation Model in Single-Cell RNA Sequencing. <i>Statistics in Biosciences</i> , 2021, 13, 543-562.	0.6	5
1890	Macrophages in SHH subgroup medulloblastoma display dynamic heterogeneity that varies with treatment modality. <i>Cell Reports</i> , 2021, 34, 108917.	2.9	27
1892	Computational modeling of malignant ascites reveals CCL5-SDC4 interaction in the immune microenvironment of ovarian cancer. <i>Molecular Carcinogenesis</i> , 2021, 60, 297-312.	1.3	15
1894	NTRK Fusions Can Co-Occur With H3K27M Mutations and May Define Druggable Subclones Within Diffuse Midline Gliomas. <i>Journal of Neuropathology and Experimental Neurology</i> , 2021, 80, 345-353.	0.9	5
1895	Toward a Consensus in the Repertoire of Hemocytes Identified in <i>Drosophila</i> . <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 643712.	1.8	25
1896	Methods and tools for spatial mapping of single-cell RNAseq clusters in <i>Drosophila</i> . <i>Genetics</i> , 2021, 217, .	1.2	10
1898	Development of double-positive thymocytes at single-cell resolution. <i>Genome Medicine</i> , 2021, 13, 49.	3.6	17
1900	Circulating mucosal-associated invariant T cells identify patients responding to anti-PD-1 therapy. <i>Nature Communications</i> , 2021, 12, 1669.	5.8	48
1901	Î³Î´ T cells regulate the intestinal response to nutrient sensing. <i>Science</i> , 2021, 371, .	6.0	78
1902	Transcriptome Profiling of the Ovarian Cells at the Single-Cell Resolution in Adult Asian Seabass. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 647892.	1.8	7
1903	Resolving Human Lactation Heterogeneity Using Single Milk-Derived Cells, a Resource at the Ready. <i>Journal of Mammary Gland Biology and Neoplasia</i> , 2021, 26, 3-8.	1.0	3
1904	A modified vaccinia Ankara vector-based vaccine protects macaques from SARS-CoV-2 infection, immune pathology, and dysfunction in the lungs. <i>Immunity</i> , 2021, 54, 542-556.e9.	6.6	72
1905	Implication of TIGIT+ human memory B cells in immune regulation. <i>Nature Communications</i> , 2021, 12, 1534.	5.8	41

#	ARTICLE	IF	CITATIONS
1906	Skeletal muscle regeneration via the chemical induction and expansion of myogenic stem cells in situ or in vitro. <i>Nature Biomedical Engineering</i> , 2021, 5, 864-879.	11.6	23
1907	The CD33 short isoform is a gain-of-function variant that enhances AÎ²1â€™42 phagocytosis in microglia. <i>Molecular Neurodegeneration</i> , 2021, 16, 19.	4.4	46
1909	Cellular plasticity balances the metabolic and proliferation dynamics of a regenerating liver. <i>Genome Research</i> , 2021, 31, 576-591.	2.4	53
1910	Patterns of transcription factor programs and immune pathway activation define four major subtypes of SCLC with distinct therapeutic vulnerabilities. <i>Cancer Cell</i> , 2021, 39, 346-360.e7.	7.7	422
1912	Ex utero mouse embryogenesis from pre-gastrulation to late organogenesis. <i>Nature</i> , 2021, 593, 119-124.	13.7	124
1918	Unraveling Heterogeneity of Tumor Cells and Microenvironment and Its Clinical Implications for Triple Negative Breast Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 557477.	1.3	15
1920	Alignment of single-cell RNA-seq samples without overcorrection using kernel density matching. <i>Genome Research</i> , 2021, 31, 698-712.	2.4	4
1921	Mononuclear phagocytic system and fibrosis: back to the future?. <i>European Respiratory Journal</i> , 2021, 57, 2004466.	3.1	2
1922	Algorithmic advances in machine learning for single-cell expression analysis. <i>Current Opinion in Systems Biology</i> , 2021, 25, 27-33.	1.3	20
1923	Characterizing the molecular regulation of inhibitory immune checkpoints with multimodal single-cell screens. <i>Nature Genetics</i> , 2021, 53, 322-331.	9.4	96
1925	Appyters: Turning Jupyter Notebooks into data-driven web apps. <i>Patterns</i> , 2021, 2, 100213.	3.1	58
1926	A single-cell atlas of the healthy breast tissues reveals clinically relevant clusters of breast epithelial cells. <i>Cell Reports Medicine</i> , 2021, 2, 100219.	3.3	48
1927	Predicting recognition between T cell receptors and epitopes with TCRGP. <i>PLoS Computational Biology</i> , 2021, 17, e1008814.	1.5	67
1928	Estrogen receptor alpha in the brain mediates tamoxifen-induced changes in physiology in mice. <i>ELife</i> , 2021, 10, .	2.8	17
1929	Characterization of Gene Expression Signatures for the Identification of Cellular Heterogeneity in the Developing Mammary Gland. <i>Journal of Mammary Gland Biology and Neoplasia</i> , 2021, 26, 43-66.	1.0	14
1930	Enhanced expression of immune checkpoint receptors during SARS-CoV-2 viral infection. <i>Molecular Therapy - Methods and Clinical Development</i> , 2021, 20, 109-121.	1.8	41
1931	Defective metabolic programming impairs early neuronal morphogenesis in neural cultures and an organoid model of Leigh syndrome. <i>Nature Communications</i> , 2021, 12, 1929.	5.8	55
1932	ACE2 Shedding and Furin Abundance in Target Organs may Influence the Efficiency of SARS-CoV-2 Entry. <i>Open Bioinformatics Journal</i> , 2021, 14, 1-12.	1.0	3

#	ARTICLE	IF	CITATIONS
1933	Inhibitory CD161 receptor identified in glioma-infiltrating T cells by single-cell analysis. <i>Cell</i> , 2021, 184, 1281-1298.e26.	13.5	210
1934	Genomic, epigenomic, and biophysical cues controlling the emergence of the lung alveolus. <i>Science</i> , 2021, 371, .	6.0	108
1935	Single-nucleus RNA and ATAC sequencing reveals the impact of chromatin accessibility on gene expression in Arabidopsis roots at the single-cell level. <i>Molecular Plant</i> , 2021, 14, 372-383.	3.9	153
1936	Transcriptomic profiling of SARS-CoV-2 infected human cell lines identifies HSP90 as target for COVID-19 therapy. <i>Science</i> , 2021, 24, 102151.	1.9	202
1938	Functional States in Tumor-Initiating Cell Differentiation in Human Colorectal Cancer. <i>Cancers</i> , 2021, 13, 1097.	1.7	11
1943	From Bite to Byte: Dental Structures Resolved at a Single-Cell Resolution. <i>Journal of Dental Research</i> , 2021, 100, 002203452110018.	2.5	13
1945	WASP: a versatile, web-accessible single cell RNA-Seq processing platform. <i>BMC Genomics</i> , 2021, 22, 195.	1.2	6
1946	Dynamic Expression of Imprinted Genes in the Developing and Postnatal Pituitary Gland. <i>Genes</i> , 2021, 12, 509.	1.0	9
1952	Single-cell data clustering based on sparse optimization and low-rank matrix factorization. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	1
1954	A cross-talk between CAR T cell subsets and the tumor microenvironment is essential for sustained cytotoxic activity. <i>Science Immunology</i> , 2021, 6, .	5.6	105
1956	Hematopoietic Stem Cell Heterogeneity Is Linked to the Initiation and Therapeutic Response of Myeloproliferative Neoplasms. <i>Cell Stem Cell</i> , 2021, 28, 502-513.e6.	5.2	36
1958	Single-cell transcriptional changes associated with drug tolerance and response to combination therapies in cancer. <i>Nature Communications</i> , 2021, 12, 1628.	5.8	103
1959	Strategies to Identify Mesenchymal Stromal Cells in Minimally Manipulated Human Bone Marrow Aspirate Concentrate Lack Consensus. <i>American Journal of Sports Medicine</i> , 2021, 49, 1313-1322.	1.9	10
1960	A distinct microglial subset at the tumor-stroma interface of glioma. <i>Glia</i> , 2021, 69, 1767-1781.	2.5	18
1961	How to Get Started with Single Cell RNA Sequencing Data Analysis. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 1279-1292.	3.0	19
1962	Disparate temperature-dependent virus-host dynamics for SARS-CoV-2 and SARS-CoV in the human respiratory epithelium. <i>PLoS Biology</i> , 2021, 19, e3001158.	2.6	79
1963	Somatic mutations and single-cell transcriptomes reveal the root of malignant rhabdoid tumours. <i>Nature Communications</i> , 2021, 12, 1407.	5.8	41
1964	Hedgehog-induced PD-L1 on tumor-associated macrophages is critical for suppression of tumor-infiltrating CD8+ T cell function. <i>JCI Insight</i> , 2021, 6, .	2.3	47

#	ARTICLE	IF	CITATIONS
1965	Modelling human blastocysts by reprogramming fibroblasts into iBlastoids. <i>Nature</i> , 2021, 591, 627-632.	13.7	211
1966	A hitchhiker's guide to single-cell transcriptomics and data analysis pipelines. <i>Genomics</i> , 2021, 113, 606-619.	1.3	44
1967	Canonical and early lineage-specific stem cell types identified in planarian SirNeoblasts. <i>Cell Regeneration</i> , 2021, 10, 15.	1.1	9
1972	CMV Status Drives Distinct Trajectories of CD4+ T Cell Differentiation. <i>Frontiers in Immunology</i> , 2021, 12, 620386.	2.2	15
1978	Multimiomics integrative analysis identifies APOE allele-specific blood biomarkers associated to Alzheimer's disease etiopathogenesis. <i>Aging</i> , 2021, 13, 9277-9329.	1.4	15
1979	Single-cell RNA sequencing of mouse islets exposed to proinflammatory cytokines. <i>Life Science Alliance</i> , 2021, 4, e202000949.	1.3	16
1982	An NKX2-1/ERK/WNT feedback loop modulates gastric identity and response to targeted therapy in lung adenocarcinoma. <i>ELife</i> , 2021, 10, .	2.8	15
1983	The molecular landscape of neural differentiation in the developing <i>Drosophila</i> brain revealed by targeted scRNA-seq and multi-informatic analysis. <i>Cell Reports</i> , 2021, 35, 109039.	2.9	21
1984	System Genetics Including Causal Inference Identify Immune Targets for Coronary Artery Disease and the Lifespan. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003196.	1.6	7
1985	Single-cell chromatin accessibility landscape identifies tissue repair program in human regulatory T cells. <i>Immunity</i> , 2021, 54, 702-720.e17.	6.6	78
1986	Topography of transcriptionally active chromatin in glioblastoma. <i>Science Advances</i> , 2021, 7, .	4.7	19
1987	A flexible microfluidic system for single-cell transcriptome profiling elucidates phased transcriptional regulators of cell cycle. <i>Scientific Reports</i> , 2021, 11, 7918.	1.6	7
1988	Negative elongation factor regulates muscle progenitor expansion for efficient myofiber repair and stem cell pool repopulation. <i>Developmental Cell</i> , 2021, 56, 1014-1029.e7.	3.1	18
1989	MicroRNA-21-Dependent Macrophage-to-Fibroblast Signaling Determines the Cardiac Response to Pressure Overload. <i>Circulation</i> , 2021, 143, 1513-1525.	1.6	67
1990	Single-Cell Transcriptome Analysis of Human Adipose-Derived Stromal Cells Identifies a Contractile Cell Subpopulation. <i>Stem Cells International</i> , 2021, 2021, 1-12.	1.2	2
1991	Genetically engineered myeloid cells rebalance the core immune suppression program in metastasis. <i>Cell</i> , 2021, 184, 2033-2052.e21.	13.5	107
1992	IFN- γ and TNF- α drive a CXCL10+ CCL2+ macrophage phenotype expanded in severe COVID-19 lungs and inflammatory diseases with tissue inflammation. <i>Genome Medicine</i> , 2021, 13, 64.	3.6	128
1993	Leveraging Single-Cell Sequencing for Chimeric Antigen Receptor T Cell Therapies. <i>Trends in Biotechnology</i> , 2021, 39, 1308-1320.	4.9	18

#	ARTICLE	IF	CITATIONS
1994	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20.	7.7	327
1995	Integration, exploration, and analysis of high-dimensional single-cell cytometry data using Spectre. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2022, 101, 237-253.	1.1	78
1996	Single-cell characterization of a model of poly I:C-stimulated peripheral blood mononuclear cells in severe asthma. <i>Respiratory Research</i> , 2021, 22, 122.	1.4	8
2001	Fast identification of differential distributions in single-cell RNA-sequencing data with waddR. <i>Bioinformatics</i> , 2021, 37, 3204-3211.	1.8	14
2002	Vascular smooth muscle-derived Trpv1+ progenitors are a source of cold-induced thermogenic adipocytes. <i>Nature Metabolism</i> , 2021, 3, 485-495.	5.1	64
2005	TIM4 expression by dendritic cells mediates uptake of tumor-associated antigens and anti-tumor responses. <i>Nature Communications</i> , 2021, 12, 2237.	5.8	35
2007	Taming Cell-to-Cell Heterogeneity in Acute Myeloid Leukaemia With Machine Learning. <i>Frontiers in Oncology</i> , 2021, 11, 666829.	1.3	3
2011	Single-Cell Sequencing Methodologies: From Transcriptome to Multi-Dimensional Measurement. <i>Small Methods</i> , 2021, 5, e2100111.	4.6	17
2012	Single-cell transcriptomics reveals involution mimicry during the specification of the basal breast cancer subtype. <i>Cell Reports</i> , 2021, 35, 108945.	2.9	38
2013	CD8+ T cell self-tolerance permits responsiveness but limits tissue damage. <i>ELife</i> , 2021, 10, .	2.8	9
2014	Single-Cell Transcriptomics: Current Methods and Challenges in Data Acquisition and Analysis. <i>Frontiers in Neuroscience</i> , 2021, 15, 591122.	1.4	53
2015	Machine learning workflows identify a microRNA signature of insulin transcription in human tissues. <i>IScience</i> , 2021, 24, 102379.	1.9	17
2016	Testicular germ cell tumors arise in the absence of sex-specific differentiation. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	12
2017	High-content, targeted RNA-seq screening in organoids for drug discovery in colorectal cancer. <i>Cell Reports</i> , 2021, 35, 109026.	2.9	35
2018	Lymphohematopoietic graft-versus-host responses promote mixed chimerism in patients receiving intestinal transplantation. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	31
2019	STARTRAC analyses of scRNAseq data from tumor models reveal T cell dynamics and therapeutic targets. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	15
2022	The <i>alx3</i> gene shapes the zebrafish neurocranium by regulating frontonasal neural crest cell differentiation timing. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	19
2027	CASB: a concanavalin A-based sample barcoding strategy for single-cell sequencing. <i>Molecular Systems Biology</i> , 2021, 17, e10060.	3.2	14

#	ARTICLE	IF	CITATIONS
2028	Integrin $\alpha 2 \beta 5$ heterodimer is a specific marker of human pancreatic beta cells. <i>Scientific Reports</i> , 2021, 11, 8315.	1.6	4
2029	A computational method for direct imputation of cell type-specific expression profiles and cellular compositions from bulk-tissue RNA-Seq in brain disorders. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab056.	1.5	5
2030	A fetal wave of human type 3 effector $\gamma \delta$ cells with restricted TCR diversity persists into adulthood. <i>Science Immunology</i> , 2021, 6, .	5.6	52
2033	Identification of transcriptomic signatures and crucial pathways involved in non-alcoholic steatohepatitis. <i>Endocrine</i> , 2021, 73, 52-64.	1.1	17
2035	CytoTalk: De novo construction of signal transduction networks using single-cell transcriptomic data. <i>Science Advances</i> , 2021, 7, .	4.7	51
2036	Single-cell transcriptome sequencing on the Nanopore platform with ScNapBar. <i>Rna</i> , 2021, 27, 763-770.	1.6	12
2037	Platypus: an open-access software for integrating lymphocyte single-cell immune repertoires with transcriptomes. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab023.	1.5	27
2038	Single nucleus RNA-sequencing defines unexpected diversity of cholinergic neuron types in the adult mouse spinal cord. <i>Nature Communications</i> , 2021, 12, 2471.	5.8	71
2039	Meningeal lymphatics affect microglia responses and anti- $\text{A}\beta^2$ immunotherapy. <i>Nature</i> , 2021, 593, 255-260.	13.7	179
2041	Single-Cell TCR Sequencing Reveals the Dynamics of T Cell Repertoire Profiling During Pneumocystis Infection. <i>Frontiers in Microbiology</i> , 2021, 12, 637500.	1.5	8
2043	Kidney intercalated cells are phagocytic and acidify internalized uropathogenic Escherichia coli. <i>Nature Communications</i> , 2021, 12, 2405.	5.8	23
2044	TIPS: trajectory inference of pathway significance through pseudotime comparison for functional assessment of single-cell RNAseq data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	8
2045	Deep embedded clustering with multiple objectives on scRNA-seq data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	7
2046	MIR503HG Loss Promotes Endothelial-to-Mesenchymal Transition in Vascular Disease. <i>Circulation Research</i> , 2021, 128, 1173-1190.	2.0	41
2048	COVID-19 immune features revealed by a large-scale single-cell transcriptome atlas. <i>Cell</i> , 2021, 184, 1895-1913.e19.	13.5	512
2050	Donor cell memory confers a metastable state of directly converted cells. <i>Cell Stem Cell</i> , 2021, 28, 1291-1306.e10.	5.2	5
2052	Single-Cell Atlas Reveals Fatty Acid Metabolites Regulate the Functional Heterogeneity of Mesenchymal Stem Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 653308.	1.8	7
2055	Uncovering transcriptional dark matter via gene annotation independent single-cell RNA sequencing analysis. <i>Nature Communications</i> , 2021, 12, 2158.	5.8	9

#	ARTICLE	IF	CITATIONS
2056	MR1-Restricted MAIT Cells From The Human Lung Mucosal Surface Have Distinct Phenotypic, Functional, and Transcriptomic Features That Are Preserved in HIV Infection. <i>Frontiers in Immunology</i> , 2021, 12, 631410.	2.2	12
2059	Synthetic single cell RNA sequencing data from small pilot studies using deep generative models. <i>Scientific Reports</i> , 2021, 11, 9403.	1.6	5
2061	Decoding Cell Death: From a Veritable Library of Babel to <i>Vade Mecum</i> ?. <i>Annual Review of Immunology</i> , 2021, 39, 791-817.	9.5	7
2062	Single-Cell RNA Sequencing Reveals Tissue Compartment-Specific Plasticity of Mycosis Fungoides Tumor Cells. <i>Frontiers in Immunology</i> , 2021, 12, 666935.	2.2	27
2064	Single-Cell Multiomic Approaches Reveal Diverse Labeling of the Nervous System by Common Cre-Drivers. <i>Frontiers in Cellular Neuroscience</i> , 2021, 15, 648570.	1.8	5
2065	Atlas of breast cancer infiltrated B-lymphocytes revealed by paired single-cell RNA-sequencing and antigen receptor profiling. <i>Nature Communications</i> , 2021, 12, 2186.	5.8	86
2066	Single-cell brain atlas of Parkinson's disease mouse model. <i>Journal of Genetics and Genomics</i> , 2021, 48, 277-288.	1.7	20
2067	Deficiency of macrophage PHACTR1 impairs efferocytosis and promotes atherosclerotic plaque necrosis. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	31
2068	Iterative single-cell multi-omic integration using online learning. <i>Nature Biotechnology</i> , 2021, 39, 1000-1007.	9.4	53
2069	A non-canonical type 2 immune response coordinates tuberculous granuloma formation and epithelialization. <i>Cell</i> , 2021, 184, 1757-1774.e14.	13.5	63
2070	Single human oocyte transcriptome analysis reveals distinct maturation stage-dependent pathways impacted by age. <i>Aging Cell</i> , 2021, 20, e13360.	3.0	43
2073	Complement C5a promotes antigen cross-presentation by Peyer's patch monocyte-derived dendritic cells and drives a protective CD8+ T cell response. <i>Cell Reports</i> , 2021, 35, 108995.	2.9	13
2074	Decoding neuronal composition and ontogeny of individual hypothalamic nuclei. <i>Neuron</i> , 2021, 109, 1150-1167.e6.	3.8	18
2075	The melanocortin-3 receptor is a pharmacological target for the regulation of anorexia. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	31
2077	Independence of chromatin conformation and gene regulation during <i>Drosophila</i> dorsoventral patterning. <i>Nature Genetics</i> , 2021, 53, 487-499.	9.4	108
2078	Chimeric contribution of human extended pluripotent stem cells to monkey embryos <i>ex Vivo</i> . <i>Cell</i> , 2021, 184, 2020-2032.e14.	13.5	85
2079	Single-cell sequencing of human white adipose tissue identifies new cell states in health and obesity. <i>Nature Immunology</i> , 2021, 22, 639-653.	7.0	169
2080	Single-cell analysis of the developing human testis reveals somatic niche cell specification and fetal germline stem cell establishment. <i>Cell Stem Cell</i> , 2021, 28, 764-778.e4.	5.2	104

#	ARTICLE	IF	CITATIONS
2081	Comparative Transcriptomic Analysis of the Hematopoietic System between Human and Mouse by Single Cell RNA Sequencing. <i>Cells</i> , 2021, 10, 973.	1.8	6
2082	Transcriptional signatures in prefrontal cortex confer vulnerability versus resilience to food and cocaine addiction-like behavior. <i>Scientific Reports</i> , 2021, 11, 9076.	1.6	17
2083	CBA: Cluster-Guided Batch Alignment for Single Cell RNA-seq. <i>Frontiers in Genetics</i> , 2021, 12, 644211.	1.1	3
2084	Critical downstream analysis steps for single-cell RNA sequencing data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	33
2085	Immune cells lacking Y chromosome show dysregulation of autosomal gene expression. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 4019-4033.	2.4	54
2087	Cellular fate of intersex differentiation. <i>Cell Death and Disease</i> , 2021, 12, 388.	2.7	8
2088	scConsensus: combining supervised and unsupervised clustering for cell type identification in single-cell RNA sequencing data. <i>BMC Bioinformatics</i> , 2021, 22, 186.	1.2	14
2090	Implications of cardiac markers in risk-stratification and management for COVID-19 patients. <i>Critical Care</i> , 2021, 25, 158.	2.5	16
2091	Single-cell transcriptomics identifies limbal stem cell population and cell types mapping its differentiation trajectory in limbal basal epithelium of human cornea. <i>Ocular Surface</i> , 2021, 20, 20-32.	2.2	55
2092	Phase I Trial of N-803, an IL15 Receptor Agonist, with Rituximab in Patients with Indolent Non-Hodgkin Lymphoma. <i>Clinical Cancer Research</i> , 2021, 27, 3339-3350.	3.2	26
2093	Statistical mechanics meets single-cell biology. <i>Nature Reviews Genetics</i> , 2021, 22, 459-476.	7.7	65
2094	Single-cell resolution of lineage trajectories in the Arabidopsis stomatal lineage and developing leaf. <i>Developmental Cell</i> , 2021, 56, 1043-1055.e4.	3.1	125
2095	White matter aging drives microglial diversity. <i>Neuron</i> , 2021, 109, 1100-1117.e10.	3.8	208
2096	An intercrypt subpopulation of goblet cells is essential for colonic mucus barrier function. <i>Science</i> , 2021, 372, .	6.0	144
2097	Single-Cell Transcriptomic Atlas of Different Human Cardiac Arteries Identifies Cell Types Associated With Vascular Physiology. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2021, 41, 1408-1427.	1.1	48
2098	Activated Regulatory T-Cells, Dysfunctional and Senescent T-Cells Hinder the Immunity in Pancreatic Cancer. <i>Cancers</i> , 2021, 13, 1776.	1.7	24
2100	The hypothalamus predates the origin of vertebrates. <i>Science Advances</i> , 2021, 7, .	4.7	16
2102	Recovering Spatially-Varying Cell-Specific Gene Co-expression Networks for Single-Cell Spatial Expression Data. <i>Frontiers in Genetics</i> , 2021, 12, 656637.	1.1	0

#	ARTICLE	IF	CITATIONS
2103	Identification of a novel subset of alveolar type 2 cells enriched in PD-L1 and expanded following pneumonectomy. <i>European Respiratory Journal</i> , 2021, 58, 2004168.	3.1	31
2104	Combined epigenetic/genetic study identified an ALS age of onset modifier. <i>Acta Neuropathologica Communications</i> , 2021, 9, 75.	2.4	7
2107	Cannabinoid Receptor Type-2 in B Cells Is Associated with Tumor Immunity in Melanoma. <i>Cancers</i> , 2021, 13, 1934.	1.7	5
2112	Single-cell transcriptomics identifies gene expression networks driving differentiation and tumorigenesis in the human fallopian tube. <i>Cell Reports</i> , 2021, 35, 108978.	2.9	48
2113	Host IL11 Signaling Suppresses CD4+ T cell-Mediated Antitumor Responses to Colon Cancer in Mice. <i>Cancer Immunology Research</i> , 2021, 9, 735-747.	1.6	23
2115	Sex-Specific Control of Human Heart Maturation by the Progesterone Receptor. <i>Circulation</i> , 2021, 143, 1614-1628.	1.6	42
2116	Astrocytes and neurons share region-specific transcriptional signatures that confer regional identity to neuronal reprogramming. <i>Science Advances</i> , 2021, 7, .	4.7	65
2117	The Transcription Regulator Patz1 Is Essential for Neural Stem Cell Maintenance and Proliferation. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 657149.	1.8	5
2119	Irx3 and Irx5 in Ins2-Cre+ cells regulate hypothalamic postnatal neurogenesis and leptin response. <i>Nature Metabolism</i> , 2021, 3, 701-713.	5.1	18
2120	Stabilized epithelial phenotype of cancer cells in primary tumors leads to increased colonization of liver metastasis in pancreatic cancer. <i>Cell Reports</i> , 2021, 35, 108990.	2.9	49
2121	Transcriptional landscapes of floral meristems in barley. <i>Science Advances</i> , 2021, 7, .	4.7	33
2122	Surface antigen-guided CRISPR screens identify regulators of myeloid leukemia differentiation. <i>Cell Stem Cell</i> , 2021, 28, 718-731.e6.	5.2	38
2123	Single-cell transcriptome and genome analyses of pituitary neuroendocrine tumors. <i>Neuro-Oncology</i> , 2021, 23, 1859-1871.	0.6	29
2124	Transcriptional profiling of mouse peripheral nerves to the single-cell level to build a sciatic nerve Atlas (SNAT). <i>ELife</i> , 2021, 10, .	2.8	84
2125	Brain proteome-wide association study implicates novel proteins in depression pathogenesis. <i>Nature Neuroscience</i> , 2021, 24, 810-817.	7.1	85
2126	Maternal Angiotensin Increases Placental Leptin in Early Gestation via an Alternative Renin-Angiotensin System Pathway. <i>Hypertension</i> , 2021, 77, 1723-1736.	1.3	19
2134	Reprogramming epiblast stem cells into pre-implantation blastocyst cell-like cells. <i>Stem Cell Reports</i> , 2021, 16, 1197-1209.	2.3	6
2135	<scp>SAREV</scp>: A review on statistical analytics of single-cell RNA sequencing data. <i>Wiley Interdisciplinary Reviews: Computational Statistics</i> , 2022, 14, e1558.	2.1	2

#	ARTICLE	IF	CITATIONS
2137	Human photoreceptor cells from different macular subregions have distinct transcriptional profiles. <i>Human Molecular Genetics</i> , 2021, 30, 1543-1558.	1.4	17
2139	A single-cell RNA expression atlas of normal, preneoplastic and tumorigenic states in the human breast. <i>EMBO Journal</i> , 2021, 40, e107333.	3.5	170
2140	The nuclear receptor HNF4 drives a brush border gene program conserved across murine intestine, kidney, and embryonic yolk sac. <i>Nature Communications</i> , 2021, 12, 2886.	5.8	24
2142	Single Cell Transcriptomic Analyses Reveal the Impact of bHLH Factors on Human Retinal Organoid Development. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 653305.	1.8	9
2143	ASCL1 represses a SOX9 ⁺ neural crest stem-like state in small cell lung cancer. <i>Genes and Development</i> , 2021, 35, 847-869.	2.7	32
2144	Cell-level metadata are indispensable for documenting single-cell sequencing datasets. <i>PLoS Biology</i> , 2021, 19, e3001077.	2.6	7
2145	The healing myocardium mobilizes a distinct B-cell subset through a CXCL13-CXCR5-dependent mechanism. <i>Cardiovascular Research</i> , 2021, 117, 2664-2676.	1.8	30
2146	Single-cell RNA sequencing of cultured human endometrial CD140b ⁺ CD146 ⁺ perivascular cells highlights the importance of in vivo microenvironment. <i>Stem Cell Research and Therapy</i> , 2021, 12, 306.	2.4	16
2149	A single-cell map of intratumoral changes during anti-PD1 treatment of patients with breast cancer. <i>Nature Medicine</i> , 2021, 27, 820-832.	15.2	330
2150	IL-1R1-dependent signaling coordinates epithelial regeneration in response to intestinal damage. <i>Science Immunology</i> , 2021, 6, .	5.6	31
2151	clAP1/2 antagonism eliminates MHC class II-negative tumors through T cell-dependent reprogramming of mononuclear phagocytes. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	25
2152	Absence of Batf3 reveals a new dimension of cell state heterogeneity within conventional dendritic cells. <i>IScience</i> , 2021, 24, 102402.	1.9	16
2153	Expansion of FcÎ³ Receptor IIIa-Positive Macrophages, Ficolin I-Positive Monocyte-Derived Dendritic Cells, and Plasmacytoid Dendritic Cells Associated With Severe Skin Disease in Systemic Sclerosis. <i>Arthritis and Rheumatology</i> , 2022, 74, 329-341.	2.9	38
2154	Restoring miR-132 expression rescues adult hippocampal neurogenesis and memory deficits in Alzheimer's disease. <i>Cell Stem Cell</i> , 2021, 28, 1805-1821.e8.	5.2	76
2155	Differential gene expression analysis for multi-subject single-cell RNA-sequencing studies with aggregateBioVar. <i>Bioinformatics</i> , 2021, 37, 3243-3251.	1.8	18
2156	PTEN somatic mutations contribute to spectrum of cerebral overgrowth. <i>Brain</i> , 2021, 144, 2971-2978.	3.7	23
2157	A framework for highly multiplexed dextramer mapping and prediction of T cell receptor sequences to antigen specificity. <i>Science Advances</i> , 2021, 7, .	4.7	57
2158	Single-nucleus transcriptomic landscape of primate hippocampal aging. <i>Protein and Cell</i> , 2021, 12, 695-716.	4.8	49

#	ARTICLE	IF	CITATIONS
2159	Transcriptomic Profiling of Human Placenta in Gestational Diabetes Mellitus at the Single-Cell Level. <i>Frontiers in Endocrinology</i> , 2021, 12, 679582.	1.5	41
2160	Single-cell analysis can define distinct evolution of tumor sites in follicular lymphoma. <i>Blood</i> , 2021, 137, 2869-2880.	0.6	48
2161	Unraveling Root Development Through Single-Cell Omics and Reconstruction of Gene Regulatory Networks. <i>Frontiers in Plant Science</i> , 2021, 12, 661361.	1.7	4
2162	Dysregulation of the Pdx1/Ovol2/Zeb2 axis in dedifferentiated β 2-cells triggers the induction of genes associated with epithelialâ€mesenchymal transition in diabetes. <i>Molecular Metabolism</i> , 2021, 53, 101248.	3.0	14
2164	Altered oligodendroglia and astroglia in chronic traumatic encephalopathy. <i>Acta Neuropathologica</i> , 2021, 142, 295-321.	3.9	26
2165	Tumor and immune reprogramming during immunotherapy in advanced renal cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 649-661.e5.	7.7	263
2166	Cell Type-Specific Differentiation Between Indica and Japonica Rice Root Tip Responses to Different Environments Based on Single-Cell RNA Sequencing. <i>Frontiers in Genetics</i> , 2021, 12, 659500.	1.1	4
2167	Single-cell sequencing reveals suppressive transcriptional programs regulated by MIS/AMH in neonatal ovaries. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	35
2168	A hypothetical role for autophagy during the day/night rhythmâ€regulated melatonin synthesis in the rat pineal gland. <i>Journal of Pineal Research</i> , 2021, 71, e12742.	3.4	7
2170	SSBER: removing batch effect for single-cell RNA sequencing data. <i>BMC Bioinformatics</i> , 2021, 22, 249.	1.2	3
2171	A Cancer Cell Cluster Marked by LincRNA MEG3 Leads Pancreatic Ductal Adenocarcinoma Metastasis. <i>Frontiers in Oncology</i> , 2021, 11, 656564.	1.3	13
2175	Stromal Heterogeneity in the Human Proliferative Endometriumâ€A Single-Cell RNA Sequencing Study. <i>Journal of Personalized Medicine</i> , 2021, 11, 448.	1.1	30
2177	Immu-Mela: An open resource for exploring immunotherapy-related multidimensional genomic profiles in melanoma. <i>Journal of Genetics and Genomics</i> , 2021, 48, 361-368.	1.7	3
2179	Association of Premature Immune Aging and Cytomegalovirus After Solid Organ Transplant. <i>Frontiers in Immunology</i> , 2021, 12, 661551.	2.2	13
2181	Epigenetic silencing by SETDB1 suppresses tumour intrinsic immunogenicity. <i>Nature</i> , 2021, 595, 309-314.	13.7	181
2182	Expression of lactate dehydrogenase A and B isoforms in the mouse kidney. <i>American Journal of Physiology - Renal Physiology</i> , 2021, 320, F706-F718.	1.3	18
2183	CD27hiCD38hi plasmablasts are activated B cells of mixed origin with distinct function. <i>IScience</i> , 2021, 24, 102482.	1.9	12
2184	Transcriptional analysis of cystic fibrosis airways at single-cell resolution reveals altered epithelial cell states and composition. <i>Nature Medicine</i> , 2021, 27, 806-814.	15.2	101

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2185	Single-cell transcriptomics trajectory and molecular convergence of clinically relevant mutations in Brugada syndrome. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2021, 320, H1935-H1948.	1.5	6
2186	Fibroblast dedifferentiation as a determinant of successful regeneration. <i>Developmental Cell</i> , 2021, 56, 1541-1551.e6.	3.1	68
2187	Divergent and self-reactive immune responses in the CNS of COVID-19 patients with neurological symptoms. <i>Cell Reports Medicine</i> , 2021, 2, 100288.	3.3	121
2188	Role of epigenetics in unicellular to multicellular transition in <i>Dictyostelium</i> . <i>Genome Biology</i> , 2021, 22, 134.	3.8	12
2190	Single-Cell <i>sc</i> RNA Sequencing Reveals the Breadth of Osteoblast Heterogeneity. <i>JBMR Plus</i> , 2021, 5, e10496.	1.3	14
2191	Co-evolution of tumor and immune cells during progression of multiple myeloma. <i>Nature Communications</i> , 2021, 12, 2559.	5.8	68
2192	A Subpopulation of Schwann Cell-Like Cells With Nerve Regeneration Signatures Is Identified Through Single-Cell RNA Sequencing. <i>Frontiers in Physiology</i> , 2021, 12, 637924.	1.3	5
2193	Single nucleus multi-omics regulatory landscape of the murine pituitary. <i>Nature Communications</i> , 2021, 12, 2677.	5.8	38
2194	GIMAP5 maintains liver endothelial cell homeostasis and prevents portal hypertension. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	22
2195	<i>sc</i> LGR6 marks nephron progenitor cells. <i>Developmental Dynamics</i> , 2021, 250, 1568-1583.	0.8	3
2196	Interfacing Seurat with the R tidy universe. <i>Bioinformatics</i> , 2021, 37, 4100-4107.	1.8	50
2197	A single-cell atlas of <i>Plasmodium falciparum</i> transmission through the mosquito. <i>Nature Communications</i> , 2021, 12, 3196.	5.8	54
2198	A Stat1 bound enhancer promotes Namp1 expression and function within tumor associated macrophages. <i>Nature Communications</i> , 2021, 12, 2620.	5.8	33
2200	Multomics characteristics of neurogenesis-related gene are dysregulated in tumor immune microenvironment. <i>Npj Genomic Medicine</i> , 2021, 6, 37.	1.7	7
2202	Signatures of B Cell Receptor Repertoire Following <i>Pneumocystis</i> Infection. <i>Frontiers in Microbiology</i> , 2021, 12, 636250.	1.5	3
2208	Resident memory T cells in tumor-distant tissues fortify against metastasis formation. <i>Cell Reports</i> , 2021, 35, 109118.	2.9	17
2209	Single cell RNA-seq analysis of the flexor digitorum brevis mouse myofibers. <i>Skeletal Muscle</i> , 2021, 11, 13.	1.9	6
2210	Single-Nucleus RNA-Seq Reveals Dysregulation of Striatal Cell Identity Due to Huntington's Disease Mutations. <i>Journal of Neuroscience</i> , 2021, 41, 5534-5552.	1.7	30

#	ARTICLE	IF	CITATIONS
2212	Integrating multiple references for single-cell assignment. <i>Nucleic Acids Research</i> , 2021, 49, e80-e80.	6.5	14
2213	Sarcomere function activates a p53-dependent DNA damage response that promotes polyploidization and limits in vivo cell engraftment. <i>Cell Reports</i> , 2021, 35, 109088.	2.9	11
2214	Evolution of core archetypal phenotypes in progressive high grade serous ovarian cancer. <i>Nature Communications</i> , 2021, 12, 3039.	5.8	24
2216	Predicting anti-PD-1 responders in malignant melanoma from the frequency of S100A9+ monocytes in the blood. , 2021, 9, e002171.		12
2217	Cutting Edge: Distinct B Cell Repertoires Characterize Patients with Mild and Severe COVID-19. <i>Journal of Immunology</i> , 2021, 206, 2785-2790.	0.4	31
2218	Single-cell protein activity analysis identifies recurrence-associated renal tumor macrophages. <i>Cell</i> , 2021, 184, 2988-3005.e16.	13.5	166
2220	Cross-tissue organization of the fibroblast lineage. <i>Nature</i> , 2021, 593, 575-579.	13.7	463
2221	Detection of differentially abundant cell subpopulations in scRNA-seq data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	81
2222	Coordinated changes in cellular behavior ensure the lifelong maintenance of the hippocampal stem cell population. <i>Cell Stem Cell</i> , 2021, 28, 863-876.e6.	5.2	106
2223	Uncovering genetic mechanisms of hypertension through multi-omic analysis of the kidney. <i>Nature Genetics</i> , 2021, 53, 630-637.	9.4	37
2224	scConnect: a method for exploratory analysis of cell-cell communication based on single-cell RNA-sequencing data. <i>Bioinformatics</i> , 2021, 37, 3501-3508.	1.8	18
2226	Roles of <i>Stra8</i> and <i>Tcerg1</i> in retinoic acid induced spermatogonial differentiation in mouse. <i>Biology of Reproduction</i> , 2021, 105, 503-518.	1.2	10
2227	Single-Cell RNA Sequencing Reveals a Unique Monocyte Population in Bronchoalveolar Lavage Cells of Mice Challenged With Afghanistan Particulate Matter and Allergen. <i>Toxicological Sciences</i> , 2021, 182, 297-309.	1.4	7
2229	Learning a genome-wide score of human mouse conservation at the functional genomics level. <i>Nature Communications</i> , 2021, 12, 2495.	5.8	12
2231	Divergent clonal differentiation trajectories establish CD8+ memory T cell heterogeneity during acute viral infections in humans. <i>Cell Reports</i> , 2021, 35, 109174.	2.9	9
2233	Suppressive neutrophils require PIM1 for metabolic fitness and survival during chronic viral infection. <i>Cell Reports</i> , 2021, 35, 109160.	2.9	14
2234	Characterizing the tumor microenvironment of metastatic ovarian cancer by single-cell transcriptomics. <i>Cell Reports</i> , 2021, 35, 109165.	2.9	75
2235	Single-cell analysis of pancreatic ductal adenocarcinoma identifies a novel fibroblast subtype associated with poor prognosis but better immunotherapy response. <i>Cell Discovery</i> , 2021, 7, 36.	3.1	109

#	ARTICLE	IF	CITATIONS
2236	Single-Cell Characterization of the Immune Microenvironment of Melanoma Brain and Leptomeningeal Metastases. <i>Clinical Cancer Research</i> , 2021, 27, 4109-4125.	3.2	65
2238	Treatment scheduling effects on the evolution of drug resistance in heterogeneous cancer cell populations. <i>Npj Breast Cancer</i> , 2021, 7, 60.	2.3	19
2239	Single-cell multiomics dissection of basal and antigen-specific activation states of CD19-targeted CAR T cells. , 2021, 9, e002328.		31
2240	Spatial Reconstruction of the Early Hepatic Transcriptomic Landscape After an Acetaminophen Overdose Using Single-Cell RNA-Sequencing. <i>Toxicological Sciences</i> , 2021, 182, 327-345.	1.4	19
2243	Co-occupancy identifies transcription factor co-operation for axon growth. <i>Nature Communications</i> , 2021, 12, 2555.	5.8	8
2245	The Transcriptome of SH-SY5Y at Single-Cell Resolution: A CITE-Seq Data Analysis Workflow. <i>Methods and Protocols</i> , 2021, 4, 28.	0.9	2
2247	Generative modeling of single-cell time series with PRESCIENT enables prediction of cell trajectories with interventions. <i>Nature Communications</i> , 2021, 12, 3222.	5.8	27
2250	Analysis of deficiency of adenosine deaminase 2 pathogenesis based on single-cell RNA sequencing of monocytes. <i>Journal of Leukocyte Biology</i> , 2021, 110, 409-424.	1.5	26
2251	Clump sequencing exposes the spatial expression programs of intestinal secretory cells. <i>Nature Communications</i> , 2021, 12, 3074.	5.8	43
2252	Extraction of nuclei from archived postmortem tissues for single-nucleus sequencing applications. <i>Nature Protocols</i> , 2021, 16, 2788-2801.	5.5	15
2254	Adaptive cell invasion maintains lateral line organ homeostasis in response to environmental changes. <i>Developmental Cell</i> , 2021, 56, 1296-1312.e7.	3.1	17
2255	Big data analytics in single-cell transcriptomics: Five grand opportunities. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2021, 11, e1414.	4.6	1
2256	Integrative analysis of the human brain mural cell transcriptome. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2021, 41, 3052-3068.	2.4	15
2258	CDSeqR: fast complete deconvolution for gene expression data from bulk tissues. <i>BMC Bioinformatics</i> , 2021, 22, 262.	1.2	11
2259	NEBULA is a fast negative binomial mixed model for differential or co-expression analysis of large-scale multi-subject single-cell data. <i>Communications Biology</i> , 2021, 4, 629.	2.0	50
2261	A sustained type I IFN-neutrophil-IL-18 axis drives pathology during mucosal viral infection. <i>ELife</i> , 2021, 10, .	2.8	15
2262	Hox dosage contributes to flight appendage morphology in <i>Drosophila</i> . <i>Nature Communications</i> , 2021, 12, 2892.	5.8	30
2263	Machine Intelligence in Single-Cell Data Analysis: Advances and New Challenges. <i>Frontiers in Genetics</i> , 2021, 12, 655536.	1.1	33

#	ARTICLE	IF	CITATIONS
2264	A potential role for somatostatin signaling in regulating retinal neurogenesis. <i>Scientific Reports</i> , 2021, 11, 10962.	1.6	7
2265	The neutrotime transcriptional signature defines a single continuum of neutrophils across biological compartments. <i>Nature Communications</i> , 2021, 12, 2856.	5.8	149
2266	Applications of single-cell and bulk RNA sequencing in onco-immunology. <i>European Journal of Cancer</i> , 2021, 149, 193-210.	1.3	62
2268	Single-cell analysis of cell identity in the Arabidopsis root apical meristem: insights and opportunities. <i>Journal of Experimental Botany</i> , 2021, 72, 6679-6686.	2.4	28
2269	The complement system drives local inflammatory tissue priming by metabolic reprogramming of synovial fibroblasts. <i>Immunity</i> , 2021, 54, 1002-1021.e10.	6.6	106
2270	Longitudinal single-cell profiling reveals molecular heterogeneity and tumor-immune evolution in refractory mantle cell lymphoma. <i>Nature Communications</i> , 2021, 12, 2877.	5.8	35
2271	Discrete limbal epithelial stem cell populations mediate corneal homeostasis and wound healing. <i>Cell Stem Cell</i> , 2021, 28, 1248-1261.e8.	5.2	63
2272	Deep generative model embedding of single-cell RNA-Seq profiles on hyperspheres and hyperbolic spaces. <i>Nature Communications</i> , 2021, 12, 2554.	5.8	48
2273	Understanding the Adult Mammalian Heart at Single-Cell RNA-Seq Resolution. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 645276.	1.8	11
2275	Functionally distinct POMC-expressing neuron subpopulations in hypothalamus revealed by intersectional targeting. <i>Nature Neuroscience</i> , 2021, 24, 913-929.	7.1	64
2277	Tutorial: guidelines for annotating single-cell transcriptomic maps using automated and manual methods. <i>Nature Protocols</i> , 2021, 16, 2749-2764.	5.5	100
2279	Selective removal of astrocytic APOE4 strongly protects against tau-mediated neurodegeneration and decreases synaptic phagocytosis by microglia. <i>Neuron</i> , 2021, 109, 1657-1674.e7.	3.8	151
2280	AKR1C2 and AKR1C3 expression in adipose tissue: Association with body fat distribution and regulatory variants. <i>Molecular and Cellular Endocrinology</i> , 2021, 527, 111220.	1.6	11
2284	Cryptic developmental events determine medulloblastoma radiosensitivity and cellular heterogeneity without altering transcriptomic profile. <i>Communications Biology</i> , 2021, 4, 616.	2.0	13
2288	The <i>Drosophila</i> brain on cocaine at single-cell resolution. <i>Genome Research</i> , 2021, 31, 1927-1937.	2.4	23
2289	scDesign2: a transparent simulator that generates high-fidelity single-cell gene expression count data with gene correlations captured. <i>Genome Biology</i> , 2021, 22, 163.	3.8	48
2291	Single-cell RNA sequencing reveals the sustained immune cell dysfunction in the pathogenesis of sepsis secondary to bacterial pneumonia. <i>Genomics</i> , 2021, 113, 1219-1233.	1.3	29
2292	Direct contribution of skeletal muscle mesenchymal progenitors to bone repair. <i>Nature Communications</i> , 2021, 12, 2860.	5.8	53

#	ARTICLE	IF	CITATIONS
2293	A robust method of nuclei isolation for single-cell RNA sequencing of solid tissues from the plant genus <i>Populus</i> . <i>PLoS ONE</i> , 2021, 16, e0251149.	1.1	23
2294	Single-cell RNA sequencing reveals Nestin+ active neural stem cells outside the central canal after spinal cord injury. <i>Science China Life Sciences</i> , 2022, 65, 295-308.	2.3	24
2295	Neuronal ApoE upregulates MHC-I expression to drive selective neurodegeneration in Alzheimer's disease. <i>Nature Neuroscience</i> , 2021, 24, 786-798.	7.1	91
2296	Progressive immune dysfunction with advancing disease stage in renal cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 632-648.e8.	7.7	230
2297	The Cellular Composition of Bovine Coccygeal Intervertebral Discs: A Comprehensive Single-Cell RNAseq Analysis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4917.	1.8	24
2299	A coordinated progression of progenitor cell states initiates urinary tract development. <i>Nature Communications</i> , 2021, 12, 2627.	5.8	19
2300	Generation of mature compact ventricular cardiomyocytes from human pluripotent stem cells. <i>Nature Communications</i> , 2021, 12, 3155.	5.8	93
2304	Tumor-associated hematopoietic stem and progenitor cells positively linked to glioblastoma progression. <i>Nature Communications</i> , 2021, 12, 3895.	5.8	28
2306	Loss of Gap Junction Delta-2 (GJD2) gene orthologs leads to refractive error in zebrafish. <i>Communications Biology</i> , 2021, 4, 676.	2.0	19
2307	Skin and gut imprinted helper T cell subsets exhibit distinct functional phenotypes in central nervous system autoimmunity. <i>Nature Immunology</i> , 2021, 22, 880-892.	7.0	34
2309	Visualization and Analysis of Gene Expression in Stanford Type A Aortic Dissection Tissue Section by Spatial Transcriptomics. <i>Frontiers in Genetics</i> , 2021, 12, 698124.	1.1	12
2311	A regulatory role for CHD4 in maintenance of the spermatogonial stem cell pool. <i>Stem Cell Reports</i> , 2021, 16, 1555-1567.	2.3	12
2312	Therapeutic Targeting of Transcription Factors to Control the Cytokine Release Syndrome in COVID-19. <i>Frontiers in Pharmacology</i> , 2021, 12, 673485.	1.6	10
2314	An in vitro model of tumor heterogeneity resolves genetic, epigenetic, and stochastic sources of cell state variability. <i>PLoS Biology</i> , 2021, 19, e3000797.	2.6	21
2317	Spatial and cell type transcriptional landscape of human cerebellar development. <i>Nature Neuroscience</i> , 2021, 24, 1163-1175.	7.1	98
2319	Single-cell biology to decode the immune cellular composition of kidney inflammation. <i>Cell and Tissue Research</i> , 2021, 385, 435-443.	1.5	5
2320	Diversity and intratumoral heterogeneity in human gallbladder cancer progression revealed by single-cell RNA sequencing. <i>Clinical and Translational Medicine</i> , 2021, 11, e462.	1.7	21
2321	Cell segmentation-free inference of cell types from in situ transcriptomics data. <i>Nature Communications</i> , 2021, 12, 3545.	5.8	52

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2323	Integration of spatial and single-cell transcriptomics localizes epithelial cell-immune cross-talk in kidney injury. <i>JCI Insight</i> , 2021, 6, .	2.3	83
2324	Single-cell transcriptome atlas of the leaf and root of rice seedlings. <i>Journal of Genetics and Genomics</i> , 2021, 48, 881-898.	1.7	84
2325	CloneSeq: A highly sensitive analysis platform for the characterization of 3D-cultured single-cell-derived clones. <i>Developmental Cell</i> , 2021, 56, 1804-1817.e7.	3.1	4
2326	The triumphs and limitations of computational methods for scRNA-seq. <i>Nature Methods</i> , 2021, 18, 723-732.	9.0	133
2327	Single cell transcriptome atlas of mouse mammary epithelial cells across development. <i>Breast Cancer Research</i> , 2021, 23, 69.	2.2	26
2328	Prmt5 promotes vascular morphogenesis independently of its methyltransferase activity. <i>PLoS Genetics</i> , 2021, 17, e1009641.	1.5	10
2330	Detection of Hematopoietic Stem Cell Transcriptome in Human Fetal Kidneys and Kidney Organoids Derived From Human Induced Pluripotent Stem Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 668833.	1.8	4
2331	Normalization by distributional resampling of high throughput single-cell RNA-sequencing data. <i>Bioinformatics</i> , 2021, 37, 4123-4128.	1.8	13
2332	REBET: a method to determine the number of cell clusters based on batch effect removal. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	2
2333	Unveiling the sensory and interneuronal pathways of the neuroendocrine connectome in <i>Drosophila</i> . <i>ELife</i> , 2021, 10, .	2.8	25
2334	RNA-seq analysis of laser microdissected <i>Arabidopsis thaliana</i> leaf epidermis, mesophyll and vasculature defines tissue-specific transcriptional responses to multiple stress treatments. <i>Plant Journal</i> , 2021, 107, 938-955.	2.8	31
2335	Single-Cell RNA-Seq Reveals Transcriptomic Heterogeneity and Post-Traumatic Osteoarthritis-Associated Early Molecular Changes in Mouse Articular Chondrocytes. <i>Cells</i> , 2021, 10, 1462.	1.8	44
2338	Leveraging Novel Integrated Single-Cell Analyses to Define HIV-1 Latency Reversal. <i>Viruses</i> , 2021, 13, 1197.	1.5	3
2339	Distinct populations of antigen specific tissue resident CD8 T cells in human cervix mucosa. <i>JCI Insight</i> , 2021, 6, .	2.3	10
2344	IL-6 contributes to metastatic switch via the differentiation of monocytic-dendritic progenitors into prometastatic immune cells. , 2021, 9, e002856.		19
2346	Single-cell RNA-seq landscape midbrain cell responses to red spotted grouper nervous necrosis virus infection. <i>PLoS Pathogens</i> , 2021, 17, e1009665.	2.1	20
2348	Metabolomic profiling of single enlarged lysosomes. <i>Nature Methods</i> , 2021, 18, 788-798.	9.0	46
2349	Systemic GLP-1R agonist treatment reverses mouse glial and neurovascular cell transcriptomic aging signatures in a genome-wide manner. <i>Communications Biology</i> , 2021, 4, 656.	2.0	9

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2352	Single-cell RNA-seq analysis reveals penaeid shrimp hemocyte subpopulations and cell differentiation process. <i>ELife</i> , 2021, 10, .	2.8	53
2353	TIM-3 restrains anti-tumour immunity by regulating inflammasome activation. <i>Nature</i> , 2021, 595, 101-106.	13.7	169
2354	A map of transcriptional heterogeneity and regulatory variation in human microglia. <i>Nature Genetics</i> , 2021, 53, 861-868.	9.4	115
2355	Single-cell RNA sequencing of human liver reveals hepatic stellate cell heterogeneity. <i>JHEP Reports</i> , 2021, 3, 100278.	2.6	57
2356	High-resolution transcriptional landscape of xeno-free human induced pluripotent stem cell-derived cerebellar organoids. <i>Scientific Reports</i> , 2021, 11, 12959.	1.6	32
2357	The molecular and epigenetic mechanisms of innate lymphoid cell (ILC) memory and its relevance for asthma. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	31
2358	In silico analysis of the transcriptional regulatory logic of neuronal identity specification throughout the <i>C. elegans</i> nervous system. <i>ELife</i> , 2021, 10, .	2.8	16
2359	Analysis of single-cell RNA sequencing data based on autoencoders. <i>BMC Bioinformatics</i> , 2021, 22, 309.	1.2	15
2360	Secreted inhibitors drive the loss of regeneration competence in <i>Xenopus</i> limbs. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	20
2361	IP3-mediated Ca ²⁺ signals regulate larval to pupal transition under nutrient stress through the H3K36 methyltransferase <i>Set2</i> . <i>Development (Cambridge)</i> , 2021, 148, .	1.2	1
2365	Distinctive waves of innate immune response in the retina in experimental autoimmune encephalomyelitis. <i>JCI Insight</i> , 2021, 6, .	2.3	14
2366	Single-cell immunophenotyping of the skin lesion erythema migrans identifies IgM memory B cells. <i>JCI Insight</i> , 2021, 6, .	2.3	10
2367	A single cell characterisation of human embryogenesis identifies pluripotency transitions and putative anterior hypoblast centre. <i>Nature Communications</i> , 2021, 12, 3679.	5.8	63
2368	Silk gel recruits specific cell populations for scarless skin regeneration. <i>Applied Materials Today</i> , 2021, 23, 101004.	2.3	4
2370	Direct and indirect immune effects of CMP-001, a virus-like particle containing a TLR9 agonist. , 2021, 9, e002484.		16
2371	Sublayer- and cell-type-specific neurodegenerative transcriptional trajectories in hippocampal sclerosis. <i>Cell Reports</i> , 2021, 35, 109229.	2.9	20
2372	A transitory signaling center controls timing of primordial germ cell differentiation. <i>Developmental Cell</i> , 2021, 56, 1742-1755.e4.	3.1	10
2373	Essential role for <i>Gata2</i> in modulating lineage output from hematopoietic stem cells in zebrafish. <i>Blood Advances</i> , 2021, 5, 2687-2700.	2.5	21

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2374	Combined EZH2 Inhibition and IKAROS Degradation Leads to Enhanced Antitumor Activity in Diffuse Large B-cell Lymphoma. <i>Clinical Cancer Research</i> , 2021, 27, 5401-5414.	3.2	16
2375	Consensus clustering of single-cell RNA-seq data by enhancing network affinity. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	24
2376	Advances and Opportunities in Single-Cell Transcriptomics for Plant Research. <i>Annual Review of Plant Biology</i> , 2021, 72, 847-866.	8.6	101
2377	A taxonomy of transcriptomic cell types across the isocortex and hippocampal formation. <i>Cell</i> , 2021, 184, 3222-3241.e26.	13.5	479
2381	Unsupervised gene selection for predicting cell spatial positions in the Drosophila embryo. <i>F1000Research</i> , 0, 9, 124.	0.8	0
2382	coupleCoC+: An information-theoretic co-clustering-based transfer learning framework for the integrative analysis of single-cell genomic data. <i>PLoS Computational Biology</i> , 2021, 17, e1009064.	1.5	11
2383	Neural G0: a quiescent-like state found in neuroepithelial-derived cells and glioma. <i>Molecular Systems Biology</i> , 2021, 17, e9522.	3.2	24
2384	Ketogenic diet restrains aging-induced exacerbation of coronavirus infection in mice. <i>ELife</i> , 2021, 10, .	2.8	37
2385	Network medicine links SARS-CoV-2/COVID-19 infection to brain microvascular injury and neuroinflammation in dementia-like cognitive impairment. <i>Alzheimer's Research and Therapy</i> , 2021, 13, 110.	3.0	108
2386	Multi-omic profiling reveals widespread dysregulation of innate immunity and hematopoiesis in COVID-19. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	139
2388	Identification of SARS-CoV-2-induced pathways reveals drug repurposing strategies. <i>Science Advances</i> , 2021, 7, .	4.7	34
2389	Overexpression of Replication-Dependent Histone Signifies a Subset of Dedifferentiated Liposarcoma with Increased Aggressiveness. <i>Cancers</i> , 2021, 13, 3122.	1.7	7
2391	Systematic analysis of exonic germline and postzygotic de novo mutations in bipolar disorder. <i>Nature Communications</i> , 2021, 12, 3750.	5.8	15
2397	Single-cell transcriptomic analysis reveals disparate effector differentiation pathways in human Treg compartment. <i>Nature Communications</i> , 2021, 12, 3913.	5.8	27
2399	Single-cell technologies and analyses in hematopoiesis and hematological malignancies. <i>Experimental Hematology</i> , 2021, 98, 1-13.	0.2	11
2400	Generation of excitatory and inhibitory neurons from common progenitors via Notch signaling in the cerebellum. <i>Cell Reports</i> , 2021, 35, 109208.	2.9	18
2401	Systems genetics in diversity outbred mice inform BMD GWAS and identify determinants of bone strength. <i>Nature Communications</i> , 2021, 12, 3408.	5.8	31
2402	Charting human development using a multi-endodermal organ atlas and organoid models. <i>Cell</i> , 2021, 184, 3281-3298.e22.	13.5	82

#	ARTICLE	IF	CITATIONS
2403	Single-cell RNA sequencing reveals the mechanism of sonodynamic therapy combined with a RAS inhibitor in the setting of hepatocellular carcinoma. <i>Journal of Nanobiotechnology</i> , 2021, 19, 177.	4.2	18
2404	Machine learning for perturbational single-cell omics. <i>Cell Systems</i> , 2021, 12, 522-537.	2.9	52
2405	Capturing human trophoblast development with naive pluripotent stem cells in vitro. <i>Cell Stem Cell</i> , 2021, 28, 1023-1039.e13.	5.2	164
2406	scGCN is a graph convolutional networks algorithm for knowledge transfer in single cell omics. <i>Nature Communications</i> , 2021, 12, 3826.	5.8	40
2407	Single-Nucleus RNA Sequencing Identifies New Classes of Proximal Tubular Epithelial Cells in Kidney Fibrosis. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 2501-2516.	3.0	38
2409	Monocyte and macrophage derived myofibroblasts: Is it fate? A review of the current evidence. <i>Wound Repair and Regeneration</i> , 2021, 29, 548-562.	1.5	27
2410	Cell type hierarchy reconstruction via reconciliation of multi-resolution cluster tree. <i>Nucleic Acids Research</i> , 2021, 49, e91-e91.	6.5	11
2411	Single-cell analysis of the cellular heterogeneity and interactions in the injured mouse spinal cord. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	121
2412	cGAS restricts colon cancer development by protecting intestinal barrier integrity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	31
2413	Gata2-L359V impairs primitive and definitive hematopoiesis and blocks cell differentiation in murine chronic myelogenous leukemia model. <i>Cell Death and Disease</i> , 2021, 12, 568.	2.7	6
2419	Single cell analysis of host response to helminth infection reveals the clonal breadth, heterogeneity, and tissue-specific programming of the responding CD4+ T cell repertoire. <i>PLoS Pathogens</i> , 2021, 17, e1009602.	2.1	7
2420	Single-Cell Transcriptome Analysis Reveals the M2 Macrophages and Exhausted T Cells and Intratumoral Heterogeneity in Triple-Negative Breast Cancer. <i>Anti-Cancer Agents in Medicinal Chemistry</i> , 2022, 22, 294-312.	0.9	7
2421	Surfactant protein C mutation links postnatal type 2 cell dysfunction to adult disease. <i>JCI Insight</i> , 2021, 6, .	2.3	11
2422	Long non-coding RNA exploration for mesenchymal stem cell characterisation. <i>BMC Genomics</i> , 2021, 22, 412.	1.2	3
2424	Post-myocardial infarction heart failure dysregulates the bone vascular niche. <i>Nature Communications</i> , 2021, 12, 3964.	5.8	23
2425	Single-cell transcriptomics defines heterogeneity of epicardial cells and fibroblasts within the infarcted murine heart. <i>ELife</i> , 2021, 10, .	2.8	42
2426	Reciprocal repulsions instruct the precise assembly of parallel hippocampal networks. <i>Science</i> , 2021, 372, 1068-1073.	6.0	38
2427	Single-Cell RNA Sequencing Uncovers Paracrine Functions of the Epicardial-Derived Cells in Arrhythmogenic Cardiomyopathy. <i>Circulation</i> , 2021, 143, 2169-2187.	1.6	22

#	ARTICLE	IF	CITATIONS
2429	SARS-CoV-2-mediated dysregulation of metabolism and autophagy uncovers host-targeting antivirals. Nature Communications, 2021, 12, 3818.	5.8	172
2430	The cellular architecture of the antimicrobial response network in human leprosy granulomas. Nature Immunology, 2021, 22, 839-850.	7.0	60
2431	Scalable, multimodal profiling of chromatin accessibility, gene expression and protein levels in single cells. Nature Biotechnology, 2021, 39, 1246-1258.	9.4	244
2434	Single-cell multi-omics sequencing: application trends, COVID-19, data analysis issues and prospects. Briefings in Bioinformatics, 2021, 22, .	3.2	14
2435	Notch1 switches progenitor competence in inducing medulloblastoma. Science Advances, 2021, 7, .	4.7	6
2436	Human Monocytes Plasticity in Neurodegeneration. Biomedicines, 2021, 9, 717.	1.4	5
2437	Resolving the graft ischemia-reperfusion injury during liver transplantation at the single cell resolution. Cell Death and Disease, 2021, 12, 589.	2.7	23
2438	Tumor cells in light-chain amyloidosis and myeloma show distinct transcriptional rewiring of normal plasma cell development. Blood, 2021, 138, 1583-1589.	0.6	11
2439	Inhibition of host Ogr1 enhances effector CD8+ T-cell function by modulating acidic microenvironment. Cancer Gene Therapy, 2021, 28, 1213-1224.	2.2	13
2440	Collection and preprocessing of fine needle aspirate patient samples for single cell profiling and data analysis. STAR Protocols, 2021, 2, 100581.	0.5	1
2441	Integration of millions of transcriptomes using batch-aware triplet neural networks. Nature Machine Intelligence, 2021, 3, 705-715.	8.3	19
2444	The regulatory landscape of Arabidopsis thaliana roots at single-cell resolution. Nature Communications, 2021, 12, 3334.	5.8	84
2445	Glomerular Endothelial Cells Are the Coordinator in the Development of Diabetic Nephropathy. Frontiers in Medicine, 2021, 8, 655639.	1.2	10
2446	MYC deficiency impairs the development of effector/memory T lymphocytes. IScience, 2021, 24, 102761.	1.9	10
2449	The Prognostic Potential of Human Prostate Cancer-Associated Macrophage Subtypes as Revealed by Single-Cell Transcriptomics. Molecular Cancer Research, 2021, 19, 1778-1791.	1.5	20
2450	Machine learning for single-cell genomics data analysis. Current Opinion in Systems Biology, 2021, 26, 64-71.	1.3	15
2451	A Role for Protease Activated Receptor Type 3 (PAR3) in Nociception Demonstrated Through Development of a Novel Peptide Agonist. Journal of Pain, 2021, 22, 692-706.	0.7	7
2452	Integrating longitudinal clinical laboratory tests with targeted proteomic and transcriptomic analyses reveal the landscape of host responses in COVID-19. Cell Discovery, 2021, 7, 42.	3.1	23

#	ARTICLE	IF	CITATIONS
2453	Microscopic examination of spatial transcriptome using Seq-Scope. <i>Cell</i> , 2021, 184, 3559-3572.e22.	13.5	233
2454	Overexpression of human BAG3P209L in mice causes restrictive cardiomyopathy. <i>Nature Communications</i> , 2021, 12, 3575.	5.8	17
2455	Plasticity and heterogeneity of thermogenic adipose tissue. <i>Nature Metabolism</i> , 2021, 3, 751-761.	5.1	29
2456	A method for cryopreservation and single nucleus RNA-sequencing of normal adult human interventricular septum heart tissue reveals cellular diversity and function. <i>BMC Medical Genomics</i> , 2021, 14, 161.	0.7	16
2457	COTAN: scRNA-seq data analysis based on gene co-expression. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab072.	1.5	11
2458	A Bayesian inference transcription factor activity model for the analysis of single-cell transcriptomes. <i>Genome Research</i> , 2021, 31, 1296-1311.	2.4	7
2459	Interleukin-6 is an activator of pituitary stem cells upon local damage, a competence quenched in the aging gland. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	25
2460	Single-Cell RNA Sequencing Analysis of Chicken Anterior Pituitary: A Bird's-Eye View on Vertebrate Pituitary. <i>Frontiers in Physiology</i> , 2021, 12, 562817.	1.3	12
2462	B cell genomics behind cross-neutralization of SARS-CoV-2 variants and SARS-CoV. <i>Cell</i> , 2021, 184, 3205-3221.e24.	13.5	73
2463	Phospholipids of APOE lipoproteins activate microglia in an isoform-specific manner in preclinical models of Alzheimer's disease. <i>Nature Communications</i> , 2021, 12, 3416.	5.8	57
2464	Targeting of the CD80/86 proinflammatory axis as a therapeutic strategy to prevent severe COVID-19. <i>Scientific Reports</i> , 2021, 11, 11462.	1.6	11
2465	Integrating single-cell and spatial transcriptomics to elucidate intercellular tissue dynamics. <i>Nature Reviews Genetics</i> , 2021, 22, 627-644.	7.7	423
2466	Axial elongation of caudalized human organoids mimics aspects of neural tube development. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	47
2467	Tumor-Infiltrating B Lymphocyte Profiling Identifies IgG-Biased, Clonally Expanded Prognostic Phenotypes in Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2021, 81, 4290-4304.	0.4	40
2468	Plant PhysioSpace: a robust tool to compare stress response across plant species. <i>Plant Physiology</i> , 2021, 187, 1795-1811.	2.3	3
2469	Single-cell analysis of human skin identifies CD14+ type 3 dendritic cells co-producing IL1B and IL23A in psoriasis. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	68
2470	Preoptic BRS3 neurons increase body temperature and heart rate via multiple pathways. <i>Cell Metabolism</i> , 2021, 33, 1389-1403.e6.	7.2	29
2472	Exploring the role of autophagy during early human embryonic development through single-cell transcriptome and methylome analyses. <i>Science China Life Sciences</i> , 2022, 65, 940-952.	2.3	9

#	ARTICLE	IF	CITATIONS
2473	Extrathymic Aire-expressing cells support maternal-fetal tolerance. <i>Science Immunology</i> , 2021, 6, .	5.6	17
2474	EGR1 dysregulation defines an inflammatory and leukemic program in cell trajectory of human-aged hematopoietic stem cells (HSC). <i>Stem Cell Research and Therapy</i> , 2021, 12, 419.	2.4	17
2475	Oncogenic cooperation between TCF7-SPI1 and NRAS(G12D) requires β -catenin activity to drive T-cell acute lymphoblastic leukemia. <i>Nature Communications</i> , 2021, 12, 4164.	5.8	9
2476	Discovery of potential imaging and therapeutic targets for severe inflammation in COVID-19 patients. <i>Scientific Reports</i> , 2021, 11, 14151.	1.6	8
2477	Bulk and single-cell transcriptome profiling reveal the metabolic heterogeneity in human breast cancers. <i>Molecular Therapy</i> , 2021, 29, 2350-2365.	3.7	49
2479	Cigarette Smoke Specifically Affects Small Airway Epithelial Cell Populations and Triggers the Expansion of Inflammatory and Squamous Differentiation Associated Basal Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7646.	1.8	16
2480	Airway basal stem cells reutilize the embryonic proliferation regulator, Tgf β 2-Id2 axis, for tissue regeneration. <i>Developmental Cell</i> , 2021, 56, 1917-1929.e9.	3.1	29
2481	Mapping Angiopoietin1 Expression in the Developing and Adult Brain. <i>Developmental Neuroscience</i> , 2021, 43, 321-334.	1.0	2
2482	Hypoxia-inducible factors individually facilitate inflammatory myeloid metabolism and inefficient cardiac repair. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	27
2484	Single-cell transcriptomic profiling reveals distinct mechanical responses between normal and diseased tendon progenitor cells. <i>Cell Reports Medicine</i> , 2021, 2, 100343.	3.3	10
2485	Diversity of Reactive Astrogliosis in CNS Pathology: Heterogeneity or Plasticity?. <i>Frontiers in Cellular Neuroscience</i> , 2021, 15, 703810.	1.8	34
2486	Intercellular Arc Signaling Regulates Vasodilation. <i>Journal of Neuroscience</i> , 2021, 41, 7712-7726.	1.7	12
2487	Delineating spatiotemporal and hierarchical development of human fetal innate lymphoid cells. <i>Cell Research</i> , 2021, 31, 1106-1122.	5.7	25
2488	Human Primary Airway Basal Cells Display a Continuum of Molecular Phases from Health to Disease in Chronic Obstructive Pulmonary Disease. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2021, 65, 103-113.	1.4	13
2489	Butyrophilin-like 2 regulates site-specific adaptations of intestinal β intraepithelial lymphocytes. <i>Communications Biology</i> , 2021, 4, 913.	2.0	3
2491	Intra-Tumoral Activation of Endosomal TLR Pathways Reveals a Distinct Role for TLR3 Agonist Dependent Type-1 Interferons in Shaping the Tumor Immune Microenvironment. <i>Frontiers in Oncology</i> , 2021, 11, 711673.	1.3	10
2492	An otopetrin family proton channel promotes cellular acid efflux critical for biomineralization in a marine calcifier. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	22
2493	AutoGeneS: Automatic gene selection using multi-objective optimization for RNA-seq deconvolution. <i>Cell Systems</i> , 2021, 12, 706-715.e4.	2.9	44

#	ARTICLE	IF	CITATIONS
2494	Differential immune responses in pregnant patients recovered from COVID-19. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 289.	7.1	28
2496	Differential Expression Levels of Sox9 in Early Neocortical Radial Glial Cells Regulate the Decision between Stem Cell Maintenance and Differentiation. <i>Journal of Neuroscience</i> , 2021, 41, 6969-6986.	1.7	12
2497	Generation of functional human thymic cells from induced pluripotent stem cells. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 149, 767-781.e6.	1.5	16
2498	RCA2: a scalable supervised clustering algorithm that reduces batch effects in scRNA-seq data. <i>Nucleic Acids Research</i> , 2021, 49, 8505-8519.	6.5	7
2499	Pulmonary Aerosol Delivery of Letâ€b microRNA Confers a Striking Inhibitory Effect on Lung Carcinogenesis through Targeting the Tumor Immune Microenvironment. <i>Advanced Science</i> , 2021, 8, e2100629.	5.6	17
2500	Preparation of single-cell suspensions of mouse glomeruli for high-throughput analysis. <i>Nature Protocols</i> , 2021, 16, 4068-4083.	5.5	10
2503	Uptake of oxidized lipids by the scavenger receptor CD36 promotes lipid peroxidation and dysfunction in CD8+ T cells in tumors. <i>Immunity</i> , 2021, 54, 1561-1577.e7.	6.6	260
2504	Murine muscle stem cell response to perturbations of the neuromuscular junction are attenuated with aging. <i>ELife</i> , 2021, 10, .	2.8	20
2505	Landscape of innate lymphoid cells in human head and neck cancer reveals divergent NK cell states in the tumor microenvironment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	50
2507	Integrative Single-Cell Transcriptomic Analysis of Human Fetal Thymocyte Development. <i>Frontiers in Genetics</i> , 2021, 12, 679616.	1.1	5
2509	NF-ÎBâ€dependent IRF1 activation programs cDC1 dendritic cells to drive antitumor immunity. <i>Science Immunology</i> , 2021, 6, .	5.6	55
2510	Single-Cell Transcriptome Profiling Simulation Reveals the Impact of Sequencing Parameters and Algorithms on Clustering. <i>Life</i> , 2021, 11, 716.	1.1	0
2512	Constrained TCRÎ³Î´-associated Syk activity engages PI3K to facilitate thymic development of IL-17Aâ€secreting Î³Î´ T cells. <i>Science Signaling</i> , 2021, 14, .	1.6	12
2513	Single-Cell Transcriptomics Identifies a Unique Entity and Signature Markers of Transit-Amplifying Cells in Human Corneal Limbus. , 2021, 62, 36.		26
2517	Multimodal single-cell omics analysis identifies epitheliumâ€immune cell interactions and immune vulnerability associated with sex differences in COVID-19. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 292.	7.1	13
2518	Epigenetic scarring of exhausted T cells hinders memory differentiation upon eliminating chronic antigenic stimulation. <i>Nature Immunology</i> , 2021, 22, 1008-1019.	7.0	116
2519	UCSC Cell Browser: visualize your single-cell data. <i>Bioinformatics</i> , 2021, 37, 4578-4580.	1.8	105
2522	FlowGrid enables fast clustering of very large single-cell RNA-seq data. <i>Bioinformatics</i> , 2021, 38, 282-283.	1.8	3

#	ARTICLE	IF	CITATIONS
2523	Leukocytes with chromosome Y loss have reduced abundance of the cell surface immunoprotein CD99. <i>Scientific Reports</i> , 2021, 11, 15160.	1.6	23
2524	Scaling up reproducible research for single-cell transcriptomics using MetaNeighbor. <i>Nature Protocols</i> , 2021, 16, 4031-4067.	5.5	19
2525	Single-nucleus chromatin accessibility and transcriptomic characterization of Alzheimer's disease. <i>Nature Genetics</i> , 2021, 53, 1143-1155.	9.4	264
2526	Transcriptomic encoding of sensorimotor transformation in the midbrain. <i>ELife</i> , 2021, 10, .	2.8	27
2527	Modeling High-Grade Serous Ovarian Carcinoma Using a Combination of <i>In Vivo</i> Fallopian Tube Electroporation and CRISPR-Cas9-Mediated Genome Editing. <i>Cancer Research</i> , 2021, 81, 5147-5160.	0.4	11
2528	ChrNet: A re-trainable chromosome-based 1D convolutional neural network for predicting immune cell types. <i>Genomics</i> , 2021, 113, 2023-2031.	1.3	5
2529	Transcriptome landscape of double negative T cells by single-cell RNA sequencing. <i>Journal of Autoimmunity</i> , 2021, 121, 102653.	3.0	20
2532	A Preliminary Single-Cell RNA-Seq Analysis of Embryonic Cells That Express Brachyury in the Amphioxus, <i>Branchiostoma japonicum</i> . <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 696875.	1.8	8
2533	Single-cell RNA-seq reveals cellular heterogeneity of mouse carotid artery under disturbed flow. <i>Cell Death Discovery</i> , 2021, 7, 180.	2.0	26
2535	An active learning approach for clustering single-cell RNA-seq data. <i>Laboratory Investigation</i> , 2022, 102, 227-235.	1.7	8
2536	Roles of tetraspanins during trophoblast development: bioinformatics and new perspectives. <i>Cell and Tissue Research</i> , 2021, 386, 157-171.	1.5	1
2537	Tim-4+ cavity-resident macrophages impair anti-tumor CD8+ T cell immunity. <i>Cancer Cell</i> , 2021, 39, 973-988.e9.	7.7	93
2538	Co-delivery of novel bispecific and trispecific engagers by an amplicon vector augments the therapeutic effect of an HSV-based oncolytic virotherapy. , 2021, 9, e002454.		7
2542	Exploiting Single-Cell Tools in Gene and Cell Therapy. <i>Frontiers in Immunology</i> , 2021, 12, 702636.	2.2	21
2543	Tumor-derived NKG2D ligand sMIC reprograms NK cells to an inflammatory phenotype through CBM signalosome activation. <i>Communications Biology</i> , 2021, 4, 905.	2.0	10
2544	Developmental Alcohol Exposure in <i>Drosophila</i> : Effects on Adult Phenotypes and Gene Expression in the Brain. <i>Frontiers in Psychiatry</i> , 2021, 12, 699033.	1.3	13
2545	scRNA sequencing uncovers a TCF4-dependent transcription factor network regulating commissure development in mouse. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	8
2547	Single-Cell RNA Sequencing Reveals the Immunological Profiles of Renal Allograft Rejection in Mice. <i>Frontiers in Immunology</i> , 2021, 12, 693608.	2.2	13

#	ARTICLE	IF	CITATIONS
2548	High Coexpression of the Ghrelin and LEAP2 Receptor GHSR With Pancreatic Polypeptide in Mouse and Human Islets. <i>Endocrinology</i> , 2021, 162, .	1.4	14
2549	Single-cell analysis of mosquito hemocytes identifies signatures of immune cell subtypes and cell differentiation. <i>ELife</i> , 2021, 10, .	2.8	31
2550	rPanglaoDB: an R package to download and merge labeled single-cell RNA-seq data from the PanglaoDB database. <i>Bioinformatics</i> , 2022, 38, 580-582.	1.8	7
2551	Regional specialization and fate specification of bone stromal cells in skeletal development. <i>Cell Reports</i> , 2021, 36, 109352.	2.9	59
2557	High-grade serous tubo-ovarian cancer refined with single-cell RNA sequencing: specific cell subtypes influence survival and determine molecular subtype classification. <i>Genome Medicine</i> , 2021, 13, 111.	3.6	70
2559	Identification and characterization of relapse-initiating cells in MLL-rearranged infant ALL by single-cell transcriptomics. <i>Leukemia</i> , 2022, 36, 58-67.	3.3	9
2560	Single-Cell Transcriptomics-Based Study of Transcriptional Regulatory Features in the Mouse Brain Vasculature. <i>BioMed Research International</i> , 2021, 2021, 1-15.	0.9	20
2561	Plaque-associated human microglia accumulate lipid droplets in a chimeric model of Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2021, 16, 50.	4.4	65
2562	Single-cell transcriptome and TCR profiling reveal activated and expanded T cell populations in Parkinson's disease. <i>Cell Discovery</i> , 2021, 7, 52.	3.1	51
2563	HLA-dependent heterogeneity and macrophage immunoproteasome activation during lung COVID-19 disease. <i>Journal of Translational Medicine</i> , 2021, 19, 290.	1.8	16
2564	Genetic Trends in Fusarium Head Blight Resistance from 20 Years of Winter Wheat Breeding and Cooperative Testing in the Northern U.S.A.. <i>Plant Disease</i> , 2022, 106, 364-372.	0.7	6
2567	The predicting roles of carcinoembryonic antigen and its underlying mechanism in the progression of coronavirus disease 2019. <i>Critical Care</i> , 2021, 25, 234.	2.5	10
2568	Neuronal VCP loss of function recapitulates FTLD-TDP pathology. <i>Cell Reports</i> , 2021, 36, 109399.	2.9	25
2569	CALLR: a semi-supervised cell-type annotation method for single-cell RNA sequencing data. <i>Bioinformatics</i> , 2021, 37, i51-i58.	1.8	17
2570	Molecular characterization of projection neuron subtypes in the mouse olfactory bulb. <i>ELife</i> , 2021, 10, .	2.8	22
2572	Single-cell transcriptomics of the early developing mouse cerebral cortex disentangle the spatial and temporal components of neuronal fate acquisition. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	32
2573	Blocking Short-Form Ron Eliminates Breast Cancer Metastases through Accumulation of Stem-Like CD4+ T Cells That Subvert Immunosuppression. <i>Cancer Discovery</i> , 2021, 11, 3178-3197.	7.7	7
2574	Single-Cell RNA-Sequencing Reveals Lineage-Specific Regulatory Changes of Fibroblasts and Vascular Endothelial Cells in Keloids. <i>Journal of Investigative Dermatology</i> , 2022, 142, 124-135.e11.	0.3	52

#	ARTICLE	IF	CITATIONS
2575	Key molecular alterations in endothelial cells in human glioblastoma uncovered through single-cell RNA sequencing. <i>JCI Insight</i> , 2021, 6, .	2.3	47
2576	Spatiotemporal dynamics of inner ear sensory and non-sensory cells revealed by single-cell transcriptomics. <i>Cell Reports</i> , 2021, 36, 109358.	2.9	31
2577	Single-cell RNA sequencing in vision research: Insights into human retinal health and disease. <i>Progress in Retinal and Eye Research</i> , 2021, 83, 100934.	7.3	24
2578	High-content single-cell combinatorial indexing. <i>Nature Biotechnology</i> , 2021, 39, 1574-1580.	9.4	39
2579	Gucy2d selectively marks inhibitory dynorphin neurons in the spinal dorsal horn but is dispensable for pain and itch sensitivity. <i>Pain Reports</i> , 2021, 6, e947.	1.4	2
2580	i2dash: Creation of Flexible, Interactive, and Web-Based Dashboards for Visualization of Omics Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 568-577.	3.0	1
2581	Characterizing the Metabolic and Immune Landscape of Non-small Cell Lung Cancer Reveals Prognostic Biomarkers Through Omics Data Integration. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 702112.	1.8	7
2583	Single-cell transcriptomics reveals immune response of intestinal cell types to viral infection. <i>Molecular Systems Biology</i> , 2021, 17, e9833.	3.2	24
2585	Dynamic Transcriptional and Epigenetic Changes Drive Cellular Plasticity in the Liver. <i>Hepatology</i> , 2021, 74, 444-457.	3.6	20
2586	Single-cell transcriptome of bronchoalveolar lavage fluid reveals sequential change of macrophages during SARS-CoV-2 infection in ferrets. <i>Nature Communications</i> , 2021, 12, 4567.	5.8	43
2587	A DNA repair pathway can regulate transcriptional noise to promote cell fate transitions. <i>Science</i> , 2021, 373, .	6.0	58
2588	Single-cell transcriptome analysis of the zebrafish embryonic trunk. <i>PLoS ONE</i> , 2021, 16, e0254024.	1.1	14
2591	Unstable regulatory T cells, enriched for na ⁺ ve and Nrp1 ^{neg} cells, are purged after fate challenge. <i>Science Immunology</i> , 2021, 6, .	5.6	13
2592	Cre Recombinase Driver Mice Reveal Lineage-Dependent and -Independent Expression of <i>Brs3</i> in the Mouse Brain. <i>ENeuro</i> , 2021, 8, ENEURO.0252-21.2021.	0.9	2
2593	Direct cardiac reprogramming comes of age: Recent advance and remaining challenges. <i>Seminars in Cell and Developmental Biology</i> , 2022, 122, 37-43.	2.3	10
2596	CDK7 and MITF repress a transcription program involved in survival and drug tolerance in melanoma. <i>EMBO Reports</i> , 2021, 22, e51683.	2.0	10
2597	Revealing consensus gene pathways associated with respiratory functions and disrupted by PM2.5 nitrate exposure at bulk tissue and single cell resolution. <i>Environmental Pollution</i> , 2021, 280, 116951.	3.7	12
2598	Single-Cell Analyses Reveal Diverse Mechanisms of Resistance to EGFR Tyrosine Kinase Inhibitors in Lung Cancer. <i>Cancer Research</i> , 2021, 81, 4835-4848.	0.4	31

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2599	Bifidobacteria-mediated immune system imprinting early in life. <i>Cell</i> , 2021, 184, 3884-3898.e11.	13.5	312
2600	CD14 Expressing Precursors Give Rise to Highly Functional Conventional Dendritic Cells for Use as Dendritic Cell Vaccine. <i>Cancers</i> , 2021, 13, 3818.	1.7	2
2601	Multi-Omics Analysis Showed the Clinical Value of Gene Signatures of C1QC+ and SPP1+ TAMs in Cervical Cancer. <i>Frontiers in Immunology</i> , 2021, 12, 694801.	2.2	21
2602	High-resolution characterization of gene function using single-cell CRISPR tiling screen. <i>Nature Communications</i> , 2021, 12, 4063.	5.8	23
2604	Creation of a Single Cell RNASeq Meta-Atlas to Define Human Liver Immune Homeostasis. <i>Frontiers in Immunology</i> , 2021, 12, 679521.	2.2	11
2608	Cannabinoid signaling promotes the deâ€differentiation and proliferation of MÃ¼ller gliaâ€derived progenitor cells. <i>Glia</i> , 2021, 69, 2503-2521.	2.5	20
2609	Dimensionality reduction by UMAP reinforces sample heterogeneity analysis in bulk transcriptomic data. <i>Cell Reports</i> , 2021, 36, 109442.	2.9	67
2612	Patterns of Tâ€Cell Phenotypes in Rheumatic Diseases From Singleâ€Cell Studies of Tissue. <i>ACR Open Rheumatology</i> , 2021, 3, 601-613.	0.9	8
2617	Single-cell RNA sequencing of freshly isolated bovine milk cells and cultured primary mammary epithelial cells. <i>Scientific Data</i> , 2021, 8, 177.	2.4	7
2618	LAG3 is not expressed in human and murine neurons and does not modulate Î±â€synucleinopathies. <i>EMBO Molecular Medicine</i> , 2021, 13, e14745.	3.3	44
2619	The loss of RNA N6-adenosine methyltransferase Mettl14 in tumor-associated macrophages promotes CD8+ Tâ€Cell dysfunction and tumor growth. <i>Cancer Cell</i> , 2021, 39, 945-957.e10.	7.7	124
2620	Single-cell RNA sequencing reveals distinct cellular factors for response to immunotherapy targeting CD73 and PD-1 in colorectal cancer. , 2021, 9, e002503.		36
2621	A human three-dimensional neural-perivascular â€assembloidâ€™ promotes astrocytic development and enables modeling of SARS-CoV-2 neuropathology. <i>Nature Medicine</i> , 2021, 27, 1600-1606.	15.2	94
2622	Neurotensin is an anti-thermogenic peptide produced by lymphatic endothelial cells. <i>Cell Metabolism</i> , 2021, 33, 1449-1465.e6.	7.2	38
2623	Identification of a special cell type as a determinant of the kidney tropism of SARSâ€CoVâ€2. <i>FEBS Journal</i> , 2021, 288, 5163-5178.	2.2	5
2624	Immune cell residency in the nasal mucosa may partially explain respiratory disease severity across the age range. <i>Scientific Reports</i> , 2021, 11, 15927.	1.6	16
2625	Spatiotemporal Immune Landscape of Colorectal Cancer Liver Metastasis at Single-Cell Level. <i>Cancer Discovery</i> , 2022, 12, 134-153.	7.7	286
2626	Single-cell sequencing of immune cells from anticitrullinated peptide antibody positive and negative rheumatoid arthritis. <i>Nature Communications</i> , 2021, 12, 4977.	5.8	73

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2632	Single cell RNA sequencing detects persistent cell type- and methylmercury exposure paradigm-specific effects in a human cortical neurodevelopmental model. <i>Food and Chemical Toxicology</i> , 2021, 154, 112288.	1.8	10
2633	The exon-junction complex helicase eIF4A3 controls cell fate via coordinated regulation of ribosome biogenesis and translational output. <i>Science Advances</i> , 2021, 7, .	4.7	25
2634	TooManyPeaks identifies drug-resistant-specific regulatory elements from single-cell leukemic epigenomes. <i>Cell Reports</i> , 2021, 36, 109575.	2.9	7
2635	NANOS2 suppresses the cell cycle by repressing mTORC1 activators in embryonic male germ cells. <i>iScience</i> , 2021, 24, 102890.	1.9	14
2636	Anti-PD-1/L1 lead-in before MAPK inhibitor combination maximizes antitumor immunity and efficacy. <i>Cancer Cell</i> , 2021, 39, 1375-1387.e6.	7.7	78
2637	Tracing colonic embryonic transcriptional profiles and their reactivation upon intestinal damage. <i>Cell Reports</i> , 2021, 36, 109484.	2.9	18
2639	A TALE/HOX code unlocks WNT signalling response towards paraxial mesoderm. <i>Nature Communications</i> , 2021, 12, 5136.	5.8	10
2640	Neuroinflammatory astrocyte subtypes in the mouse brain. <i>Nature Neuroscience</i> , 2021, 24, 1475-1487.	7.1	285
2641	A human forebrain organoid model of fragile X syndrome exhibits altered neurogenesis and highlights new treatment strategies. <i>Nature Neuroscience</i> , 2021, 24, 1377-1391.	7.1	80
2642	Sclerostin Depletion Induces Inflammation in the Bone Marrow of Mice. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9111.	1.8	5
2643	Attenuated activation of pulmonary immune cells in mRNA-1273â€“vaccinated hamsters after SARS-CoV-2 infection. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	23
2644	Glucocorticoids and Androgens Protect From Gastric Metaplasia by Suppressing Group 2 Innate Lymphoid Cell Activation. <i>Gastroenterology</i> , 2021, 161, 637-652.e4.	0.6	25
2645	The Application of Single-Cell RNA Sequencing in Mammalian Meiosis Studies. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 673642.	1.8	7
2646	Community-wide hackathons to identify central themes in single-cell multi-omics. <i>Genome Biology</i> , 2021, 22, 220.	3.8	9
2647	ExpressHeart: Web Portal to Visualize Transcriptome Profiles of Non-Cardiomyocyte Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8943.	1.8	3
2648	Transcriptional, Epigenetic, and Functional Reprogramming of Monocytes From Non-Human Primates Following Chronic Alcohol Drinking. <i>Frontiers in Immunology</i> , 2021, 12, 724015.	2.2	11
2649	Embedding to reference t-SNE space addresses batch effects in single-cell classification. <i>Machine Learning</i> , 2023, 112, 721-740.	3.4	10
2651	Epigenetic promoter alterations in GI tumour immune-editing and resistance to immune checkpoint inhibition. <i>Gut</i> , 2022, 71, 1277-1288.	6.1	23

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2652	Dendritic cells maintain anti-tumor immunity by positioning CD8 skin-resident memory T cells. <i>Life Science Alliance</i> , 2021, 4, e202101056.	1.3	16
2653	Liver-fibrosis-activated transcriptional networks govern hepatocyte reprogramming and intra-hepatic communication. <i>Cell Metabolism</i> , 2021, 33, 1685-1700.e9.	7.2	73
2656	Improving In Vitro Culture of Human Male Fetal Germ Cells. <i>Cells</i> , 2021, 10, 2033.	1.8	5
2658	Live cell tagging tracking and isolation for spatial transcriptomics using photoactivatable cell dyes. <i>Nature Communications</i> , 2021, 12, 4995.	5.8	25
2660	Unveiling Complexity and Multipotentiality of Early Heart Fields. <i>Circulation Research</i> , 2021, 129, 474-487.	2.0	50
2661	Single-cell transcriptomes reveal heterogeneity of high-grade serous ovarian carcinoma. <i>Clinical and Translational Medicine</i> , 2021, 11, e500.	1.7	34
2662	LISA2: Learning Complex Single-Cell Trajectory and Expression Trends. <i>Frontiers in Genetics</i> , 2021, 12, 681206.	1.1	1
2663	Helios represses megakaryocyte priming in hematopoietic stem and progenitor cells. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	4
2666	The canonical smooth muscle cell marker TAGLN is present in endothelial cells and is involved in angiogenesis. <i>Journal of Cell Science</i> , 2021, 134, .	1.2	20
2668	The MURAL collection of prostate cancer patient-derived xenografts enables discovery through preclinical models of uro-oncology. <i>Nature Communications</i> , 2021, 12, 5049.	5.8	33
2669	A systematic dissection of human primary osteoblasts in vivo at single-cell resolution. <i>Aging</i> , 2021, 13, 20629-20650.	1.4	19
2670	A comprehensive transcriptomic analysis of alternate interferon signaling pathways in peripheral blood mononuclear cells in rheumatoid arthritis. <i>Aging</i> , 2021, 13, 20511-20533.	1.4	5
2671	Macrophage balance fraction determines the degree of immunosuppression and metastatic ability of breast cancer. <i>International Immunopharmacology</i> , 2021, 97, 107682.	1.7	9
2672	Toward reproducible, scalable, and robust data analysis across multiplex tissue imaging platforms. <i>Cell Reports Methods</i> , 2021, 1, 100053.	1.4	22
2674	Single-cell RNA analysis identifies pre-migratory neural crest cells expressing markers of differentiated derivatives. <i>ELife</i> , 2021, 10, .	2.8	20
2676	H3K4 Trimethylation Is Required for Postnatal Pancreatic Endocrine Cell Functional Maturation. <i>Diabetes</i> , 2021, 70, 2568-2579.	0.3	5
2677	Spatially Distinct Reprogramming of the Tumor Microenvironment Based On Tumor Invasion in Diffuse-Type Gastric Cancers. <i>Clinical Cancer Research</i> , 2021, 27, 6529-6542.	3.2	50
2679	Spinal Cord Injury Induces Permanent Reprogramming of Microglia into a Disease-Associated State Which Contributes to Functional Recovery. <i>Journal of Neuroscience</i> , 2021, 41, 8441-8459.	1.7	25

#	ARTICLE	IF	CITATIONS
2680	The PEMDAC phase 2 study of pembrolizumab and entinostat in patients with metastatic uveal melanoma. <i>Nature Communications</i> , 2021, 12, 5155.	5.8	85
2681	Non-terminally exhausted tumor-resident memory HBV-specific T _H 1 cell responses correlate with relapse-free survival in hepatocellular carcinoma. <i>Immunity</i> , 2021, 54, 1825-1840.e7.	6.6	64
2682	Multimomics analyses reveal a critical role of selenium in controlling T _H 1 cell differentiation in Crohn's disease. <i>Immunity</i> , 2021, 54, 1728-1744.e7.	6.6	72
2683	Temporal omics analysis in Syrian hamsters unravel cellular effector responses to moderate COVID-19. <i>Nature Communications</i> , 2021, 12, 4869.	5.8	68
2684	Histone crotonylation regulates neural stem cell fate decisions by activating bivalent promoters. <i>EMBO Reports</i> , 2021, 22, e52023.	2.0	21
2686	HDAC1 is required for GATA-1 transcription activity, global chromatin occupancy and hematopoiesis. <i>Nucleic Acids Research</i> , 2021, 49, 9783-9798.	6.5	12
2687	AHR signaling is induced by infection with coronaviruses. <i>Nature Communications</i> , 2021, 12, 5148.	5.8	38
2688	Identification of neural oscillations and epileptiform changes in human brain organoids. <i>Nature Neuroscience</i> , 2021, 24, 1488-1500.	7.1	112
2689	Myonuclear transcriptional dynamics in response to exercise following satellite cell depletion. <i>IScience</i> , 2021, 24, 102838.	1.9	28
2690	Human sensorimotor organoids derived from healthy and amyotrophic lateral sclerosis stem cells form neuromuscular junctions. <i>Nature Communications</i> , 2021, 12, 4744.	5.8	69
2691	A comprehensive analysis of gene expression changes in a high replicate and open-source dataset of differentiating hiPSC-derived cardiomyocytes. <i>Scientific Reports</i> , 2021, 11, 15845.	1.6	28
2692	Mesomelic dysplasias associated with the HOXD locus are caused by regulatory reallocations. <i>Nature Communications</i> , 2021, 12, 5013.	5.8	14
2693	<i>Enterococcus</i> peptidoglycan remodeling promotes checkpoint inhibitor cancer immunotherapy. <i>Science</i> , 2021, 373, 1040-1046.	6.0	158
2694	A reference-free approach for cell type classification with scRNA-seq. <i>IScience</i> , 2021, 24, 102855.	1.9	6
2695	STAT5 Represses a STAT3-Independent Th17-like Program during Th9 Cell Differentiation. <i>Journal of Immunology</i> , 2021, 207, 1265-1274.	0.4	7
2696	Amnion signals are essential for mesoderm formation in primates. <i>Nature Communications</i> , 2021, 12, 5126.	5.8	59
2697	Reconstruction of lateral root formation through single-cell RNA sequencing reveals order of tissue initiation. <i>Molecular Plant</i> , 2021, 14, 1362-1378.	3.9	44
2699	Supervised application of internal validation measures to benchmark dimensionality reduction methods in scRNA-seq data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	9

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2702	Study of cellular heterogeneity and differential dynamics of autophagy in human embryonic kidney development by single-cell RNA sequencing. <i>Cancer Cell International</i> , 2021, 21, 460.	1.8	3
2704	MondoAâ€™Thioredoxin-Interacting Protein Axis Maintains Regulatory T-Cell Identity and Function in Colorectal Cancer Microenvironment. <i>Gastroenterology</i> , 2021, 161, 575-591.e16.	0.6	44
2705	Single-cell analysis of cell fate bifurcation in the chordate <i>Ciona</i> . <i>BMC Biology</i> , 2021, 19, 180.	1.7	6
2706	Granzyme A and CD160 expression delineates ILC1 with graded functions in the mouse liver. <i>European Journal of Immunology</i> , 2021, 51, 2568-2575.	1.6	28
2707	From bench to bedside: Single-cell analysis for cancer immunotherapy. <i>Cancer Cell</i> , 2021, 39, 1062-1080.	7.7	67
2708	Myeloid-Derived Suppressive Cells Deficient in Liver X Receptor Î± Protected From Autoimmune Hepatitis. <i>Frontiers in Immunology</i> , 2021, 12, 732102.	2.2	5
2709	Identification of asthma-associated microRNAs in bronchial biopsies. <i>European Respiratory Journal</i> , 2022, 59, 2101294.	3.1	19
2711	Profound Treg perturbations correlate with COVID-19 severity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	104
2712	Heterogeneity of HSCs in a Mouse Model of NASH. <i>Hepatology</i> , 2021, 74, 667-685.	3.6	71
2713	Sc-compReg enables the comparison of gene regulatory networks between conditions using single-cell data. <i>Nature Communications</i> , 2021, 12, 4763.	5.8	12
2715	DeepFeature: feature selection in nonimage data using convolutional neural network. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	31
2716	deepMNN: Deep Learning-Based Single-Cell RNA Sequencing Data Batch Correction Using Mutual Nearest Neighbors. <i>Frontiers in Genetics</i> , 2021, 12, 708981.	1.1	14
2717	NPAS4 regulates the transcriptional response of the suprachiasmatic nucleus to light and circadian behavior. <i>Neuron</i> , 2021, 109, 3268-3282.e6.	3.8	46
2718	Spatially Resolved Immunometabolism to Understand Infectious Disease Progression. <i>Frontiers in Microbiology</i> , 2021, 12, 709728.	1.5	6
2719	A Catalogus Immune Muris of the mouse immune responses to diverse pathogens. <i>Cell Death and Disease</i> , 2021, 12, 798.	2.7	0
2720	Roles of the Immune/Methylation/Autophagy Landscape on Single-Cell Genotypes and Stroke Risk in Breast Cancer Microenvironment. <i>Oxidative Medicine and Cellular Longevity</i> , 2021, 2021, 1-32.	1.9	23
2721	Distinct immune microenvironment profiles of therapeutic responders emerge in combined TGFÎ²/PD-L1 blockade-treated squamous cell carcinoma. <i>Communications Biology</i> , 2021, 4, 1005.	2.0	10
2725	Single-Cell RNA-Sequencing Portraying Functional Diversity and Clinical Implications of IFI6 in Ovarian Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 677697.	1.8	11

#	ARTICLE	IF	CITATIONS
2726	Extracardiac Progenitors: Moving Beyond the First and Second Heart Field. <i>Circulation Research</i> , 2021, 129, 488-490.	2.0	0
2728	Single-cell omics: Overview, analysis, and application in biomedical science. <i>Journal of Cellular Biochemistry</i> , 2021, 122, 1571-1578.	1.2	18
2729	A clinically applicable integrative molecular classification of meningiomas. <i>Nature</i> , 2021, 597, 119-125.	13.7	180
2730	Molecular characteristics and spatial distribution of adult human corneal cell subtypes. <i>Scientific Reports</i> , 2021, 11, 16323.	1.6	33
2731	Genome accessibility dynamics in response to phosphate limitation is controlled by the PHR1 family of transcription factors in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	38
2733	Improved integration of single-cell transcriptome and surface protein expression by LinQ-View. <i>Cell Reports Methods</i> , 2021, 1, 100056.	1.4	10
2734	Silencing Myeloid Netrin-1 Induces Inflammation Resolution and Plaque Regression. <i>Circulation Research</i> , 2021, 129, 530-546.	2.0	25
2735	Integrative Analysis Identified MCT4 as an Independent Prognostic Factor for Bladder Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 704857.	1.3	7
2736	Lung Epithelial Signaling Mediates Early Vaccine-Induced CD4 ⁺ T Cell Activation and <i>Mycobacterium tuberculosis</i> Control. <i>MBio</i> , 2021, 12, e0146821.	1.8	11
2737	Overexpressing low-density lipoprotein receptor reduces tau-associated neurodegeneration in relation to apoE-linked mechanisms. <i>Neuron</i> , 2021, 109, 2413-2426.e7.	3.8	57
2738	The CD155/TIGIT axis promotes and maintains immune evasion in neoantigen-expressing pancreatic cancer. <i>Cancer Cell</i> , 2021, 39, 1342-1360.e14.	7.7	119
2739	Characterization of human FDCs reveals regulation of T cells and antigen presentation to B cells. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	30
2740	FastCount. , 2021, , .		0
2741	FRMC: a fast and robust method for the imputation of scRNA-seq data. <i>RNA Biology</i> , 2021, , 1-10.	1.5	1
2742	Clinical Perspectives of Single-Cell RNA Sequencing. <i>Biomolecules</i> , 2021, 11, 1161.	1.8	11
2744	Towards high throughput and high information coverage: advanced single-cell mass spectrometric techniques. <i>Analytical and Bioanalytical Chemistry</i> , 2022, 414, 219-233.	1.9	10
2745	TCF-1 controls Treg cell functions that regulate inflammation, CD8 ⁺ T cell cytotoxicity and severity of colon cancer. <i>Nature Immunology</i> , 2021, 22, 1152-1162.	7.0	42
2747	Foxm1 regulates neural progenitor fate during spinal cord regeneration. <i>EMBO Reports</i> , 2021, 22, e50932.	2.0	9

#	ARTICLE	IF	CITATIONS
2749	Developmental HCN channelopathy results in decreased neural progenitor proliferation and microcephaly in mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	6
2751	An in vitro platform supports generation of human innate lymphoid cells from CD34+ hematopoietic progenitors that recapitulate ex vivo identity. <i>Immunity</i> , 2021, 54, 2417-2432.e5.	6.6	32
2752	Stochastic gene expression drives mesophyll protoplast regeneration. <i>Science Advances</i> , 2021, 7, .	4.7	44
2754	Single-cell RNA-seq of T Cells in ALL Patients Reveals an Exhausted Subset with Remarkable Heterogeneity. <i>Advanced Science</i> , 2021, 8, e2101447.	5.6	24
2755	Single-cell transcriptomic landscape reveals tumor specific innate lymphoid cells associated with colorectal cancer progression. <i>Cell Reports Medicine</i> , 2021, 2, 100353.	3.3	44
2756	ELAVL4, splicing, and glutamatergic dysfunction precede neuron loss in MAPT mutation cerebral organoids. <i>Cell</i> , 2021, 184, 4547-4563.e17.	13.5	73
2757	Single-cell transcriptomic analyses of T cells in chronic HCV-infected patients dominated by DAA-induced interferon signaling changes. <i>PLoS Pathogens</i> , 2021, 17, e1009799.	2.1	7
2758	Elevated Fibronectin Levels in Profibrotic CD14+ Monocytes and CD14+ Macrophages in Systemic Sclerosis. <i>Frontiers in Immunology</i> , 2021, 12, 642891.	2.2	20
2759	Importins: Diverse roles in male fertility. <i>Seminars in Cell and Developmental Biology</i> , 2022, 121, 82-98.	2.3	10
2760	Tissue signals imprint Aiolos expression in ILC2s to modulate type 2 immunity. <i>Mucosal Immunology</i> , 2021, 14, 1306-1322.	2.7	15
2762	Allosteric inhibition reveals SHP2-mediated tumor immunosuppression in colon cancer by single-cell transcriptomics. <i>Acta Pharmaceutica Sinica B</i> , 2022, 12, 149-166.	5.7	25
2763	Single-cell RNA sequencing of intramedullary canal tissue to improve methods for studying fracture repair biology. <i>BioTechniques</i> , 2021, 71, 431-438.	0.8	1
2764	CXCR6 positions cytotoxic T cells to receive critical survival signals in the tumor microenvironment. <i>Cell</i> , 2021, 184, 4512-4530.e22.	13.5	180
2765	Exploring tissue architecture using spatial transcriptomics. <i>Nature</i> , 2021, 596, 211-220.	13.7	593
2766	Single-cell RNA-seq analysis identifies unique chondrocyte subsets and reveals involvement of ferroptosis in human intervertebral disc degeneration. <i>Osteoarthritis and Cartilage</i> , 2021, 29, 1324-1334.	0.6	62
2768	PsiNorm: a scalable normalization for single-cell RNA-seq data. <i>Bioinformatics</i> , 2021, 38, 164-172.	1.8	14
2769	Single-cell transcriptomics reveal DHX9 in mature B cell as a dynamic network biomarker before lymph node metastasis in CRC. <i>Molecular Therapy - Oncolytics</i> , 2021, 22, 495-506.	2.0	7
2770	Single cell transcriptomic analysis of external genitalia reveals complex and sexually dimorphic cell populations in the early genital tubercle. <i>Developmental Biology</i> , 2021, 477, 145-154.	0.9	5

#	ARTICLE	IF	CITATIONS
2771	Glycomic and glycotranscriptomic profiling of mucin-type O-glycans in planarian <i>Schmidtea mediterranea</i> . <i>Glycobiology</i> , 2021, , .	1.3	0
2773	Macrophage-derived interleukin-6 is necessary and sufficient for choroidal angiogenesis. <i>Scientific Reports</i> , 2021, 11, 18084.	1.6	20
2774	The establishment of variant surface glycoprotein monoallelic expression revealed by single-cell RNA-seq of <i>Trypanosoma brucei</i> in the tsetse fly salivary glands. <i>PLoS Pathogens</i> , 2021, 17, e1009904.	2.1	29
2775	Fluorescent Multiplex Immunohistochemistry Coupled With Other State-Of-The-Art Techniques to Systematically Characterize the Tumor Immune Microenvironment. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 673042.	1.6	19
2776	Oviduct epithelial cells constitute two developmentally distinct lineages that are spatially separated along the distal-proximal axis. <i>Cell Reports</i> , 2021, 36, 109677.	2.9	27
2778	Troy/Tnfrsf19 marks epidermal cells that govern interfollicular epidermal renewal and cornification. <i>Stem Cell Reports</i> , 2021, 16, 2379-2394.	2.3	2
2779	Combinatorial transcription factor profiles predict mature and functional human islet β 1 and β 2 cells. <i>JCI Insight</i> , 2021, 6, .	2.3	22
2780	Radiation-activated secretory proteins of Scgb1a1+ club cells increase the efficacy of immune checkpoint blockade in lung cancer. <i>Nature Cancer</i> , 2021, 2, 919-931.	5.7	26
2781	Mapping Gene Expression in the Spatial Dimension. <i>Small Methods</i> , 2021, 5, e2100722.	4.6	9
2783	Single-Cell Analyses Reveal Mechanisms of Cancer Stem Cell Maintenance and Epithelialâ€“Mesenchymal Transition in Recurrent Bladder Cancer. <i>Clinical Cancer Research</i> , 2022, 27, 6265-6278.	3.2	43
2784	Attenuated monoamine oxidase a impairs endometrial receptivity in women with adenomyosis via downregulation of FOXO1. <i>Biology of Reproduction</i> , 2021, 105, 1443-1457.	1.2	8
2785	Integration and gene co-expression network analysis of scRNA-seq transcriptomes reveal heterogeneity and key functional genes in human spermatogenesis. <i>Scientific Reports</i> , 2021, 11, 19089.	1.6	12
2787	Singleâ€“cell transcriptomic landscape of cardiac neural crest cell derivatives during development. <i>EMBO Reports</i> , 2021, 22, e52389.	2.0	13
2788	Dysregulation of mitochondrial and proteolysosomal genes in Parkinsonâ€™s disease myeloid cells. <i>Nature Aging</i> , 2021, 1, 850-863.	5.3	16
2791	Olfactory bulb astrocytes mediate sensory circuit processing through Sox9 in the mouse brain. <i>Nature Communications</i> , 2021, 12, 5230.	5.8	24
2794	Transcriptional progression during meiotic prophase I reveals sex-specific features and X chromosome dynamics in human fetal female germline. <i>PLoS Genetics</i> , 2021, 17, e1009773.	1.5	8
2795	Resolving monocytes generated through TRAM deletion attenuate atherosclerosis. <i>JCI Insight</i> , 2021, 6, .	2.3	18
2796	Recipient APOL1 risk alleles associate with death-censored renal allograft survival and rejection episodes. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	33

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2797	Early IFN- γ signatures and persistent dysfunction are distinguishing features of NK cells in severe COVID-19. <i>Immunity</i> , 2021, 54, 2650-2669.e14.	6.6	145
2798	FlowCT for the analysis of large immunophenotypic data sets and biomarker discovery in cancer immunology. <i>Blood Advances</i> , 2022, 6, 690-703.	2.5	19
2799	Autoimmunity affecting the biliary tract fuels the immunosurveillance of cholangiocarcinoma. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	20
2800	Distinct human Langerhans cell subsets orchestrate reciprocal functions and require different developmental regulation. <i>Immunity</i> , 2021, 54, 2305-2320.e11.	6.6	38
2802	Human microglia states are conserved across experimental models and regulate neural stem cell responses in chimeric organoids. <i>Cell Stem Cell</i> , 2021, 28, 2153-2166.e6.	5.2	98
2803	A subset of Kupffer cells regulates metabolism through the expression of CD36. <i>Immunity</i> , 2021, 54, 2101-2116.e6.	6.6	99
2804	Single-cell ATAC and RNA sequencing reveal pre-existing and persistent cells associated with prostate cancer relapse. <i>Nature Communications</i> , 2021, 12, 5307.	5.8	58
2806	Epithelial memory of inflammation limits tissue damage while promoting pancreatic tumorigenesis. <i>Science</i> , 2021, 373, eabj0486.	6.0	99
2807	Pro-inflammatory and proliferative microglia drive progression of glioblastoma. <i>Cell Reports</i> , 2021, 36, 109718.	2.9	72
2809	Discovery and construction of prognostic model for clear cell renal cell carcinoma based on single-cell and bulk transcriptome analysis. <i>Translational Andrology and Urology</i> , 2021, 10, 3540-3554.	0.6	3
2810	Impaired local intrinsic immunity to SARS-CoV-2 infection in severe COVID-19. <i>Cell</i> , 2021, 184, 4713-4733.e22.	13.5	206
2811	Semicoordinated allelic-bursting shape dynamic random monoallelic expression in pregastrulation embryos. <i>iScience</i> , 2021, 24, 102954.	1.9	9
2812	MLG: multilayer graph clustering for multi-condition scRNA-seq data. <i>Nucleic Acids Research</i> , 2021, 49, e127-e127.	6.5	2
2814	Modeling glioblastoma heterogeneity as a dynamic network of cell states. <i>Molecular Systems Biology</i> , 2021, 17, e10105.	3.2	19
2816	Functional coordination of non- α myocytes plays a key role in adult zebrafish heart regeneration. <i>EMBO Reports</i> , 2021, 22, e52901.	2.0	17
2818	Smoking shifts human small airway epithelium club cells toward a lesser differentiated population. <i>Npj Genomic Medicine</i> , 2021, 6, 73.	1.7	12
2821	Antigen dominance hierarchies shape TCF1+ progenitor CD8 T cell phenotypes in tumors. <i>Cell</i> , 2021, 184, 4996-5014.e26.	13.5	84
2822	NMDARs Drive the Expression of Neuropsychiatric Disorder Risk Genes Within GABAergic Interneuron Subtypes in the Juvenile Brain. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 712609.	1.4	9

#	ARTICLE	IF	CITATIONS
2823	SCReadCounts: estimation of cell-level SNVs expression from scRNA-seq data. BMC Genomics, 2021, 22, 689.	1.2	13
2824	A pathogenic DMC1 frameshift mutation causes nonobstructive azoospermia but not primary ovarian insufficiency in humans. Molecular Human Reproduction, 2021, 27, .	1.3	9
2825	Identifying Cellâ€Typeâ€Specific Metabolic Signatures Using Transcriptome and Proteome Analyses. Current Protocols, 2021, 1, e245.	1.3	3
2826	Single-cell RNA sequencing reveals markers of disease progression in primary cutaneous T-cell lymphoma. Molecular Cancer, 2021, 20, 124.	7.9	24
2828	Biogenesis of P-TEFb in CD4+ T cells to reverse HIV latency is mediated by protein kinase C (PKC)-independent signaling pathways. PLoS Pathogens, 2021, 17, e1009581.	2.1	13
2830	CCR2 deficiency alters activation of microglia subsets in traumatic brain injury. Cell Reports, 2021, 36, 109727.	2.9	23
2833	Podocyte-specific KLF4 is required to maintain parietal epithelial cell quiescence in the kidney. Science Advances, 2021, 7, eabg6600.	4.7	12
2834	Comprehensive Analysis of a Nine-Gene Signature Related to Tumor Microenvironment in Lung Adenocarcinoma. Frontiers in Cell and Developmental Biology, 2021, 9, 700607.	1.8	23
2835	A chemical biology approach reveals a dependency of glioblastoma on biotin distribution. Science Advances, 2021, 7, eabf6033.	4.7	10
2836	Role of hypothalamic MAPK/ERK signaling and central action of FGF1 in diabetes remission. IScience, 2021, 24, 102944.	1.9	18
2839	Programmatic introduction of parenchymal cell types into blood vessel organoids. Stem Cell Reports, 2021, 16, 2432-2441.	2.3	11
2840	Multomics Analysis Reveals the Prognostic Non-tumor Cell Landscape in Glioblastoma Niches. Frontiers in Genetics, 2021, 12, 741325.	1.1	0
2841	Identification of immune correlates of fatal outcomes in critically ill COVID-19 patients. PLoS Pathogens, 2021, 17, e1009804.	2.1	39
2842	A role for translational regulation by S6 kinase and a downstream target in inflammatory pain. British Journal of Pharmacology, 2021, 178, 4675-4690.	2.7	5
2843	The nasal symbiont Staphylococcus species restricts the transcription of SARS-CoV-2 entry factors in human nasal epithelium. IScience, 2021, 24, 103172.	1.9	5
2844	SATB2 preserves colon stem cell identity and mediates ileum-colon conversion via enhancer remodeling. Cell Stem Cell, 2022, 29, 101-115.e10.	5.2	31
2845	Disruption of the endopeptidase ADAM10-Notch signaling axis leads to skin dysbiosis and innate lymphoid cell-mediated hair follicle destruction. Immunity, 2021, 54, 2321-2337.e10.	6.6	35
2846	A harmonized atlas of mouse spinal cord cell types and their spatial organization. Nature Communications, 2021, 12, 5722.	5.8	116

#	ARTICLE	IF	CITATIONS
2847	The developmental hourglass model is applicable to the spinal cord based on single-cell transcriptomes and non-conserved cis-regulatory elements. <i>Development Growth and Differentiation</i> , 2021, 63, 372-391.	0.6	2
2849	Single-cell analysis defines a pancreatic fibroblast lineage that supports anti-tumor immunity. <i>Cancer Cell</i> , 2021, 39, 1227-1244.e20.	7.7	158
2850	IL13 Acts Directly on Gastric Epithelial Cells to Promote Metaplasia Development During Chronic Gastritis. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2022, 13, 623-642.	2.3	19
2851	Improved SNV Discovery in Barcode-Stratified scRNA-seq Alignments. <i>Genes</i> , 2021, 12, 1558.	1.0	7
2852	Identifying Risk Factors for Secondary Infection Post-SARS-CoV-2 Infection in Patients With Severe and Critical COVID-19. <i>Frontiers in Immunology</i> , 2021, 12, 715023.	2.2	9
2853	Single-Cell RNA Sequencing Analysis Reveals Greater Epithelial Ridge Cells Degeneration During Postnatal Development of Cochlea in Rats. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 719491.	1.8	4
2855	A comparison of deep learning-based pre-processing and clustering approaches for single-cell RNA sequencing data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	14
2856	Complement factor C1q mediates sleep spindle loss and epileptic spikes after mild brain injury. <i>Science</i> , 2021, 373, eabj2685.	6.0	55
2858	IL-33 causes thermogenic failure in aging by expanding dysfunctional adipose ILC2. <i>Cell Metabolism</i> , 2021, 33, 2277-2287.e5.	7.2	42
2859	Detailed characterization of the transcriptome of single B cells in mantle cell lymphoma suggesting a potential use for SOX4. <i>Scientific Reports</i> , 2021, 11, 19092.	1.6	3
2860	scDEA: differential expression analysis in single-cell RNA-sequencing data via ensemble learning. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	12
2861	Single-Cell Analysis Reveals Major Histocompatibility Complex II-Expressing Keratinocytes in Pressure Ulcers with Worse Healing Outcomes. <i>Journal of Investigative Dermatology</i> , 2022, 142, 705-716.	0.3	14
2862	Rare variants in the endocytic pathway are associated with Alzheimer's disease, its related phenotypes, and functional consequences. <i>PLoS Genetics</i> , 2021, 17, e1009772.	1.5	1
2867	Cardiac Myoediting Attenuates Cardiac Abnormalities in Human and Mouse Models of Duchenne Muscular Dystrophy. <i>Circulation Research</i> , 2021, 129, 602-616.	2.0	16
2868	Fatal cytokine release syndrome by an aberrant FLIP/STAT3 axis. <i>Cell Death and Differentiation</i> , 2022, 29, 420-438.	5.0	14
2869	Single-cell RNA sequencing reveals the epithelial cell heterogeneity and invasive subpopulation in human bladder cancer. <i>International Journal of Cancer</i> , 2021, 149, 2099-2115.	2.3	40
2870	Integrin β 7+ T cells direct intestinal stem cell fate decisions via adhesion signaling. <i>Cell Research</i> , 2021, 31, 1291-1307.	5.7	13
2871	Molecular Profiling of Coronavirus Disease 2019 (COVID-19) Autopsies Uncovers Novel Disease Mechanisms. <i>American Journal of Pathology</i> , 2021, 191, 2064-2071.	1.9	14

#	ARTICLE	IF	CITATIONS
2872	Disabling de novo DNA methylation in embryonic stem cells allows an illegitimate fate trajectory. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	14
2873	A cell-type-specific atlas of the inner ear transcriptional response to acoustic trauma. <i>Cell Reports</i> , 2021, 36, 109758.	2.9	59
2874	The landscape of tumor cell states and ecosystems in diffuse large B cell lymphoma. <i>Cancer Cell</i> , 2021, 39, 1422-1437.e10.	7.7	102
2876	Atlas of clinically distinct cell states and ecosystems across human solid tumors. <i>Cell</i> , 2021, 184, 5482-5496.e28.	13.5	116
2878	Fetal Brain Elicits Sexually Conflicting Transcriptional Response to the Ablation of Uterine Forkhead Box A2 (Foxa2) in Mice. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9693.	1.8	8
2880	Single-nuclei chromatin profiling of ventral midbrain reveals cell identity transcription factors and cell-type-specific gene regulatory variation. <i>Epigenetics and Chromatin</i> , 2021, 14, 43.	1.8	5
2881	Cannabinoid receptor 1 signaling in hepatocytes and stellate cells does not contribute to NAFLD. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	23
2882	Spatially organized multicellular immune hubs in human colorectal cancer. <i>Cell</i> , 2021, 184, 4734-4752.e20.	13.5	256
2884	Hedgehog interacting proteinâ€‘expressing lung fibroblasts suppress lymphocytic inflammation in mice. <i>JCI Insight</i> , 2021, 6, .	2.3	9
2885	Nrf1 promotes heart regeneration and repair by regulating proteostasis and redox balance. <i>Nature Communications</i> , 2021, 12, 5270.	5.8	59
2886	TIPE2 is a checkpoint of natural killer cell maturation and antitumor immunity. <i>Science Advances</i> , 2021, 7, eabi6515.	4.7	20
2887	Singleâ€‘nucleus RNA sequencing of plant tissues using a nanowellâ€‘based system. <i>Plant Journal</i> , 2021, 108, 859-869.	2.8	27
2888	Tumor microenvironment is associated with clinical and genetic properties of diffuse gliomas and predicts overall survival. <i>Cancer Immunology, Immunotherapy</i> , 2022, 71, 953-966.	2.0	8
2889	Single cell RNA sequencing (scRNA-Seq) deciphering pathological alterations in streptozotocin-induced diabetic retinas. <i>Experimental Eye Research</i> , 2021, 210, 108718.	1.2	23
2890	A single-cell atlas of liver metastases of colorectal cancer reveals reprogramming of the tumor microenvironment in response to preoperative chemotherapy. <i>Cell Discovery</i> , 2021, 7, 80.	3.1	55
2891	AMULET: a novel read count-based method for effective multiplet detection from single nucleus ATAC-seq data. <i>Genome Biology</i> , 2021, 22, 252.	3.8	36
2894	Single-cell RNA-seq unravels alterations of the human spermatogonial stem cell compartment in patients with impaired spermatogenesis. <i>Cell Reports Medicine</i> , 2021, 2, 100395.	3.3	33
2895	Single-nucleus transcriptome analysis reveals cell-type-specific molecular signatures across reward circuitry in the human brain. <i>Neuron</i> , 2021, 109, 3088-3103.e5.	3.8	95

#	ARTICLE	IF	CITATIONS
2897	The Prognostic Model Based on Tumor Cell Evolution Trajectory Reveals a Different Risk Group of Hepatocellular Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 737723.	1.8	3
2899	A lymphocyte–microglia–astrocyte axis in chronic active multiple sclerosis. <i>Nature</i> , 2021, 597, 709-714.	13.7	307
2900	Learning interpretable cellular and gene signature embeddings from single-cell transcriptomic data. <i>Nature Communications</i> , 2021, 12, 5261.	5.8	38
2903	NG2 glia-derived GABA release tunes inhibitory synapses and contributes to stress-induced anxiety. <i>Nature Communications</i> , 2021, 12, 5740.	5.8	43
2904	A single-cell tumor immune atlas for precision oncology. <i>Genome Research</i> , 2021, 31, 1913-1926.	2.4	87
2905	Shortening of 3' UTRs in most cell types composing tumor tissues implicates alternative polyadenylation in protein metabolism. <i>Rna</i> , 2021, 27, 1459-1470.	1.6	6
2907	A molecular toolkit for superorganisms. <i>Trends in Genetics</i> , 2021, 37, 846-859.	2.9	6
2908	Molecular diversity of diencephalic astrocytes reveals adult astrogenesis regulated by Smad4. <i>EMBO Journal</i> , 2021, 40, e107532.	3.5	26
2909	Integrating single-cell datasets with ambiguous batch information by incorporating molecular network features. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	5
2910	Single-Cell Transcriptome Sequencing and Proteomics Reveal Neonatal Ileum Dynamic Developmental Potentials. <i>MSystems</i> , 2021, 6, e0072521.	1.7	11
2911	Intricacies of single-cell multi-omics data integration. <i>Trends in Genetics</i> , 2022, 38, 128-139.	2.9	25
2912	Fine-tuned repression of Drp1-driven mitochondrial fission primes a stem/progenitor-like state to support neoplastic transformation. <i>ELife</i> , 2021, 10, .	2.8	7
2914	Resident memory CD8+ T cells in regional lymph nodes mediate immunity to metastatic melanoma. <i>Immunity</i> , 2021, 54, 2117-2132.e7.	6.6	50
2916	Single-cell and single-nucleus RNA-seq uncovers shared and distinct axes of variation in dorsal LGN neurons in mice, non-human primates, and humans. <i>ELife</i> , 2021, 10, .	2.8	41
2919	Tumor-Infiltrating PD-1hiCD8+-T-Cell Signature as an Effective Biomarker for Immune Checkpoint Inhibitor Therapy Response Across Multiple Cancers. <i>Frontiers in Oncology</i> , 2021, 11, 695006.	1.3	9
2920	Proneural genes define ground-state rules to regulate neurogenic patterning and cortical folding. <i>Neuron</i> , 2021, 109, 2847-2863.e11.	3.8	26
2922	Use of human tissue stem cell-derived organoid cultures to model enterohepatic circulation. <i>American Journal of Physiology - Renal Physiology</i> , 2021, 321, G270-G279.	1.6	7
2924	Evaluation of some aspects in supervised cell type identification for single-cell RNA-seq: classifier, feature selection, and reference construction. <i>Genome Biology</i> , 2021, 22, 264.	3.8	21

#	ARTICLE	IF	CITATIONS
2925	Single-Cell RNA Sequencing Identifies New Inflammation-Promoting Cell Subsets in Asian Patients With Chronic Periodontitis. <i>Frontiers in Immunology</i> , 2021, 12, 711337.	2.2	22
2926	Developmental programming and lineage branching of early human telencephalon. <i>EMBO Journal</i> , 2021, 40, e107277.	3.5	10
2927	Microdissection of the Bulk Transcriptome at Single-Cell Resolution Reveals Clinical Significance and Myeloid Cells Heterogeneity in Lung Adenocarcinoma. <i>Frontiers in Immunology</i> , 2021, 12, 723908.	2.2	1
2929	Dysregulation of cholesterol homeostasis in human lung cancer tissue and tumour-associated macrophages. <i>EBioMedicine</i> , 2021, 72, 103578.	2.7	43
2930	Enhanced chemo-photodynamic therapy of an enzyme-responsive prodrug in bladder cancer patient-derived xenograft models. <i>Biomaterials</i> , 2021, 277, 121061.	5.7	62
2931	Intrathymic differentiation of natural antibody-producing plasma cells in human neonates. <i>Nature Communications</i> , 2021, 12, 5761.	5.8	12
2932	Immune checkpoint blockade sensitivity and progression-free survival associates with baseline CD8 ⁺ T cell clone size and cytotoxicity. <i>Science Immunology</i> , 2021, 6, eabj8825.	5.6	41
2933	Single-Cell RNA Sequencing Reveals Endothelial Cell Transcriptome Heterogeneity Under Homeostatic Laminar Flow. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2021, 41, 2575-2584.	1.1	19
2934	Charting oncogenicity of genes and variants across lineages via multiplexed screens in teratomas. <i>IScience</i> , 2021, 24, 103149.	1.9	2
2935	Immunogenomics of Colorectal Cancer Response to Checkpoint Blockade: Analysis of the KEYNOTE 177 Trial and Validation Cohorts. <i>Gastroenterology</i> , 2021, 161, 1179-1193.	0.6	62
2936	Advances in spatial transcriptomic data analysis. <i>Genome Research</i> , 2021, 31, 1706-1718.	2.4	102
2937	G-CSF secreted by mutant IDH1 glioma stem cells abolishes myeloid cell immunosuppression and enhances the efficacy of immunotherapy. <i>Science Advances</i> , 2021, 7, eabh3243.	4.7	53
2938	Antitumor immune effects of preoperative sitravatinib and nivolumab in oral cavity cancer: SNOW window-of-opportunity study. , 2021, 9, e003476.		20
2939	Nonbone Marrow CD34 ⁺ Cells Are Crucial for Endothelial Repair of Injured Artery. <i>Circulation Research</i> , 2021, 129, e146-e165.	2.0	28
2940	Evolutionary cell type mapping with single-cell genomics. <i>Trends in Genetics</i> , 2021, 37, 919-932.	2.9	43
2942	Subtype heterogeneity and epigenetic convergence in neuroendocrine prostate cancer. <i>Nature Communications</i> , 2021, 12, 5775.	5.8	59
2943	A survey of the mouse hindbrain in the fed and fasted states using single-nucleus RNA sequencing. <i>Molecular Metabolism</i> , 2021, 53, 101240.	3.0	41
2944	Myeloid cell-specific Irf5 deficiency stabilizes atherosclerotic plaques in Apoe mice. <i>Molecular Metabolism</i> , 2021, 53, 101250.	3.0	6

#	ARTICLE	IF	CITATIONS
2945	Single cell functional genomics reveals plasticity of subcutaneous white adipose tissue (WAT) during early postnatal development. <i>Molecular Metabolism</i> , 2021, 53, 101307.	3.0	14
2946	Overexpression of transposable elements is associated with immune evasion and poor outcome in colorectal cancer. <i>European Journal of Cancer</i> , 2021, 157, 94-107.	1.3	12
2947	Combinatorial therapy in tumor microenvironment: Where do we stand?. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2021, 1876, 188585.	3.3	48
2948	Acquisition of murine splenic myeloid cells for protein and gene expression profiling by advanced flow cytometry and CITE-seq. <i>STAR Protocols</i> , 2021, 2, 100842.	0.5	2
2949	Delineating chromatin accessibility re-patterning at single cell level during early stage of direct cardiac reprogramming. <i>Journal of Molecular and Cellular Cardiology</i> , 2022, 162, 62-71.	0.9	19
2953	Regulation of cancer stem cells in triple negative breast cancer. , 2021, 4, 321-342.		28
2954	The evolution of alternative splicing in glioblastoma under therapy. <i>Genome Biology</i> , 2021, 22, 48.	3.8	23
2956	Chromatin accessibility profiling methods. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	95
2957	Codependency and mutual exclusivity for gene community detection from sparse single-cell transcriptome data. <i>Nucleic Acids Research</i> , 2021, 49, e104-e104.	6.5	3
2958	Single-Cell Transcription Profiling of the Developing <i>Drosophila</i> Heart Reveals New Cardiac Cell Types and Conserved Pathways for Cardiomyocyte Maturation. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
2959	Traumatic Brain Injury Causes Chronic Cortical Inflammation and Neuronal Dysfunction Mediated by Microglia. <i>Journal of Neuroscience</i> , 2021, 41, 1597-1616.	1.7	168
2960	Distinct metabolic programs established in the thymus control effector functions of $\hat{\gamma}$ T cell subsets in tumor microenvironments. <i>Nature Immunology</i> , 2021, 22, 179-192.	7.0	99
2962	Integrating human brain proteomes with genome-wide association data implicates new proteins in Alzheimer's disease pathogenesis. <i>Nature Genetics</i> , 2021, 53, 143-146.	9.4	158
2963	An organoid-derived bronchioalveolar model for SARS-CoV-2 infection of human alveolar type II-like cells. <i>EMBO Journal</i> , 2021, 40, e105912.	3.5	153
2964	scRNA-Seq Reveals New Enteric Nervous System Roles for GDNF, NRTN, and TBX3. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021, 11, 1548-1592.e1.	2.3	55
2965	scReQTL: an approach to correlate SNVs to gene expression from individual scRNA-seq datasets. <i>BMC Genomics</i> , 2021, 22, 40.	1.2	11
2966	Bi-fated tendon-to-bone attachment cells are regulated by shared enhancers and KLF transcription factors. <i>ELife</i> , 2021, 10, .	2.8	36
2968	Probabilistic harmonization and annotation of single-cell transcriptomics data with deep generative models. <i>Molecular Systems Biology</i> , 2021, 17, e9620.	3.2	211

#	ARTICLE	IF	CITATIONS
2969	Single-cell dissection of intratumoral heterogeneity and lineage diversity in metastatic gastric adenocarcinoma. <i>Nature Medicine</i> , 2021, 27, 141-151.	15.2	134
2970	PD-L2 based immune signature confers poor prognosis in HNSCC. <i>Oncolimmunology</i> , 2021, 10, 1947569.	2.1	21
2973	Single-Cell Mapping of Progressive Fetal-to-Adult Transition in Human Naive T Cells. <i>Cell Reports</i> , 2021, 34, 108573.	2.9	25
2976	BET bromodomain inhibitor JQ1 regulates spermatid development by changing chromatin conformation in mouse spermatogenesis. <i>Genes and Diseases</i> , 2022, 9, 1062-1073.	1.5	1
2979	Zebrafish model for spondylo-megaepiphyseal-metaphyseal dysplasia reveals post-embryonic roles of Nkx3.2 in the skeleton. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	7
2980	Pax9 is essential for granulopoiesis but dispensable for erythropoiesis in zebrafish. <i>Biochemical and Biophysical Research Communications</i> , 2021, 534, 359-366.	1.0	4
2984	Evidence for phloem loading via the abaxial bundle sheath cells in maize leaves. <i>Plant Cell</i> , 2021, 33, 531-547.	3.1	85
2985	Elucidating the cellular dynamics of the brain with single-cell RNA sequencing. <i>RNA Biology</i> , 2021, 18, 1063-1084.	1.5	14
2986	Ancestral developmental potentials in early bony fish contributed to vertebrate water-to-land transition. <i>Zoological Research</i> , 2021, 42, 135-137.	0.9	5
2987	An <i>in vitro</i> vascularized micro-tumor model of human colorectal cancer recapitulates <i>in vivo</i> responses to standard-of-care therapy. <i>Lab on A Chip</i> , 2021, 21, 1333-1351.	3.1	58
2988	Dimensionality Reduction of Single-Cell RNA-Seq Data. <i>Methods in Molecular Biology</i> , 2021, 2284, 331-342.	0.4	6
2992	Single-cell resolution landscape of equine peripheral blood mononuclear cells reveals diverse cell types including T-bet+ B cells. <i>BMC Biology</i> , 2021, 19, 13.	1.7	25
2993	Spontaneous cell fusions as a mechanism of parasexual recombination in tumour cell populations. <i>Nature Ecology and Evolution</i> , 2021, 5, 379-391.	3.4	38
2994	Gut-licensed IFN γ + NK cells drive LAMP1+TRAIL+ anti-inflammatory astrocytes. <i>Nature</i> , 2021, 590, 473-479.	13.7	178
2995	The aging transcriptome and cellular landscape of the human lung in relation to SARS-CoV-2. <i>Nature Communications</i> , 2021, 12, 4.	5.8	63
2996	scMC learns biological variation through the alignment of multiple single-cell genomics datasets. <i>Genome Biology</i> , 2021, 22, 10.	3.8	534
2997	Endothelial cell infection and dysfunction, immune activation in severe COVID-19. <i>Theranostics</i> , 2021, 11, 8076-8091.	4.6	70
2998	Global computational alignment of tumor and cell line transcriptional profiles. <i>Nature Communications</i> , 2021, 12, 22.	5.8	71

#	ARTICLE	IF	CITATIONS
2999	HiDeF: identifying persistent structures in multiscale omics data. <i>Genome Biology</i> , 2021, 22, 21.	3.8	29
3000	Analysis of Transcriptional Profiling of Immune Cells at the Single-Cell Level. <i>Methods in Molecular Biology</i> , 2020, 2111, 47-57.	0.4	8
3001	Profiling Cell Type Abundance and Expression in Bulk Tissues with CIBERSORTx. <i>Methods in Molecular Biology</i> , 2020, 2117, 135-157.	0.4	249
3002	Visualization of Single Cell RNA-Seq Data Using t-SNE in R. <i>Methods in Molecular Biology</i> , 2020, 2117, 159-167.	0.4	46
3003	Single-Cell Transcriptome Analysis of T Cells. <i>Methods in Molecular Biology</i> , 2019, 2048, 155-205.	0.4	3
3004	Clustering of Small-Sample Single-Cell RNA-Seq Data via Feature Clustering and Selection. <i>Lecture Notes in Computer Science</i> , 2019, , 445-456.	1.0	4
3005	Medulloblastoma Arises from the Persistence of a Rare and Transient Sox2+ Granule Neuron Precursor. <i>Cell Reports</i> , 2020, 31, 107511.	2.9	35
3006	Excessive E2F Transcription in Single Cancer Cells Precludes Transient Cell-Cycle Exit after DNA Damage. <i>Cell Reports</i> , 2020, 33, 108449.	2.9	16
3007	Single-Cell Transcriptomics Reveal Immune Mechanisms of the Onset and Progression of IgA Nephropathy. <i>Cell Reports</i> , 2020, 33, 108525.	2.9	49
3008	Ageing-Associated Alterations in Mammary Epithelia and Stroma Revealed by Single-Cell RNA Sequencing. <i>Cell Reports</i> , 2020, 33, 108566.	2.9	75
3009	Evaluation of Cell Type Annotation R Packages on Single-cell RNA-seq Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 267-281.	3.0	68
3010	Heterogenous Populations of Tissue-Resident CD8+ T Cells Are Generated in Response to Infection and Malignancy. <i>Immunity</i> , 2020, 52, 808-824.e7.	6.6	149
3011	Developmental Relationships of Four Exhausted CD8+ T Cell Subsets Reveals Underlying Transcriptional and Epigenetic Landscape Control Mechanisms. <i>Immunity</i> , 2020, 52, 825-841.e8.	6.6	497
3012	Single-Cell RNA Sequencing of Tumor-Infiltrating NK Cells Reveals that Inhibition of Transcription Factor HIF-1 α Unleashes NK Cell Activity. <i>Immunity</i> , 2020, 52, 1075-1087.e8.	6.6	167
3013	MCH Neurons Regulate Permeability of the Median Eminence Barrier. <i>Neuron</i> , 2020, 107, 306-319.e9.	3.8	45
3014	Spatiotemporal Analysis Reveals Overlap of Key Proepicardial Markers in the Developing Murine Heart. <i>Stem Cell Reports</i> , 2020, 14, 770-787.	2.3	52
3015	Generation and isolation of single cells from mouse brain with mosaic analysis with double markers-induced uniparental chromosome disomy. <i>STAR Protocols</i> , 2020, 1, 100215.	0.5	11
3016	Kindlin-2 regulates skeletal homeostasis by modulating PTH1R in mice. <i>Signal Transduction and Targeted Therapy</i> , 2020, 5, 297.	7.1	31

#	ARTICLE	IF	CITATIONS
3017	Focal adhesion protein Kindlin-2 regulates bone homeostasis in mice. <i>Bone Research</i> , 2020, 8, 2.	5.4	50
3018	Single-cell RNA sequencing reveals regulation of fetal ovary development in the monkey (<i>Macaca Tj</i>). <i>ETQq1</i> 1 0.784314 rgBT JOverlode	3.1	19
3019	Single-cell analysis of murine fibroblasts identifies neonatal to adult switching that regulates cardiomyocyte maturation. <i>Nature Communications</i> , 2020, 11, 2585.	5.8	71
3020	Sensitive high-throughput single-cell RNA-seq reveals within-clonal transcript correlations in yeast populations. <i>Nature Microbiology</i> , 2019, 4, 683-692.	5.9	61
3021	Prokaryotic single-cell RNA sequencing by in situ combinatorial indexing. <i>Nature Microbiology</i> , 2020, 5, 1192-1201.	5.9	103
3022	MAFG-driven astrocytes promote CNS inflammation. <i>Nature</i> , 2020, 578, 593-599.	13.7	282
3023	Lineage-dependent gene expression programs influence the immune landscape of colorectal cancer. <i>Nature Genetics</i> , 2020, 52, 594-603.	9.4	380
3024	Neuronal defects in a human cellular model of 22q11.2 deletion syndrome. <i>Nature Medicine</i> , 2020, 26, 1888-1898.	15.2	113
3025	An optimized workflow for single-cell transcriptomics and repertoire profiling of purified lymphocytes from clinical samples. <i>Scientific Reports</i> , 2020, 10, 2219.	1.6	25
3026	Single-cell analyses reveal increased intratumoral heterogeneity after the onset of therapy resistance in small-cell lung cancer. <i>Nature Cancer</i> , 2020, 1, 423-436.	5.7	218
3027	Single-cell RNA sequencing of adult mouse testes. <i>Scientific Data</i> , 2018, 5, 180192.	2.4	48
3028	Single cell approaches to address adipose tissue stromal cell heterogeneity. <i>Biochemical Journal</i> , 2020, 477, 583-600.	1.7	58
3029	Plant stem-cell organization and differentiation at single-cell resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 33689-33699.	3.3	134
3030	Different lineage contexts direct common pro-neural factors to specify distinct retinal cell subtypes. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	16
3031	Phenotypic and functional characterization of first-trimester human placental macrophages, Hofbauer cells. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	98
3032	SoupX removes ambient RNA contamination from droplet-based single-cell RNA sequencing data. <i>GigaScience</i> , 2020, 9, .	3.3	578
3033	Acoel Single-Cell Transcriptomics: Cell Type Analysis of a Deep Branching Bilaterian. <i>Molecular Biology and Evolution</i> , 2021, 38, 1888-1904.	3.5	14
3034	Integration of single-cell datasets reveals novel transcriptomic signatures of β 2-cells in human type 2 diabetes. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa097.	1.5	15

#	ARTICLE	IF	CITATIONS
3035	Identification of diverse tumor endothelial cell populations in malignant glioma. <i>Neuro-Oncology</i> , 2021, 23, 932-944.	0.6	32
3036	Single-nucleus characterization of adult mouse spinal dynorphin-lineage cells and identification of persistent transcriptional effects of neonatal hindpaw incision. <i>Pain</i> , 2021, 162, 203-218.	2.0	12
3542	Context-dependent functional compensation between Ythdf m⁶A reader proteins. <i>Genes and Development</i> , 2020, 34, 1373-1391.	2.7	158
3543	Accurately Clustering Single-cell RNA-seq data by Capturing Structural Relations between Cells through Graph Convolutional Network. , 2020, , .		26
3544	Intrinsic apoptosis shapes the tumor spectrum linked to inactivation of the deubiquitinase BAP1. <i>Science</i> , 2019, 364, 283-285.	6.0	71
3545	A latent lineage potential in resident neural stem cells enables spinal cord repair. <i>Science</i> , 2020, 370, .	6.0	89
3546	IRF5 guides monocytes toward an inflammatory CD11c ⁺ macrophage phenotype and promotes intestinal inflammation. <i>Science Immunology</i> , 2020, 5, .	5.6	48
3547	LISA: Accurate reconstruction of cell trajectory and pseudo-time for massive single cell RNA-seq data. , 2018, , .		2
3548	Alterations in the Transcriptional Programs of Myeloma Cells and the Microenvironment during Extramedullary Progression Affect Proliferation and Immune Evasion. <i>Clinical Cancer Research</i> , 2020, 26, 935-944.	3.2	51
3549	Timed Ang2-Targeted Therapy Identifies the Angiopoietinâ€Tie Pathway as Key Regulator of Fatal Lymphogenous Metastasis. <i>Cancer Discovery</i> , 2021, 11, 424-445.	7.7	18
3550	Integrated RNA Sequencing Reveals Epigenetic Impacts of Diesel Particulate Matter Exposure in Human Cerebral Organoids. <i>Developmental Neuroscience</i> , 2020, 42, 195-207.	1.0	12
3551	Single-Cell RNA Sequencing Analysis Reveals a Crucial Role for CTHRC1 (Collagen Triple Helix Repeat) Tj ETQq1 1 0.784314 rgBT /Ove to	1.6	132
3552	Environment-Sensing Aryl Hydrocarbon Receptor Inhibits the Chondrogenic Fate of Modulated Smooth Muscle Cells in Atherosclerotic Lesions. <i>Circulation</i> , 2020, 142, 575-590.	1.6	57
3553	Organoid single cell profiling identifies a transcriptional signature of glomerular disease. <i>JCI Insight</i> , 2019, 4, .	2.3	73
3554	Single-cell RNA sequencing identifies TGF-Î² as a key regenerative cue following LPS-induced lung injury. <i>JCI Insight</i> , 2019, 4, .	2.3	111
3555	Single cell RNA sequencing identifies unique inflammatory airspace macrophage subsets. <i>JCI Insight</i> , 2019, 4, .	2.3	167
3556	Cellular heterogeneity during mouse pancreatic ductal adenocarcinoma progression at single-cell resolution. <i>JCI Insight</i> , 2019, 4, .	2.3	169
3557	Syndecan-1 promotes lung fibrosis by regulating epithelial reprogramming through extracellular vesicles. <i>JCI Insight</i> , 2019, 4, .	2.3	50

#	ARTICLE	IF	CITATIONS
3558	Transcriptional heterogeneity of fibroblasts is a hallmark of the aging heart. JCI Insight, 2019, 4, .	2.3	101
3559	MicroRNA-146a regulates immune-related adverse events caused by immune checkpoint inhibitors. JCI Insight, 2020, 5, .	2.3	49
3560	Heme oxygenase-1 orchestrates the immunosuppressive program of tumor-associated macrophages. JCI Insight, 2020, 5, .	2.3	32
3561	Myocardial B cells are a subset of circulating lymphocytes with delayed transit through the heart. JCI Insight, 2020, 5, .	2.3	57
3562	Type I IFN response associated with mTOR activation in the TAFRO subtype of idiopathic multicentric Castleman disease. JCI Insight, 2020, 5, .	2.3	35
3563	Identification of pathogenic TRAIL-expressing innate immune cells during HIV-1 infection in humanized mice by scRNA-seq. JCI Insight, 2020, 5, .	2.3	8
3564	Host immunology and rational immunotherapy for carbapenem-resistant Klebsiella pneumoniae infection. JCI Insight, 2020, 5, .	2.3	13
3565	Single cell RNA sequencing identifies an early monocyte gene signature in acute respiratory distress syndrome. JCI Insight, 2020, 5, .	2.3	39
3566	Single-cell repertoire tracing identifies rituximab-resistant B cells during myasthenia gravis relapses. JCI Insight, 2020, 5, .	2.3	37
3567	CCL5 mediates CD40-driven CD4+ T cell tumor infiltration and immunity. JCI Insight, 2020, 5, .	2.3	72
3568	The cellular basis of protease activated receptor type 2 (PAR2) evoked mechanical and affective pain. JCI Insight, 2020, 5, .	2.3	18
3569	Single-cell transcriptomics of alloreactive CD4+ T cells over time reveals divergent fates during gut graft-versus-host disease. JCI Insight, 2020, 5, .	2.3	12
3570	Epigenetic regulation of the PGE2 pathway modulates macrophage phenotype in normal and pathologic wound repair. JCI Insight, 2020, 5, .	2.3	37
3571	Contribution of plasma cells and B cells to hidradenitis suppurativa pathogenesis. JCI Insight, 2020, 5, .	2.3	105
3572	Single-cell omics analysis reveals functional diversification of hepatocytes during liver regeneration. JCI Insight, 2020, 5, .	2.3	43
3573	Preoperative stimulation of resolution and inflammation blockade eradicates micrometastases. Journal of Clinical Investigation, 2019, 129, 2964-2979.	3.9	94
3574	Increased expression of anion transporter SLC26A9 delays diabetes onset in cystic fibrosis. Journal of Clinical Investigation, 2019, 130, 272-286.	3.9	33
3575	Dermal adipose tissue has high plasticity and undergoes reversible dedifferentiation in mice. Journal of Clinical Investigation, 2019, 129, 5327-5342.	3.9	112

#	ARTICLE	IF	CITATIONS
3576	Angiopoietin-2 blockade ameliorates autoimmune neuroinflammation by inhibiting leukocyte recruitment into the CNS. <i>Journal of Clinical Investigation</i> , 2020, 130, 1977-1990.	3.9	26
3577	Epithelial splicing regulatory protein 2-mediated alternative splicing reprograms hepatocytes in severe alcoholic hepatitis. <i>Journal of Clinical Investigation</i> , 2020, 130, 2129-2145.	3.9	49
3578	Targeting tumor-associated macrophages and granulocytic myeloid-derived suppressor cells augments PD-1 blockade in cholangiocarcinoma. <i>Journal of Clinical Investigation</i> , 2020, 130, 5380-5396.	3.9	185
3579	Epithelial-derived gasdermin D mediates nonlytic IL-1 β release during experimental colitis. <i>Journal of Clinical Investigation</i> , 2020, 130, 4218-4234.	3.9	76
3580	Data Denoising and Post-Denoising Corrections in Single Cell RNA Sequencing. <i>Statistical Science</i> , 2020, 35, .	1.6	6
3581	scClustViz - Single-cell RNAseq cluster assessment and visualization. <i>F1000Research</i> , 2018, 7, 1522.	0.8	32
3582	scClustViz - Single-cell RNAseq cluster assessment and visualization. <i>F1000Research</i> , 2018, 7, 1522.	0.8	28
3583	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. <i>F1000Research</i> , 2019, 8, 296.	0.8	49
3584	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. <i>F1000Research</i> , 0, 8, 296.	0.8	2
3585	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. <i>F1000Research</i> , 2019, 8, 296.	0.8	45
3586	scRepertoire: An R-based toolkit for single-cell immune receptor analysis. <i>F1000Research</i> , 2020, 9, 47.	0.8	114
3587	clustifyr: an R package for automated single-cell RNA sequencing cluster classification. <i>F1000Research</i> , 2020, 9, 223.	0.8	71
3588	Single Cell RNA-Sequencing for the Study of Atherosclerosis. <i>Journal of Lipid and Atherosclerosis</i> , 2019, 8, 152.	1.1	7
3589	A network medicine approach to investigation and population-based validation of disease manifestations and drug repurposing for COVID-19. <i>PLoS Biology</i> , 2020, 18, e3000970.	2.6	139
3590	Single-cell transcriptome landscape of ovarian cells during primordial follicle assembly in mice. <i>PLoS Biology</i> , 2020, 18, e3001025.	2.6	71
3591	Distinct populations of crypt-associated fibroblasts act as signaling hubs to control colon homeostasis. <i>PLoS Biology</i> , 2020, 18, e3001032.	2.6	53
3592	A simple, scalable approach to building a cross-platform transcriptome atlas. <i>PLoS Computational Biology</i> , 2020, 16, e1008219.	1.5	12
3593	Multiscale community detection in Cytoscape. <i>PLoS Computational Biology</i> , 2020, 16, e1008239.	1.5	34

#	ARTICLE	IF	CITATIONS
3594	Deconvolution of heterogeneous tumor samples using partial reference signals. <i>PLoS Computational Biology</i> , 2020, 16, e1008452.	1.5	7
3595	Dissecting Cellular Heterogeneity Using Single-Cell RNA Sequencing. <i>Molecules and Cells</i> , 2019, 42, 189-199.	1.0	45
3596	Peripheral Nerve Single-Cell Analysis Identifies Mesenchymal Ligands that Promote Axonal Growth. <i>ENeuro</i> , 2020, 7, ENEURO.0066-20.2020.	0.9	40
3597	Single-Cell Molecular and Cellular Architecture of the Mouse Neurohypophysis. <i>ENeuro</i> , 2020, 7, ENEURO.0345-19.2019.	0.9	30
3598	Single-cell transcriptome analysis reveals thyrocyte diversity in the zebrafish thyroid gland. <i>EMBO Reports</i> , 2020, 21, e50612.	2.0	23
3599	Asymmetry in the frequency and position of mitosis in the mouse embryo epiblast at gastrulation. <i>EMBO Reports</i> , 2020, 21, e50944.	2.0	10
3600	High-throughput, microscope-based sorting to dissect cellular heterogeneity. <i>Molecular Systems Biology</i> , 2020, 16, e9442.	3.2	46
3601	The transcriptome dynamics of single cells during the cell cycle. <i>Molecular Systems Biology</i> , 2020, 16, e9946.	3.2	35
3602	Single cell transcriptome research in human placenta. <i>Reproduction</i> , 2020, 160, R155-R167.	1.1	46
3603	Development and validation of a metastasis-associated prognostic signature based on single-cell RNA-seq in clear cell renal cell carcinoma. <i>Aging</i> , 2019, 11, 10183-10202.	1.4	28
3604	Glioblastoma cell differentiation trajectory predicts the immunotherapy response and overall survival of patients. <i>Aging</i> , 2020, 12, 18297-18321.	1.4	29
3605	The new technologies of high-throughput single-cell RNA sequencing. <i>Vavilovskii Zhurnal Genetiki i Seleksii</i> , 2019, 23, 508-518.	0.4	1
3606	Single-cell RNA-seq reveals the immune escape and drug resistance mechanisms of mantle cell lymphoma. <i>Cancer Biology and Medicine</i> , 2020, 17, 726-739.	1.4	25
3607	Single-Cell RNA Sequencing of Visceral Adipose Tissue Leukocytes Reveals that Caloric Restriction Following Obesity Promotes the Accumulation of a Distinct Macrophage Population with Features of Phagocytic Cells. <i>Immunometabolism</i> , 2019, 1, .	0.7	63
3608	Netrin-1 Alters Adipose Tissue Macrophage Fate and Function in Obesity. <i>Immunometabolism</i> , 2019, 1, .	0.7	41
3610	Origin and Differentiation Trajectories of Fibroblastic Reticular Cells in the Splenic White Pulp. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
3611	A Cellular Atlas of the Developing Meninges Reveals Meningeal Fibroblast Diversity and Function. <i>SSRN Electronic Journal</i> , 0, , .	0.4	3
3612	Viral Invasion and Type I Interferon Response Characterize the Immunophenotypes during COVID-19 Infection. <i>SSRN Electronic Journal</i> , 0, , .	0.4	16

#	ARTICLE	IF	CITATIONS
3613	Suppression of Androgen Receptor (AR)-ACE2/TMPRSS2 Axis by AR Antagonists May Be Therapeutically Beneficial for Male COVID-19 Patients. SSRN Electronic Journal, 0, , .	0.4	10
3614	Comprehensive Visualization of High-Dimensional Single-Cell Data With Diffusion-Based Manifold Approximation and Projection (dbMAP). SSRN Electronic Journal, 0, , .	0.4	1
3615	Murine interfollicular epidermal differentiation is gradualistic with GRHL3 controlling progression from stem to transition cell states. Nature Communications, 2020, 11, .	5.8	1
3616	Reconstructing gene regulatory networks in single-cell transcriptomic data analysis. Zoological Research, 2020, 41, 599-604.	0.9	8
3617	A Review of Complex Systems Approaches to Cancer Networks. Complex Systems, 2020, 29, 779-835.	0.9	6
3618	Dynamic changes in the regulatory T-cell heterogeneity and function by murine IL-2 mutein. Life Science Alliance, 2020, 3, e201900520.	1.3	13
3619	Single-cell RNA sequencing of human breast tumour-infiltrating immune cells reveals a $\hat{\beta}$ T-cell subtype associated with good clinical outcome. Life Science Alliance, 2021, 4, e202000680.	1.3	6
3620	Robust production of uniform human cerebral organoids from pluripotent stem cells. Life Science Alliance, 2020, 3, e202000707.	1.3	52
3621	Transcriptomic Changes of Murine Visceral Fat Exposed to Intermittent Hypoxia at Single Cell Resolution. International Journal of Molecular Sciences, 2021, 22, 261.	1.8	4
3622	Nuclei Isolation from Fresh Frozen Brain Tumors for Single-Nucleus RNA-seq and ATAC-seq. Journal of Visualized Experiments, 2020, , .	0.2	7
3623	Epigenetic Heterogeneity and Mitotic Heritability Prime Endothelial Cell Gene Induction. Journal of Immunology, 2020, 204, 1173-1187.	0.4	12
3624	Effects of Cryopreservation and Thawing on Single-Cell Transcriptomes of Human T Cells. Immune Network, 2020, 20, e34.	1.6	14
3625	Pdgfra marks a cellular lineage with distinct contributions to myofibroblasts in lung maturation and injury response. ELife, 2018, 7, .	2.8	137
3626	Insulin mutations impair beta-cell development in a patient-derived iPSC model of neonatal diabetes. ELife, 2018, 7, .	2.8	114
3627	Nephron progenitor commitment is a stochastic process influenced by cell migration. ELife, 2019, 8, .	2.8	47
3628	Specification of diverse cell types during early neurogenesis of the mouse cerebellum. ELife, 2019, 8, .	2.8	65
3629	eIF2B activator prevents neurological defects caused by a chronic integrated stress response. ELife, 2019, 8, .	2.8	124
3630	Macrophages restrict the nephrogenic field and promote endothelial connections during kidney development. ELife, 2019, 8, .	2.8	44

#	ARTICLE	IF	CITATIONS
3631	Complementary networks of cortical somatostatin interneurons enforce layer specific control. <i>ELife</i> , 2019, 8, .	2.8	89
3632	Stem cell-derived cranial and spinal motor neurons reveal proteostatic differences between ALS resistant and sensitive motor neurons. <i>ELife</i> , 2019, 8, .	2.8	30
3633	Single-cell sequencing of neonatal uterus reveals an <i>Misr2</i> + endometrial progenitor indispensable for fertility. <i>ELife</i> , 2019, 8, .	2.8	36
3634	Molecular and anatomical organization of the dorsal raphe nucleus. <i>ELife</i> , 2019, 8, .	2.8	140
3635	A chemical probe of CARM1 alters epigenetic plasticity against breast cancer cell invasion. <i>ELife</i> , 2019, 8, .	2.8	32
3636	<i>Toxoplasma gondii</i> infection drives conversion of NK cells into ILC1-like cells. <i>ELife</i> , 2019, 8, .	2.8	91
3637	A scalable platform for the development of cell-type-specific viral drivers. <i>ELife</i> , 2019, 8, .	2.8	67
3638	Single-cell transcriptomes and whole-brain projections of serotonin neurons in the mouse dorsal and median raphe nuclei. <i>ELife</i> , 2019, 8, .	2.8	189
3639	Stereotyped transcriptomic transformation of somatosensory neurons in response to injury. <i>ELife</i> , 2019, 8, .	2.8	75
3640	Single cell transcriptome atlas of the <i>Drosophila</i> larval brain. <i>ELife</i> , 2019, 8, .	2.8	101
3641	Coopted temporal patterning governs cellular hierarchy, heterogeneity and metabolism in <i>Drosophila</i> neuroblast tumors. <i>ELife</i> , 2019, 8, .	2.8	29
3642	Axon-like protrusions promote small cell lung cancer migration and metastasis. <i>ELife</i> , 2019, 8, .	2.8	37
3643	Modular transcriptional programs separately define axon and dendrite connectivity. <i>ELife</i> , 2019, 8, .	2.8	49
3644	Anatomical and single-cell transcriptional profiling of the murine habenular complex. <i>ELife</i> , 2020, 9, .	2.8	67
3645	Single-cell transcriptome reveals the novel role of T-bet in suppressing the immature NK gene signature. <i>ELife</i> , 2020, 9, .	2.8	19
3646	Endothelial heterogeneity across distinct vascular beds during homeostasis and inflammation. <i>ELife</i> , 2020, 9, .	2.8	209
3647	Functionally heterogeneous human satellite cells identified by single cell RNA sequencing. <i>ELife</i> , 2020, 9, .	2.8	82
3648	Loss of <i>Kat2a</i> enhances transcriptional noise and depletes acute myeloid leukemia stem-like cells. <i>ELife</i> , 2020, 9, .	2.8	26

#	ARTICLE	IF	CITATIONS
3649	A MAC2-positive progenitor-like microglial population is resistant to CSF1R inhibition in adult mouse brain. <i>ELife</i> , 2020, 9, .	2.8	54
3650	Single cell transcriptional signatures of the human placenta in term and preterm parturition. <i>ELife</i> , 2019, 8, .	2.8	216
3651	Chromatin accessibility dynamics and single cell RNA-Seq reveal new regulators of regeneration in neural progenitors. <i>ELife</i> , 2020, 9, .	2.8	39
3652	Defining the role of pulmonary endothelial cell heterogeneity in the response to acute lung injury. <i>ELife</i> , 2020, 9, .	2.8	151
3653	Primary and secondary anti-viral response captured by the dynamics and phenotype of individual T cell clones. <i>ELife</i> , 2020, 9, .	2.8	48
3654	Cancer systems immunology. <i>ELife</i> , 2020, 9, .	2.8	14
3655	A single-parasite transcriptional atlas of <i>Toxoplasma Gondii</i> reveals novel control of antigen expression. <i>ELife</i> , 2020, 9, .	2.8	47
3656	Semiochemical responsive olfactory sensory neurons are sexually dimorphic and plastic. <i>ELife</i> , 2020, 9, .	2.8	21
3657	Single cell transcriptomics identifies a unique adipose lineage cell population that regulates bone marrow environment. <i>ELife</i> , 2020, 9, .	2.8	191
3658	<i>Maf</i> and <i>Mafb</i> control mouse pallial interneuron fate and maturation through neuropsychiatric disease gene regulation. <i>ELife</i> , 2020, 9, .	2.8	22
3659	A new protocol for single-cell RNA-seq reveals stochastic gene expression during lag phase in budding yeast. <i>ELife</i> , 2020, 9, .	2.8	43
3660	A single-cell transcriptomic and anatomic atlas of mouse dorsal raphe <i>Pet1</i> neurons. <i>ELife</i> , 2020, 9, .	2.8	80
3661	Genetic mapping of etiologic brain cell types for obesity. <i>ELife</i> , 2020, 9, .	2.8	79
3662	The role of the NMD factor <i>UPF3B</i> in olfactory sensory neurons. <i>ELife</i> , 2020, 9, .	2.8	18
3663	Activity-dependent tuning of intrinsic excitability in mouse and human neurogliaform cells. <i>ELife</i> , 2020, 9, .	2.8	29
3664	Bimodal function of chromatin remodeler <i>Hmga1</i> in neural crest induction and Wnt-dependent emigration. <i>ELife</i> , 2020, 9, .	2.8	19
3665	Knowledge synthesis of 100 million biomedical documents augments the deep expression profiling of coronavirus receptors. <i>ELife</i> , 2020, 9, .	2.8	61
3666	An essential role for <i>MEF2C</i> in the cortical response to loss of sleep in mice. <i>ELife</i> , 2020, 9, .	2.8	25

#	ARTICLE	IF	CITATIONS
3667	Heterogeneous somatostatin-expressing neuron population in mouse ventral tegmental area. <i>ELife</i> , 2020, 9, .	2.8	9
3668	High-resolution transcriptional and morphogenetic profiling of cells from micropatterned human ESC gastruloid cultures. <i>ELife</i> , 2020, 9, .	2.8	62
3669	Common cell type nomenclature for the mammalian brain. <i>ELife</i> , 2020, 9, .	2.8	56
3670	Gene expression variability in human and chimpanzee populations share common determinants. <i>ELife</i> , 2020, 9, .	2.8	33
3671	Combined transient ablation and single-cell RNA-sequencing reveals the development of medullary thymic epithelial cells. <i>ELife</i> , 2020, 9, .	2.8	53
3672	Single nuclei RNA-seq of mouse placental labyrinth development. <i>ELife</i> , 2020, 9, .	2.8	83
3673	Mapping endothelial-cell diversity in cerebral cavernous malformations at single-cell resolution. <i>ELife</i> , 2020, 9, .	2.8	42
3674	Emergence of non-canonical parvalbumin-containing interneurons in hippocampus of a murine model of type I lissencephaly. <i>ELife</i> , 2020, 9, .	2.8	13
3675	Application of single-cell RNA sequencing technology in liver diseases: a narrative review. <i>Annals of Translational Medicine</i> , 2021, 9, 1598-1598.	0.7	3
3676	Single-Cell RNA Sequencing Depicts the Local Cell Landscape in Thyroid-Associated Ophthalmopathy. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3677	Single-cell RNA sequencing deconvolutes the <i>in vivo</i> heterogeneity of human bone marrow-derived mesenchymal stem cells. <i>International Journal of Biological Sciences</i> , 2021, 17, 4192-4206.	2.6	39
3678	Deep learning-based advances and applications for single-cell RNA-sequencing data analysis. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	19
3679	Single-Cell Transcriptional Heterogeneity Landscapes of Third Heart Field Progenitor Cells. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3680	High-throughput RNA sequencing of paraformaldehyde-fixed single cells. <i>Nature Communications</i> , 2021, 12, 5636.	5.8	29
3681	A cis-acting structural variation at the ZNF558 locus controls a gene regulatory network in human brain development. <i>Cell Stem Cell</i> , 2022, 29, 52-69.e8.	5.2	37
3682	DNAM-1 promotes inflammation-driven tumor development via enhancing IFN- γ production. <i>International Immunology</i> , 2021, , .	1.8	0
3683	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , 2021, 598, 103-110.	13.7	166
3685	IL-12 regulates type 3 immunity through interfollicular keratinocytes in psoriasisform inflammation. <i>Science Immunology</i> , 2021, 6, eabg9012.	5.6	14

#	ARTICLE	IF	CITATIONS
3688	Copy-scAT: Deconvoluting single-cell chromatin accessibility of genetic subclones in cancer. <i>Science Advances</i> , 2021, 7, eabg6045.	4.7	19
3689	Evolutionary transcriptomics implicates new genes and pathways in human pregnancy and adverse pregnancy outcomes. <i>ELife</i> , 2021, 10, .	2.8	23
3691	Clustering spatial transcriptomics data. <i>Bioinformatics</i> , 2022, 38, 997-1004.	1.8	25
3692	Integrated analysis of tumor-associated macrophage infiltration and prognosis in ovarian cancer. <i>Aging</i> , 2021, 13, 23210-23232.	1.4	22
3693	A human multi-lineage hepatic organoid model for liver fibrosis. <i>Nature Communications</i> , 2021, 12, 6138.	5.8	47
3695	Single-Cell Analysis Using Machine Learning Techniques and Its Application to Medical Research. <i>Biomedicines</i> , 2021, 9, 1513.	1.4	15
3696	How many markers are needed to robustly determine a cell's type?. <i>IScience</i> , 2021, 24, 103292.	1.9	14
3697	Microbiota triggers STING-type I IFN-dependent monocyte reprogramming of the tumor microenvironment. <i>Cell</i> , 2021, 184, 5338-5356.e21.	13.5	229
3698	Neuronal cholesterol synthesis is essential for repair of chronically demyelinated lesions in mice. <i>Cell Reports</i> , 2021, 37, 109889.	2.9	23
3699	Single-Cell Integration Analysis of Heterotopic Ossification and Fibrocartilage Developmental Lineage: Endoplasmic Reticulum Stress Effector Xbp1 Transcriptionally Regulates the Notch Signaling Pathway to Mediate Fibrocartilage Differentiation. <i>Oxidative Medicine and Cellular Longevity</i> , 2021, 2021, 1-29.	1.9	23
3700	Loss of Functional SCO2 Attenuates Oxidative Stress in Diabetic Kidney Disease. <i>Diabetes</i> , 2022, 71, 142-156.	0.3	5
3702	Cell Differentiation Trajectory-Associated Molecular Classification of Osteosarcoma. <i>Genes</i> , 2021, 12, 1685.	1.0	6
3703	Building the mega single-cell transcriptome ocular meta-atlas. <i>GigaScience</i> , 2021, 10, .	3.3	24
3707	CD127+ CD94+ innate lymphoid cells expressing granulysin and perforin are expanded in patients with Crohn's disease. <i>Nature Communications</i> , 2021, 12, 5841.	5.8	22
3708	Single-cell epigenomics reveals mechanisms of human cortical development. <i>Nature</i> , 2021, 598, 205-213.	13.7	154
3709	Human neocortical expansion involves glutamatergic neuron diversification. <i>Nature</i> , 2021, 598, 151-158.	13.7	160
3710	Escape of hair follicle stem cells causes stem cell exhaustion during aging. <i>Nature Aging</i> , 2021, 1, 889-903.	5.3	31
3711	Experimental and real-world evidence supporting the computational repurposing of bumetanide for APOE4-related Alzheimer's disease. <i>Nature Aging</i> , 2021, 1, 932-947.	5.3	58

#	ARTICLE	IF	CITATIONS
3712	Loss of Hs3st3a1 or Hs3st3b1 enzymes alters heparan sulfate to reduce epithelial morphogenesis and adult salivary gland function. <i>Matrix Biology</i> , 2021, 103-104, 37-57.	1.5	5
3713	Automatic cell type identification methods for single-cell RNA sequencing. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5874-5887.	1.9	30
3714	Human ALS/FTD brain organoid slice cultures display distinct early astrocyte and targetable neuronal pathology. <i>Nature Neuroscience</i> , 2021, 24, 1542-1554.	7.1	72
3715	Comprehensive Analysis of the Implication of PGRMC1 in Triple-Negative Breast Cancer. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 714030.	2.0	4
3716	Targeting epigenetically maladapted vascular niche alleviates liver fibrosis in nonalcoholic steatohepatitis. <i>Science Translational Medicine</i> , 2021, 13, eabd1206.	5.8	24
3718	6-Phosphogluconolactonase Promotes Hepatocellular Carcinogenesis by Activating Pentose Phosphate Pathway. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 753196.	1.8	15
3719	In situ and transcriptomic identification of microglia in synapse-rich regions of the developing zebrafish brain. <i>Nature Communications</i> , 2021, 12, 5916.	5.8	32
3720	Transcriptional and functional divergence in lateral hypothalamic glutamate neurons projecting to the lateral habenula and ventral tegmental area. <i>Neuron</i> , 2021, 109, 3823-3837.e6.	3.8	31
3723	An airway organoid-based screen identifies a role for the HIF1 α -glycolysis axis in SARS-CoV-2 infection. <i>Cell Reports</i> , 2021, 37, 109920.	2.9	36
3724	Single-Cell RNA Sequencing Revealed CD14 ⁺ Monocytes Increased in Patients With Takayasu's Arteritis Requiring Surgical Management. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 761300.	1.8	10
3725	SMC-Derived Hyaluronan Modulates Vascular SMC Phenotype in Murine Atherosclerosis. <i>Circulation Research</i> , 2021, 129, 992-1005.	2.0	12
3728	Identification of Key eRNAs for Spinal Cord Injury by Integrated Multinomial Bioinformatics Analysis. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 728242.	1.8	5
3729	Efficient stimulation of retinal regeneration from Müller glia in adult mice using combinations of proneural bHLH transcription factors. <i>Cell Reports</i> , 2021, 37, 109857.	2.9	79
3730	Single-cell transcriptomics reveal the heterogeneity and dynamic of cancer stem-like cells during breast tumor progression. <i>Cell Death and Disease</i> , 2021, 12, 979.	2.7	11
3731	Single-cell profiling of proteins and chromatin accessibility using PHAGE-ATAC. <i>Nature Biotechnology</i> , 2022, 40, 374-381.	9.4	31
3733	Modulation of fracture healing by the transient accumulation of senescent cells. <i>ELife</i> , 2021, 10, .	2.8	37
3734	Single cell T cell landscape and T cell receptor repertoire profiling of AML in context of PD-1 blockade therapy. <i>Nature Communications</i> , 2021, 12, 6071.	5.8	44
3735	Association between particulate matter containing EPFRs and neutrophilic asthma through AhR and Th17. <i>Respiratory Research</i> , 2021, 22, 275.	1.4	10

#	ARTICLE	IF	CITATIONS
3736	Human placental biology at single-cell resolution: a contemporaneous review. <i>BJOG: an International Journal of Obstetrics and Gynaecology</i> , 2022, 129, 208-220.	1.1	12
3737	A Dynamic Transcriptome Map of Different Tissue Microenvironment Cells Identified During Gastric Cancer Development Using Single-Cell RNA Sequencing. <i>Frontiers in Immunology</i> , 2021, 12, 728169.	2.2	16
3738	Single-cell RNA sequencing reveals a strong connection between Gadd45g upregulation and oncolytic HSV infection in tumor tissue. <i>Molecular Therapy - Oncolytics</i> , 2021, 23, 330-341.	2.0	1
3739	Integrated single-cell transcriptomics and epigenomics reveals strong germinal center-associated etiology of autoimmune risk loci. <i>Science Immunology</i> , 2021, 6, eabh3768.	5.6	19
3740	RgCop-A regularized copula based method for gene selection in single-cell RNA-seq data. <i>PLoS Computational Biology</i> , 2021, 17, e1009464.	1.5	9
3742	Regulation of intestinal immunity and tissue repair by enteric glia. <i>Nature</i> , 2021, 599, 125-130.	13.7	80
3743	Untimely TGF β 2 responses in COVID-19 limit antiviral functions of NK cells. <i>Nature</i> , 2021, 600, 295-301.	13.7	146
3744	Identification of Specific Cell Subpopulations and Marker Genes in Ovarian Cancer Using Single-Cell RNA Sequencing. <i>BioMed Research International</i> , 2021, 2021, 1-27.	0.9	9
3745	A Population of M2 Macrophages Associated With Bone Formation. <i>Frontiers in Immunology</i> , 2021, 12, 686769.	2.2	22
3747	NRF1 association with ALTS2-Polycomb mediates specific gene activation in the brain. <i>Molecular Cell</i> , 2021, 81, 4663-4676.e8.	4.5	23
3748	A transcriptomic atlas of mouse cerebellar cortex comprehensively defines cell types. <i>Nature</i> , 2021, 598, 214-219.	13.7	147
3753	Activation of Vitamin D Receptor Pathway Enhances Differentiating Capacity in Acute Myeloid Leukemia with Isocitrate Dehydrogenase Mutations. <i>Cancers</i> , 2021, 13, 5243.	1.7	6
3754	Identification and Validation of a Malignant Cell Subset Marker-Based Polygenic Risk Score in Stomach Adenocarcinoma Through Integrated Analysis of Bulk and Single-Cell RNA Sequencing Data. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 720649.	1.8	7
3756	Dysregulation of TFH-B-TRM lymphocyte cooperation is associated with unfavorable anti-PD-1 responses in EGFR-mutant lung cancer. <i>Nature Communications</i> , 2021, 12, 6068.	5.8	31
3757	Decoding molecular and cellular heterogeneity of mouse nucleus accumbens. <i>Nature Neuroscience</i> , 2021, 24, 1757-1771.	7.1	87
3758	Exploring the Epigenetic Regulatory Role of m6A-Associated SNPs in Type 2 Diabetes Pathogenesis. <i>Pharmacogenomics and Personalized Medicine</i> , 2021, Volume 14, 1369-1378.	0.4	6
3760	CD300a blockade enhances efferocytosis by infiltrating myeloid cells and ameliorates neuronal deficit after ischemic stroke. <i>Science Immunology</i> , 2021, 6, eabe7915.	5.6	15
3761	Co-varying neighborhood analysis identifies cell populations associated with phenotypes of interest from single-cell transcriptomics. <i>Nature Biotechnology</i> , 2022, 40, 355-363.	9.4	30

#	ARTICLE	IF	CITATIONS
3762	Inhibition of the BTK-IDO-mTOR axis promotes differentiation of monocyte-lineage dendritic cells and enhances anti-tumor T _H 1 cell immunity. <i>Immunity</i> , 2021, 54, 2354-2371.e8.	6.6	34
3763	Introductory Chapter: Applications of RNA-Seq Diagnostics in Biology and Medicine. , 0, , .		0
3767	Single-Cell Atlas of Lineage States, Tumor Microenvironment, and Subtype-Specific Expression Programs in Gastric Cancer. <i>Cancer Discovery</i> , 2022, 12, 670-691.	7.7	165
3768	Inference of high-resolution trajectories in single-cell RNA-seq data by using RNA velocity. <i>Cell Reports Methods</i> , 2021, 1, 100095.	1.4	24
3769	SCovid: single-cell atlases for exposing molecular characteristics of COVID-19 across 10 human tissues. <i>Nucleic Acids Research</i> , 2022, 50, D867-D874.	6.5	28
3771	Integrating single-cell genomics pipelines to discover mechanisms of stem cell differentiation. <i>Trends in Molecular Medicine</i> , 2021, 27, 1135-1158.	3.5	8
3773	High-Dimensional Single-Cell Transcriptomics in Melanoma and Cancer Immunotherapy. <i>Genes</i> , 2021, 12, 1629.	1.0	8
3774	An atlas of cortical arealization identifies dynamic molecular signatures. <i>Nature</i> , 2021, 598, 200-204.	13.7	132
3776	<i>CARMN</i> Is an Evolutionarily Conserved Smooth Muscle Cell-Specific LncRNA That Maintains Contractile Phenotype by Binding Myocardin. <i>Circulation</i> , 2021, 144, 1856-1875.	1.6	50
3777	Neurotransmitter signaling regulates distinct phases of multimodal human interneuron migration. <i>EMBO Journal</i> , 2021, 40, e108714.	3.5	16
3778	Arcuate Nucleus Overexpression of NHLH2 Reduces Body Mass and Attenuates Obesity-Associated Anxiety/Depression-like Behavior. <i>Journal of Neuroscience</i> , 2021, 41, 10004-10022.	1.7	8
3779	Trajectory mapping of primary Sjögren's syndrome via transcriptome learning demonstrates limitations of peripheral blood sequencing. <i>International Journal of Rheumatic Diseases</i> , 2021, 24, 1491-1499.	0.9	1
3780	Dynamic transcriptional reprogramming leads to immunotherapeutic vulnerabilities in myeloma. <i>Nature Cell Biology</i> , 2021, 23, 1199-1211.	4.6	22
3781	A model of impaired Langerhans cell maturation associated with HPV induced epithelial hyperplasia. <i>IScience</i> , 2021, 24, 103326.	1.9	7
3782	A Markov random field model for network-based differential expression analysis of single-cell RNA-seq data. <i>BMC Bioinformatics</i> , 2021, 22, 524.	1.2	5
3785	Cell-type modeling in spatial transcriptomics data elucidates spatially variable colocalization and communication between cell-types in mouse brain. <i>Cell Systems</i> , 2022, 13, 58-70.e5.	2.9	14
3786	Tumor-propagating side population cells are a dynamic subpopulation in undifferentiated pleomorphic sarcoma. <i>JCI Insight</i> , 2021, 6, .	2.3	0
3787	DUBStepR is a scalable correlation-based feature selection method for accurately clustering single-cell data. <i>Nature Communications</i> , 2021, 12, 5849.	5.8	28

#	ARTICLE	IF	CITATIONS
3788	SMILE: mutual information learning for integration of single-cell omics data. <i>Bioinformatics</i> , 2022, 38, 476-486.	1.8	29
3789	Matricellular Protein Cilp1 Promotes Myocardial Fibrosis in Response to Myocardial Infarction. <i>Circulation Research</i> , 2021, 129, 1021-1035.	2.0	23
3790	Spatial deconvolution of HER2-positive breast cancer delineates tumor-associated cell type interactions. <i>Nature Communications</i> , 2021, 12, 6012.	5.8	140
3794	Miscell: An efficient self-supervised learning approach for dissecting single-cell transcriptome. <i>IScience</i> , 2021, 24, 103200.	1.9	6
3795	The immune landscape of SARS-CoV-2-associated Multisystem Inflammatory Syndrome in Children (MIS-C) from acute disease to recovery. <i>IScience</i> , 2021, 24, 103215.	1.9	35
3796	The personalized application of biomaterials based on age and sexuality specific immune responses. <i>Biomaterials</i> , 2021, 278, 121177.	5.7	7
3797	Defining the Identity and Dynamics of Adult Gastric Isthmus Stem Cells. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
3799	Molecular Landscapes of Embryonic and Post-Embryonic Neurogenesis in the Vertebrate Retina. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3800	Single Cell RNAseq Uncovers a Robust Transcriptional Response to Morphine by Oligodendrocytes. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3833	SINGLE CELL ANALYSIS, WHAT IS IN THE FUTURE?. , 2018, , .		1
3843	Transcriptomic Approaches for Muscle Biology and Disorders. , 2019, , 79-107.		0
3844	Embedding to Reference t-SNE Space Addresses Batch Effects in Single-Cell Classification. <i>Lecture Notes in Computer Science</i> , 2019, , 246-260.	1.0	4
3845	Guidelines for Bioinformatics and the Statistical Analysis of Omic Data. , 2019, , 45-75.		0
3849	Extent, Heritability, and Functional Relevance of Single Cell Expression Variability in Highly Homogeneous Populations of Human Cells. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3850	A 3D Atlas of Hematopoietic Stem and Progenitor Cell Expansion by Multi-Dimensional RNA-Seq Analysis. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3851	Identification of a Unique Subretinal Microglia Type in Retinal Degeneration Using Single Cell RNA-Seq. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1185, 181-186.	0.8	7
3852	Sensorimotor Organoids for Neuromuscular Disease. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3853	Single-Cell Convert-Seq Decodes Regulatory Factors Driving Neuronal Diversity. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1

#	ARTICLE	IF	CITATIONS
4024	scTree: An R package to generate antibody-compatible classifiers from single-cell sequencing data. <i>Journal of Open Source Software</i> , 2020, 5, 2061.	2.0	2
4047	A transcriptomic map of murine and human alopecia areata. <i>JCI Insight</i> , 2020, 5, .	2.3	7
4097	Building an Interactive Workbench Environment for Single Cell Genomics Applications. , 2020, , .		1
4098	Applications of Community Detection Algorithms to Large Biological Datasets. <i>Methods in Molecular Biology</i> , 2021, 2243, 59-80.	0.4	2
4134	Transcriptional Differences in Lipid-Metabolizing Enzymes in Murine Sebocytes Derived from Sebaceous Glands of the Skin and Preputial Glands. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11631.	1.8	2
4136	Ectopic expression of <i>lrx3</i> and <i>lrx5</i> in the paraventricular nucleus of the hypothalamus contributes to defects in <i>Sim1</i> haploinsufficiency. <i>Science Advances</i> , 2021, 7, eabh4503.	4.7	5
4137	Clinical practices underlie COVID-19 patient respiratory microbiome composition and its interactions with the host. <i>Nature Communications</i> , 2021, 12, 6243.	5.8	42
4138	Single-Cell RNA-Sequencing Identifies Infrapatellar Fat Pad Macrophage Polarization in Acute Synovitis/Fat Pad Fibrosis and Cell Therapy. <i>Bioengineering</i> , 2021, 8, 166.	1.6	7
4139	LYVE1+ macrophages of murine peritoneal mesothelium promote omentum-independent ovarian tumor growth. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	31
4140	Evidence for shared genetic risk factors between lymphangi leiomyomatosis and pulmonary function. <i>ERJ Open Research</i> , 2022, 8, 00375-2021.	1.1	0
4141	LOW VULNERABILITY OF THE POSTERIOR EYE SEGMENT TO SARS-COV-2 INFECTION. <i>Retina</i> , 2022, 42, 236-243.	1.0	2
4143	Lack of CD8 ⁺ T cell effector differentiation during priming mediates checkpoint blockade resistance in non-small cell lung cancer. <i>Science Immunology</i> , 2021, 6, eabi8800.	5.6	58
4144	Human neural tube morphogenesis in vitro by geometric constraints. <i>Nature</i> , 2021, 599, 268-272.	13.7	107
4145	Alteration of the Immune Microenvironment in HBsAg and HBeAg Dual-Positive Pregnant Women Presenting a High HBV Viral Load. <i>Journal of Inflammation Research</i> , 2021, Volume 14, 5619-5632.	1.6	4
4147	Comprehensive characterization of tumor immune landscape following oncolytic virotherapy by single-cell RNA sequencing. <i>Cancer Immunology, Immunotherapy</i> , 2022, 71, 1479-1495.	2.0	4
4148	Single-cell analysis revealed that IL411 promoted ovarian cancer progression. <i>Journal of Translational Medicine</i> , 2021, 19, 454.	1.8	18
4149	Differential dynamics of peripheral immune responses to acute SARS-CoV-2 infection in older adults. <i>Nature Aging</i> , 2021, 1, 1038-1052.	5.3	10
4155	The serine proteases dipeptidyl-peptidase 4 and urokinase are key molecules in human and mouse scar formation. <i>Nature Communications</i> , 2021, 12, 6242.	5.8	34

#	ARTICLE	IF	CITATIONS
4156	Single-cell chromatin state analysis with Signac. <i>Nature Methods</i> , 2021, 18, 1333-1341.	9.0	595
4157	Spatially resolved transcriptomics reveals the architecture of the tumor-microenvironment interface. <i>Nature Communications</i> , 2021, 12, 6278.	5.8	112
4158	Skin inflammation activates intestinal stromal fibroblasts and promotes colitis. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	12
4159	Vascular adhesion protein-1 defines a unique subpopulation of human hematopoietic stem cells and regulates their proliferation. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 7851-7872.	2.4	1
4163	27 α -Hydroxycholesterol regulates human <i>SLC22A12</i> gene expression through estrogen receptor action. <i>FASEB Journal</i> , 2021, 35, e21262.	0.2	10
4169	DSAVE: Detection of misclassified cells in single-cell RNA-Seq data. <i>PLoS ONE</i> , 2020, 15, e0243360.	1.1	2
4174	A robust single cell clustering method based on subspace learning and partial imputation. , 2020, , .		1
4181	Interpretation of Biological Data at a Glance. <i>Journal of Biotechnology and Bioindustry</i> , 2020, 8, 38-47.	0.1	0
4191	Age-Associated Induction of Senescent Transcriptional Programs in Human Glial Progenitor Cells. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4192	Androgen action in cell fate and communication during prostate development at single-cell resolution. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	6
4200	Toward uncharted territory of cellular heterogeneity: advances and applications of single-cell RNA-seq. , 2021, 5, 1-21.		2
4201	Network Analysis of Large-Scale Data and Its Application to Immunology. <i>Methods in Molecular Biology</i> , 2020, 2131, 199-211.	0.4	1
4202	Use of SuperCT for Enhanced Characterization of Single-Cell Transcriptomic Profiles. <i>Methods in Molecular Biology</i> , 2020, 2117, 169-177.	0.4	0
4208	scRepertoire: An R-based toolkit for single-cell immune receptor analysis. <i>F1000Research</i> , 2020, 9, 47.	0.8	153
4210	Reconstitution of Prospermatogonial Specification <i>In vitro</i> from Human Induced Pluripotent Stem Cells. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4243	clustifyr: an R package for automated single-cell RNA sequencing cluster classification. <i>F1000Research</i> , 2020, 9, 223.	0.8	21
4244	Integrated Single-Cell Bioinformatics Analysis Reveals Intrinsic and Extrinsic Biological Characteristics of Hematopoietic Stem Cell Aging. <i>Frontiers in Genetics</i> , 2021, 12, 745786.	1.1	2
4245	Multiplexed droplet single-cell sequencing (Mux-Seq) of normal and transplant kidney. <i>American Journal of Transplantation</i> , 2022, 22, 876-885.	2.6	7

#	ARTICLE	IF	CITATIONS
4246	Landscape of Hopx expression in cells of the immune system. <i>Heliyon</i> , 2021, 7, e08311.	1.4	4
4248	Kr-h1 maintains distinct caste-specific neurotranscriptomes in response to socially regulated hormones. <i>Cell</i> , 2021, 184, 5807-5823.e14.	13.5	27
4249	Aging weakens Th17 cell pathogenicity and ameliorates experimental autoimmune uveitis in mice. <i>Protein and Cell</i> , 2022, 13, 422-445.	4.8	11
4250	The histone demethylase Lsd1 regulates multiple repressive gene programs during T cell development. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	4
4251	Patient-derived xenograft culture-transplant system for investigation of human breast cancer metastasis. <i>Communications Biology</i> , 2021, 4, 1268.	2.0	5
4253	Myeloid antigen-presenting cell niches sustain antitumor T cells and license PD-1 blockade via CD28 costimulation. <i>Cancer Cell</i> , 2021, 39, 1623-1642.e20.	7.7	64
4254	Interneuron origin and molecular diversity in the human fetal brain. <i>Nature Neuroscience</i> , 2021, 24, 1745-1756.	7.1	49
4256	Single-cell immunophenotyping of the fetal immune response to maternal SARS-CoV-2 infection in late gestation. <i>Pediatric Research</i> , 2022, 91, 1090-1098.	1.1	14
4258	Single-Cell RNA Sequencing of Urinary Cells Reveals Distinct Cellular Diversity in COVID-19 Associated AKI. <i>Kidney360</i> , 2022, 3, 28-36.	0.9	12
4259	Molecular programs of fibrotic change in aging human lung. <i>Nature Communications</i> , 2021, 12, 6309.	5.8	33
4260	Systems biological assessment of altered cytokine responses to bacteria and fungi reveals impaired immune functionality in schizophrenia. <i>Molecular Psychiatry</i> , 2022, 27, 1205-1216.	4.1	10
4261	Single-cell profiling of T lymphocytes in deficiency of adenosine deaminase 2. <i>Journal of Leukocyte Biology</i> , 2022, 111, 301-312.	1.5	12
4262	Single-Cell Transcriptomic Analysis Reveals a Tumor-Reactive T Cell Signature Associated With Clinical Outcome and Immunotherapy Response In Melanoma. <i>Frontiers in Immunology</i> , 2021, 12, 758288.	2.2	13
4263	Competitive binding of E3 ligases TRIM26 and WWP2 controls SOX2 in glioblastoma. <i>Nature Communications</i> , 2021, 12, 6321.	5.8	16
4265	Profiling the specificity of clonally expanded plasma cells during chronic viral infection by single-cell analysis. <i>European Journal of Immunology</i> , 2022, 52, 297-311.	1.6	11
4267	Nuclear Factor I in neurons, glia and during the formation of Müller glia-derived progenitor cells in avian, porcine and primate retinas. <i>Journal of Comparative Neurology</i> , 2022, 530, 1213-1230.	0.9	11
4268	Identification of Key Immune-Related Genes in the Progression of Septic Shock. <i>Frontiers in Genetics</i> , 2021, 12, 668527.	1.1	3
4269	Profiling cellular diversity in sponges informs animal cell type and nervous system evolution. <i>Science</i> , 2021, 374, 717-723.	6.0	111

#	ARTICLE	IF	CITATIONS
4270	Multidimensional Single-Nuclei RNA-Seq Reconstruction of Adipose Tissue Reveals Adipocyte Plasticity Underlying Thermogenic Response. <i>Cells</i> , 2021, 10, 3073.	1.8	11
4271	Single-Cell Transcriptomics Analysis of Human Small Antral Follicles. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11955.	1.8	18
4272	Epithelial-myeloid exchange of MHC class II constrains immunity and microbiota composition. <i>Cell Reports</i> , 2021, 37, 109916.	2.9	14
4274	Characterization of Alzheimer's Disease-Associated Excitatory Neurons via Single-Cell RNA Sequencing Analysis. <i>Frontiers in Aging Neuroscience</i> , 2021, 13, 742176.	1.7	7
4275	Skeletal stem cell fate defects caused by <i>Pdgfrb</i> activating mutation. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	5
4307	Developmental, cellular, and behavioral phenotypes in a mouse model of congenital hypoplasia of the dentate gyrus. <i>ELife</i> , 2020, 9, .	2.8	2
4320	A semi-automatic cell type annotation method for single-cell RNA sequencing dataset. <i>Genomics and Informatics</i> , 2020, 18, e26.	0.4	0
4343	AbSeq Protocol Using the Nano-Well Cartridge-Based Rhapsody Platform to Generate Protein and Transcript Expression Data on the Single-Cell Level. <i>STAR Protocols</i> , 2020, 1, 100092.	0.5	12
4371	Targeted urine proteomics in lupus nephritis – a meta-analysis. <i>Expert Review of Proteomics</i> , 2020, 17, 767-776.	1.3	12
4374	Sexual Dimorphism through the Lens of Genome Manipulation, Forward Genetics, and Spatiotemporal Sequencing. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
4375	LISA: Accurate reconstruction of cell trajectory and pseudo-time for massive single cell RNA-seq data. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2019, 24, 338-349.	0.7	4
4376	Single-cell RNA-Seq analysis identifies a putative epithelial stem cell population in human primary prostate cells in monolayer and organoid culture conditions. <i>American Journal of Clinical and Experimental Urology</i> , 2019, 7, 123-138.	0.4	11
4377	An optimized protocol for retina single-cell RNA sequencing. <i>Molecular Vision</i> , 2020, 26, 705-717.	1.1	13
4378	Single-cell rna seq analysis identifies the biomarkers and differentiation of chondrocyte in human osteoarthritis. <i>American Journal of Translational Research (discontinued)</i> , 2020, 12, 7326-7339.	0.0	6
4379	Single-cell transcriptomic profiling provides insights into retinal endothelial barrier properties. <i>Molecular Vision</i> , 2020, 26, 766-779.	1.1	2
4381	Single-cell RNA analysis reveals the potential risk of organ-specific cell types vulnerable to SARS-CoV-2 infections. <i>Computers in Biology and Medicine</i> , 2022, 140, 105092.	3.9	73
4382	Single-cell transcriptome analysis of Bisphenol A exposure reveals the key roles of the testicular microenvironment in male reproduction. <i>Biomedicine and Pharmacotherapy</i> , 2022, 145, 112449.	2.5	7
4383	Enhanced single-cell RNA-seq workflow reveals coronary artery disease cellular cross-talk and candidate drug targets. <i>Atherosclerosis</i> , 2022, 340, 12-22.	0.4	35

#	ARTICLE	IF	CITATIONS
4384	Single-Cell Transcriptomic Sequencing Analyses of Cell Heterogeneity During Osteogenesis of Human Adipose-Derived Mesenchymal Stem Cells. <i>Stem Cells</i> , 2021, 39, 1478-1488.	1.4	8
4386	Germline biallelic mutation affecting the transcription factor Helios causes pleiotropic defects of immunity. <i>Science Immunology</i> , 2021, 6, eabe3981.	5.6	16
4387	Dietary palmitic acid promotes a prometastatic memory via Schwann cells. <i>Nature</i> , 2021, 599, 485-490.	13.7	126
4388	A Novel Single-Cell RNA Sequencing Data Feature Extraction Method Based on Gene Function Analysis and Its Applications in Glioma Study. <i>Frontiers in Oncology</i> , 2021, 11, 797057.	1.3	1
4389	A distinct D1-MSN subpopulation down-regulates dopamine to promote negative emotional state. <i>Cell Research</i> , 2022, 32, 139-156.	5.7	34
4390	Urine Single-Cell RNA Sequencing in Focal Segmental Glomerulosclerosis Reveals Inflammatory Signatures. <i>Kidney International Reports</i> , 2022, 7, 289-304.	0.4	21
4391	Prenatal interleukin 6 elevation increases glutamatergic synapse density and disrupts hippocampal connectivity in offspring. <i>Immunity</i> , 2021, 54, 2611-2631.e8.	6.6	63
4392	Desmoplakin and periplakin genetically and functionally contribute to eosinophilic esophagitis. <i>Nature Communications</i> , 2021, 12, 6795.	5.8	23
4394	Topoisomerase II alpha inhibition can overcome taxane-resistant prostate cancer through DNA repair pathways. <i>Scientific Reports</i> , 2021, 11, 22284.	1.6	7
4395	EGFR signaling in the nucleus regulates cell cycle progression and DNA damage response. <i>Nature Communications</i> , 2021, 12, 6906.	5.8	14
4398	CRISPR screens unveil signal hubs for nutrient licensing of T cell immunity. <i>Nature</i> , 2021, 600, 308-313.	13.7	36
4399	GABAergic neuronal IL-4R mediates T cell effect on memory. <i>Neuron</i> , 2021, 109, 3609-3618.e9.	3.8	46
4400	Cell-fate transition and determination analysis of mouse male germ cells throughout development. <i>Nature Communications</i> , 2021, 12, 6839.	5.8	31
4401	NogoA-expressing astrocytes limit peripheral macrophage infiltration after ischemic brain injury in primates. <i>Nature Communications</i> , 2021, 12, 6906.	5.8	14
4402	Pluripotency acquisition in the middle cell layer of callus is required for organ regeneration. <i>Nature Plants</i> , 2021, 7, 1453-1460.	4.7	91
4405	Single-cell RNA-seq highlights a specific carcinoembryonic cluster in ovarian cancer. <i>Cell Death and Disease</i> , 2021, 12, 1082.	2.7	10
4406	Whole-animal multiplexed single-cell RNA-seq reveals transcriptional shifts across <i>Clytia</i> medusa cell types. <i>Science Advances</i> , 2021, 7, eabh1683.	4.7	47
4408	IL-17 Receptor C Signaling Controls CD4+ TH17 Immune Responses and Tissue Injury in Immune-Mediated Kidney Diseases. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 3081-3098.	3.0	14

#	ARTICLE	IF	CITATIONS
4409	Single-cell reconstruction with spatial context of migrating neural crest cells and their microenvironments during vertebrate head and neck formation. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	6
4410	Follicular T cells are clonally and transcriptionally distinct in B cell-driven mouse autoimmune disease. <i>Nature Communications</i> , 2021, 12, 6687.	5.8	12
4411	Resolving the difference between left-sided and right-sided colorectal cancer by single-cell sequencing. <i>JCI Insight</i> , 2022, 7, .	2.3	26
4412	Super-resolved spatial transcriptomics by deep data fusion. <i>Nature Biotechnology</i> , 2022, 40, 476-479.	9.4	61
4413	A growth factor-expressing macrophage subpopulation orchestrates regenerative inflammation via GDF-15. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	31
4414	FEM: mining biological meaning from cell level in single-cell RNA sequencing data. <i>PeerJ</i> , 2021, 9, e12570.	0.9	2
4415	T cell landscape and dynamics in immunoglobulin light chain amyloidosis before and after daratumumab-based therapy. <i>Clinical and Translational Medicine</i> , 2021, 11, e582.	1.7	0
4417	Nested Stochastic Block Models applied to the analysis of single cell data. <i>BMC Bioinformatics</i> , 2021, 22, 576.	1.2	8
4418	Single-nucleus transcriptomes reveal evolutionary and functional properties of cell types in the <i>Drosophila</i> accessory gland. <i>Genetics</i> , 2022, 220, .	1.2	10
4419	Single-cell RNA Sequencing Reveals Thoracolumbar Vertebra Heterogeneity and Rib-genesis in Pigs. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 423-436.	3.0	6
4421	Transcriptomic taxonomy and neurogenic trajectories of adult human, macaque, and pig hippocampal and entorhinal cells. <i>Neuron</i> , 2022, 110, 452-469.e14.	3.8	142
4423	Human and rat skeletal muscle single-nuclei multi-omic integrative analyses nominate causal cell types, regulatory elements, and SNPs for complex traits. <i>Genome Research</i> , 2021, 31, 2258-2275.	2.4	31
4425	Transcriptional landscape of highly lignified poplar stems at single-cell resolution. <i>Genome Biology</i> , 2021, 22, 319.	3.8	47
4426	Dynamic CD4+ T cell heterogeneity defines subset-specific suppression and PD-L1-blockade-driven functional restoration in chronic infection. <i>Nature Immunology</i> , 2021, 22, 1524-1537.	7.0	26
4427	Müller glial responses compensate for degenerating photoreceptors in retinitis pigmentosa. <i>Experimental and Molecular Medicine</i> , 2021, 53, 1748-1758.	3.2	18
4428	Single-cell landscape of peripheral immune responses to fatal SFTS. <i>Cell Reports</i> , 2021, 37, 110039.	2.9	19
4430	Tuft Cells Increase Following Ovine Intestinal Parasite Infections and Define Evolutionarily Conserved and Divergent Responses. <i>Frontiers in Immunology</i> , 2021, 12, 781108.	2.2	9
4431	Single-cell RNA sequencing of the <i>Strongylocentrotus purpuratus</i> larva reveals the blueprint of major cell types and nervous system of a non-chordate deuterostome. <i>ELife</i> , 2021, 10, .	2.8	33

#	ARTICLE	IF	CITATIONS
4432	Mitochondrial inhibitors circumvent adaptive resistance to venetoclax and cytarabine combination therapy in acute myeloid leukemia. <i>Nature Cancer</i> , 2021, 2, 1204-1223.	5.7	42
4433	Exploiting the STAT3 Nexus in Cancer-Associated Fibroblasts to Improve Cancer Therapy. <i>Frontiers in Immunology</i> , 2021, 12, 767939.	2.2	9
4434	Effects of Orally Administered Cannabidiol on Neuroinflammation and Intestinal Inflammation in the Attenuation of Experimental Autoimmune Encephalomyelitis. <i>Journal of NeuroImmune Pharmacology</i> , 2022, 17, 15-32.	2.1	21
4435	Single-Cell Transcriptome Profiles Reveal Fibrocytes as Potential Targets of Cell Therapies for Abdominal Aortic Aneurysm. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 753711.	1.1	10
4436	Single cell-derived spheroids capture the self-renewing subpopulations of metastatic ovarian cancer. <i>Cell Death and Differentiation</i> , 2022, 29, 614-626.	5.0	20
4438	Cancer-associated MSC drive tumor immune exclusion and resistance to immunotherapy, which can be overcome by Hedgehog inhibition. <i>Science Advances</i> , 2021, 7, eabi5790.	4.7	35
4439	Single-Cell Transcriptomics Reveals the Expression of Aging- and Senescence-Associated Genes in Distinct Cancer Cell Populations. <i>Cells</i> , 2021, 10, 3126.	1.8	18
4442	Neoadjuvant PD-1 blockade induces T cell and cDC1 activation but fails to overcome the immunosuppressive tumor associated macrophages in recurrent glioblastoma. <i>Nature Communications</i> , 2021, 12, 6938.	5.8	93
4443	Single-cell transcriptomics identifies Gadd45b as a regulator of herpesvirus-reactivating neurons. <i>EMBO Reports</i> , 2022, 23, e53543.	2.0	16
4444	Navigating the pitfalls of applying machine learning in genomics. <i>Nature Reviews Genetics</i> , 2022, 23, 169-181.	7.7	114
4446	Type I interferon activates MHC class I-dressed CD11b+ conventional dendritic cells to promote protective anti-tumor CD8+ T cell immunity. <i>Immunity</i> , 2022, 55, 308-323.e9.	6.6	126
4447	Identification of Prognostic Biomarkers Originating From the Tumor Stroma of Betel Quid-Associated Oral Cancer Tissues. <i>Frontiers in Oncology</i> , 2021, 11, 769665.	1.3	5
4448	Single-cell RNA-seq and chromatin accessibility profiling decipher the heterogeneity of mouse $\gamma\delta$ T cells. <i>Science Bulletin</i> , 2022, 67, 408-426.	4.3	16
4449	Single-cell transcriptome profiling reveals intratumoural heterogeneity and malignant progression in retinoblastoma. <i>Cell Death and Disease</i> , 2021, 12, 1100.	2.7	8
4450	Automated annotation of rare-cell types from single-cell RNA-sequencing data through synthetic oversampling. <i>BMC Bioinformatics</i> , 2021, 22, 557.	1.2	6
4451	Novel Insights into the Stemness and Immune Privilege of Mesenchymal Stem Cells from Human Wharton Jelly by Single-Cell RNA Sequencing. <i>Medical Science Monitor</i> , 2022, 28, e934660.	0.5	2
4452	Generation of functional ciliated cholangiocytes from human pluripotent stem cells. <i>Nature Communications</i> , 2021, 12, 6504.	5.8	15
4453	Single-Cell Sequencing Reveals Differential Cell Types in Skin Tissues of Liaoning Cashmere Goats and Key Genes Related Potentially to the Fineness of Cashmere Fiber. <i>Frontiers in Genetics</i> , 2021, 12, 726670.	1.1	3

#	ARTICLE	IF	CITATIONS
4454	Hif-1a suppresses ROS-induced proliferation of cardiac fibroblasts following myocardial infarction. <i>Cell Stem Cell</i> , 2022, 29, 281-297.e12.	5.2	71
4455	A deficient MIF-CD74 signaling pathway may play an important role in immunotherapy-induced hyper-progressive disease. <i>Cell Biology and Toxicology</i> , 2021, , 1.	2.4	5
4456	Stroke subtype-dependent synapse elimination by reactive gliosis in mice. <i>Nature Communications</i> , 2021, 12, 6943.	5.8	84
4457	Differential Type 1 IFN Gene Expression in CD14+ Placenta Cells Elicited by Zika Virus Infection During Pregnancy. <i>Frontiers in Virology</i> , 2021, 1, .	0.7	3
4458	Single cell multi-omic analysis identifies a Tbx1-dependent multilineage primed population in murine cardiopharyngeal mesoderm. <i>Nature Communications</i> , 2021, 12, 6645.	5.8	31
4459	Single-Cell Transcriptome Profiling Reveals Multicellular Ecosystem of Nucleus Pulposus during Degeneration Progression. <i>Advanced Science</i> , 2022, 9, e2103631.	5.6	35
4460	Noninvasive Tape-Stripping with High-Resolution RNA Profiling Effectively Captures a Preinflammatory State in Nonlesional Psoriatic Skin. <i>Journal of Investigative Dermatology</i> , 2022, 142, 1587-1596.e2.	0.3	13
4461	ecDNA hubs drive cooperative intermolecular oncogene expression. <i>Nature</i> , 2021, 600, 731-736.	13.7	123
4462	Single-cell transcriptomics reveals opposing roles of Shp2 in Myc-driven liver tumor cells and microenvironment. <i>Cell Reports</i> , 2021, 37, 109974.	2.9	26
4463	Single-cell transcriptomic profiles reveal changes associated with BCG-induced trained immunity and protective effects in circulating monocytes. <i>Cell Reports</i> , 2021, 37, 110028.	2.9	31
4464	Proteogenomics of non-small cell lung cancer reveals molecular subtypes associated with specific therapeutic targets and immune-evasion mechanisms. <i>Nature Cancer</i> , 2021, 2, 1224-1242.	5.7	37
4465	circRNAome profiling reveals circFgfr2 regulates myogenesis and muscle regeneration via a feedback loop. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2022, 13, 696-712.	2.9	28
4466	EGFR Pathway-Based Gene Signatures of Druggable Gene Mutations in Melanoma, Breast, Lung, and Thyroid Cancers. <i>Biochemistry (Moscow)</i> , 2021, 86, 1477-1488.	0.7	1
4467	Identifying phenotype-associated subpopulations by integrating bulk and single-cell sequencing data. <i>Nature Biotechnology</i> , 2022, 40, 527-538.	9.4	128
4472	Lef1 restricts ectopic crypt formation and tumor cell growth in intestinal adenomas. <i>Science Advances</i> , 2021, 7, eabj0512.	4.7	6
4473	Genome annotation with long RNA reads reveals new patterns of gene expression and improves single-cell analyses in an ant brain. <i>BMC Biology</i> , 2021, 19, 254.	1.7	11
4474	Colon Cancer-Related Genes Identification and Function Study Based on Single-Cell Multi-Omics Integration. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 789587.	1.8	4
4475	Sparsely Connected Autoencoders: A Multi-Purpose Tool for Single Cell omics Analysis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12755.	1.8	13

#	ARTICLE	IF	CITATIONS
4477	FOXN1 forms higher-order nuclear condensates displaced by mutations causing immunodeficiency. <i>Science Advances</i> , 2021, 7, eabj9247.	4.7	10
4478	Evaluating microglial phenotypes using single-cell technologies. <i>Trends in Neurosciences</i> , 2022, 45, 133-144.	4.2	11
4479	Gene biomarker prediction in glioma by integrating scRNA-seq data and gene regulatory network. <i>BMC Medical Genomics</i> , 2021, 14, 287.	0.7	3
4480	The novel BET inhibitor UM-002 reduces glioblastoma cell proliferation and invasion. <i>Scientific Reports</i> , 2021, 11, 23370.	1.6	14
4481	A principal feature analysis. <i>Journal of Computational Science</i> , 2022, 58, 101502.	1.5	4
4482	Transcriptional profiling of sequentially generated septal neuron fates. <i>ELife</i> , 2021, 10, .	2.8	12
4486	AD-linked R47H- <i>TREM2</i> mutation induces disease-enhancing microglial states via AKT hyperactivation. <i>Science Translational Medicine</i> , 2021, 13, eabe3947.	5.8	55
4488	Single-Cell RNA Sequencing of Mouse Left Ventricle Reveals Cellular Diversity and Intercommunication. <i>Physiological Genomics</i> , 2021, , .	1.0	1
4489	Mapping the temporal and spatial dynamics of the human endometrium in vivo and in vitro. <i>Nature Genetics</i> , 2021, 53, 1698-1711.	9.4	238
4490	Immune system cells from COVID-19 patients display compromised mitochondrial-nuclear expression co-regulation and rewiring toward glycolysis. <i>IScience</i> , 2021, 24, 103471.	1.9	20
4493	An NK-like CAR T cell transition in CAR T cell dysfunction. <i>Cell</i> , 2021, 184, 6081-6100.e26.	13.5	160
4494	How a cell decides its own fate: a single-cell view of molecular mechanisms and dynamics of cell-type specification. <i>Biochemical Society Transactions</i> , 2021, 49, 2509-2525.	1.6	3
4495	Spatially Resolved Transcriptomic Analysis of Acute Kidney Injury in a Female Murine Model. <i>Journal of the American Society of Nephrology: JASN</i> , 2022, 33, 279-289.	3.0	62
4496	Defining Inner Ear Cell Type Specification at Single-Cell Resolution in a Model of Human Cranial Development. <i>SSRN Electronic Journal</i> , 0, , .	0.4	6
4497	A robust and scalable graph neural network for accurate single-cell classification. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	15
4498	On the relation between input and output distributions of scRNA-seq experiments. <i>Bioinformatics</i> , 2022, 38, 1336-1343.	1.8	1
4499	Secretory MPP3 Reinforce Myeloid Differentiation Trajectory and Amplify Myeloid Cell Production. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4500	A Clustering Ensemble Method for Cell Type Detection by Multiobjective Particle Optimization. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, PP, 1-1.	1.9	1

#	ARTICLE	IF	CITATIONS
4501	A universal approach for integrating super large-scale single-cell transcriptomes by exploring gene rankings. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	2
4502	Gene Co-Expression Network Characterizing Microenvironmental Heterogeneity and Intercellular Communication in Pancreatic Ductal Adenocarcinoma: Implications of Prognostic Significance and Therapeutic Target. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4503	A scRNA-seq Based Prediction Model of EGFR-TKIs Resistance in Patients With Non-Small Cell Lung Adenocarcinoma. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4504	sc-REnF: An entropy guided robust feature selection for single-cell RNA-seq data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	10
4505	Single-Cell Analysis of Embryoids Reveals Lineage Diversification Roadmaps of Early Human Development. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
4506	STAG2 Promotes the Myelination Transcriptional Program in Oligodendrocytes. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4507	Upregulation of the Clock Gene E4BP4 in Macrophages Induces an Anti-Inflammatory Phenotype Promoting Recovery From Colitis. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4508	circMbl Functions in <i>cis</i> and in <i>trans</i> to Regulate Gene Expression With Impacts on Physiology. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4509	Single Cell Profiling of Hofbauer Cells and Fetal Brain Microglia Reveals Shared Programs and Functions. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
4510	Fast Computational Recovery of Missing Features for Large-scale Biological Data. <i>Springer Theses</i> , 2021, , 13-40.	0.0	0
4511	Single-Cell Atlas Unveils Cellular Heterogeneity and Novel Markers in Human Neonatal and Adult Intervertebral Discs. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4512	scMAGIC: accurately annotating single cells using two rounds of reference-based classification. <i>Nucleic Acids Research</i> , 2022, 50, e43-e43.	6.5	11
4514	scDIOR: single cell RNA-seq data IO software. <i>BMC Bioinformatics</i> , 2022, 23, 16.	1.2	9
4515	In Mice and Humans, Brain Vascular Barrier Homeostasis and Contractility Are Acquired Postnatally. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4516	Single-Cell RNA-Seq of Bone Marrow Cells in Aplastic Anemia. <i>Frontiers in Genetics</i> , 2021, 12, 745483.	1.1	6
4517	Unbiased visualization of single-cell genomic data with SCUBI. <i>Cell Reports Methods</i> , 2022, 2, 100135.	1.4	6
4518	A diverse fibroblastic stromal cell landscape in the spleen directs tissue homeostasis and immunity. <i>Science Immunology</i> , 2022, 7, eabj0641.	5.6	27
4519	Single cell analysis reveals inhibition of angiogenesis attenuates the progression of heterotopic ossification in <i>Mx^{Cre}/p^{Cre}</i> mice. <i>Bone Research</i> , 2022, 10, 4.	5.4	7

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4520	C-type lectin receptor CLEC4A2 promotes tissue adaptation of macrophages and protects against atherosclerosis. <i>Nature Communications</i> , 2022, 13, 215.	5.8	28
4521	OUP accepted manuscript. <i>Briefings in Bioinformatics</i> , 2022, , .	3.2	0
4522	Antigen presentation and interferon signatures in B cells driven by localized ablative cancer immunotherapy correlate with extended survival. <i>Theranostics</i> , 2022, 12, 639-656.	4.6	8
4523	Genomic Identification, Evolution, and Expression Analysis of Bromodomain Genes Family in Buffalo. <i>Genes</i> , 2022, 13, 103.	1.0	1
4524	Comparative Studies of Renin-Null Zebrafish and Mice Provide New Functional Insights. <i>Hypertension</i> , 2022, 79, HYPERTENSIONAHA12118600.	1.3	4
4525	Engagement of the costimulatory molecule ICOS in tissues promotes establishment of CD8+ tissue-resident memory T _H cells. <i>Immunity</i> , 2022, 55, 98-114.e5.	6.6	38
4526	Analysis of the glyco-code in pancreatic ductal adenocarcinoma identifies glycan-mediated immune regulatory circuits. <i>Communications Biology</i> , 2022, 5, 41.	2.0	8
4527	Heterogeneity of tumor microenvironment is associated with clinical prognosis of non-clear cell renal cell carcinoma: a single-cell genomics study. <i>Cell Death and Disease</i> , 2022, 13, 50.	2.7	8
4528	Proteogenomic characterization identifies clinically relevant subgroups of intrahepatic cholangiocarcinoma. <i>Cancer Cell</i> , 2022, 40, 70-87.e15.	7.7	120
4529	Acquisition, processing, and single-cell analysis of normal human breast tissues from a biobank. <i>STAR Protocols</i> , 2022, 3, 101047.	0.5	6
4532	Resistant Fit Regression Normalization for Single-cell RNA-seq Data. , 2020, , .		0
4533	Limited Extent and Consequences of Pancreatic SARS-CoV-2 Infection. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4534	Prudent application of single-cell RNA sequencing in understanding cellular features and functional phenotypes in cancer studies. <i>Chinese Journal of Cancer Research: Official Journal of China Anti-Cancer Association, Beijing Institute for Cancer Research</i> , 2021, 33, 719-723.	0.7	1
4535	GranatumX: A Community-engaging, Modularized, and Flexible Webtool for Single-cell Data Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 452-460.	3.0	3
4536	Differences in Immune Checkpoint Protein Expression among Immune Cells in Lung Carcinoma. , 2021, , .		0
4537	Transcriptional Differences in Luminal Epithelial Cells in Patients with and without Lymph Node Involvement in TNBC. , 2021, , .		0
4539	Drug-Resistant States in Response to EGFR Tyrosine Kinase Inhibitors in Non-Small-Cell Lung Cancer. , 2021, , .		0
4540	Single-cell immunology of SARS-CoV-2 infection. <i>Nature Biotechnology</i> , 2022, 40, 30-41.	9.4	78

#	ARTICLE	IF	CITATIONS
4542	Single-Cell RNA Sequencing Reveals the Temporal Diversity and Dynamics of Cardiac Immunity after Myocardial Infarction. <i>Small Methods</i> , 2022, 6, e2100752.	4.6	31
4543	Itaconate and derivatives reduce interferon responses and inflammation in influenza A virus infection. <i>PLoS Pathogens</i> , 2022, 18, e1010219.	2.1	35
4544	Ten-Eleven Translocation Ablation Impairs Cardiac Differentiation of Mouse Embryonic Stem Cells. <i>Stem Cells</i> , 2022, 40, 260-272.	1.4	3
4545	Analysis and Visualization of Spatial Transcriptomic Data. <i>Frontiers in Genetics</i> , 2021, 12, 785290.	1.1	23
4547	Integrated single-cell RNA sequencing analysis reveals distinct cellular and transcriptional modules associated with survival in lung cancer. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 9.	7.1	23
4548	Single-Cell Transcriptome Analysis of Chronic Antibody-Mediated Rejection After Renal Transplantation. <i>Frontiers in Immunology</i> , 2021, 12, 767618.	2.2	19
4549	Single-cell transcriptomics of human iPSC differentiation dynamics reveal a core molecular network of Parkinson's disease. <i>Communications Biology</i> , 2022, 5, 49.	2.0	10
4550	Lung emphysema and impaired macrophage elastase clearance in mucolipin 3 deficient mice. <i>Nature Communications</i> , 2022, 13, 318.	5.8	25
4554	Integration of single-cell transcriptomes and chromatin landscapes reveals regulatory programs driving pharyngeal organ development. <i>Nature Communications</i> , 2022, 13, 457.	5.8	22
4555	A functional cellular framework for sex and estrous cycle-dependent gene expression and behavior. <i>Cell</i> , 2022, 185, 654-671.e22.	13.5	52
4556	Inducing human retinal pigment epithelium-like cells from somatic tissue. <i>Stem Cell Reports</i> , 2022, 17, 289-306.	2.3	3
4557	Single-cell multi-omics reveals dyssynchrony of the innate and adaptive immune system in progressive COVID-19. <i>Nature Communications</i> , 2022, 13, 440.	5.8	100
4558	iMyoblasts for ex vivo and in vivo investigations of human myogenesis and disease modeling. <i>ELife</i> , 2022, 11, .	2.8	13
4561	Revisiting hematopoiesis: applications of the bulk and single-cell transcriptomics dissecting transcriptional heterogeneity in hematopoietic stem cells. <i>Briefings in Functional Genomics</i> , 2022, 21, 159-176.	1.3	15
4562	Temporal modelling using single-cell transcriptomics. <i>Nature Reviews Genetics</i> , 2022, 23, 355-368.	7.7	65
4564	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
4565	The Crosstalk Between Malignant Cells and Tumor-Promoting Immune Cells Relevant to Immunotherapy in Pancreatic Ductal Adenocarcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 821232.	1.8	3
4566	Single-cell analysis of human primary prostate cancer reveals the heterogeneity of tumor-associated epithelial cell states. <i>Nature Communications</i> , 2022, 13, 141.	5.8	76

#	ARTICLE	IF	CITATIONS
4567	Neuronal Yin Yang1 in the prefrontal cortex regulates transcriptional and behavioral responses to chronic stress in mice. <i>Nature Communications</i> , 2022, 13, 55.	5.8	14
4568	HSP90 Inhibitor 17-AAG Attenuates Nucleus Pulposus Inflammation and Catabolism Induced by M1-Polarized Macrophages. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 796974.	1.8	15
4569	Benchmarking of a Bayesian single cell RNAseq differential gene expression test for dose-response study designs. <i>Nucleic Acids Research</i> , 2022, 50, e48-e48.	6.5	7
4570	Tracking Immunoglobulin Repertoire and Transcriptomic Changes in Germinal Center B Cells by Single-Cell Analysis. <i>Frontiers in Immunology</i> , 2021, 12, 818758.	2.2	4
4571	Three tissue resident macrophage subsets coexist across organs with conserved origins and life cycles. <i>Science Immunology</i> , 2022, 7, eabf7777.	5.6	167
4573	Cell trajectory modeling identifies a primitive trophoblast state defined by BCAM enrichment. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	39
4575	Single-cell RNA sequencing analysis reveals the relationship of bone marrow and osteopenia in STZ-induced type 1 diabetic mice. <i>Journal of Advanced Research</i> , 2022, 41, 145-158.	4.4	3
4576	Transcriptional changes in the mammary gland during lactation revealed by single cell sequencing of cells from human milk. <i>Nature Communications</i> , 2022, 13, 562.	5.8	34
4577	Oncogenesis induced by combined Phf6 and Idh2 mutations through increased oncometabolites and impaired DNA repair. <i>Oncogene</i> , 2022, 41, 1576-1588.	2.6	3
4578	Mesenchymal stromal cell-derived septoclasts resorb cartilage during developmental ossification and fracture healing. <i>Nature Communications</i> , 2022, 13, 571.	5.8	21
4579	Accurate and fast cell marker gene identification with COSG. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	39
4581	Tfp2b specifies an embryonic melanocyte stem cell that retains adult multifate potential. <i>Cell Reports</i> , 2022, 38, 110234.	2.9	15
4582	Development of a single-cell atlas for woodland strawberry (<i>Fragaria vesca</i>) leaves during early <i>Botrytis cinerea</i> infection using single-cell RNA-seq. <i>Horticulture Research</i> , 2022, 9, .	2.9	21
4583	Molecular mechanisms governing circulating immune cell heterogeneity across different species revealed by single-cell sequencing. <i>Clinical and Translational Medicine</i> , 2022, 12, e689.	1.7	6
4585	Squidpy: a scalable framework for spatial omics analysis. <i>Nature Methods</i> , 2022, 19, 171-178.	9.0	308
4587	Transcriptional repression and apoptosis influence the effect of APOBEC3A/3B functional polymorphisms on biliary tract cancer risk. <i>International Journal of Cancer</i> , 2022, 150, 1825-1837.	2.3	8
4588	Visualization, benchmarking and characterization of nested single-cell heterogeneity as dynamic forest mixtures. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	2
4590	Single-cell sequencing and its applications in bladder cancer. <i>Expert Reviews in Molecular Medicine</i> , 2022, 24, e6.	1.6	8

#	ARTICLE	IF	CITATIONS
4591	CXCL4 drives fibrosis by promoting several key cellular and molecular processes. <i>Cell Reports</i> , 2022, 38, 110189.	2.9	31
4593	Pyruvate dehydrogenase inactivation causes glycolytic phenotype in BAP1 mutant uveal melanoma. <i>Oncogene</i> , 2022, , .	2.6	6
4594	Pre-existing Castration-resistant Prostate Cancer-like Cells in Primary Prostate Cancer Promote Resistance to Hormonal Therapy. <i>European Urology</i> , 2022, 81, 446-455.	0.9	41
4595	Cellular architecture of human brain metastases. <i>Cell</i> , 2022, 185, 729-745.e20.	13.5	69
4596	GSDMB is increased in IBD and regulates epithelial restitution/repair independent of pyroptosis. <i>Cell</i> , 2022, 185, 283-298.e17.	13.5	86
4597	Claudin-10a Deficiency Shifts Proximal Tubular Cl- Permeability to Cation Selectivity via Claudin-2 Redistribution. <i>Journal of the American Society of Nephrology: JASN</i> , 2022, 33, 699-717.	3.0	20
4599	Common and Distinctive Intercellular Communication Patterns in Human Obstructive and Nonobstructive Hypertrophic Cardiomyopathy. <i>International Journal of Molecular Sciences</i> , 2022, 23, 946.	1.8	10
4600	Evidence for Multiple Subpopulations of Herpesvirus-Latently Infected Cells. <i>MBio</i> , 2022, 13, e0347321.	1.8	12
4602	Human airway lineages derived from pluripotent stem cells reveal the epithelial responses to SARS-CoV-2 infection. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2022, 322, L462-L478.	1.3	17
4603	A Single Cell Analysis of Thymopoiesis and Thymic iNKT Cell Development in Pigs. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4604	Long non-coding RNAs (lncRNAs) NEAT1 and MALAT1 are differentially expressed in severe COVID-19 patients: An integrated single-cell analysis. <i>PLoS ONE</i> , 2022, 17, e0261242.	1.1	37
4605	Single-Cell Profiles of Age-Related Osteoarthritis Uncover Underlying Heterogeneity Associated With Disease Progression. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 748360.	1.6	8
4606	A Pro-Endocrine Pancreatic Islet Transcriptional Program Established During Development Is Retained in Human Gallbladder Epithelial Cells. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2022, 13, 1530-1553.e4.	2.3	1
4607	Spatial omics: Navigating to the golden era of cancer research. <i>Clinical and Translational Medicine</i> , 2022, 12, e696.	1.7	53
4608	Single Nuclear RNA Sequencing Highlights Intra-Tumoral Heterogeneity and Tumor Microenvironment Complexity in Testicular Embryonic Rhabdomyosarcoma. <i>Journal of Inflammation Research</i> , 2022, Volume 15, 493-507.	1.6	3
4610	Single-cell immune profiling reveals functional diversity of T cells in tuberculous pleural effusion. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	12
4611	Lysyl oxidase promotes anaplastic thyroid carcinoma cell proliferation and metastasis mediated via BMP1. <i>Gland Surgery</i> , 2022, 11, 245-257.	0.5	6
4612	Adaptive differentiation promotes intestinal villus recovery. <i>Developmental Cell</i> , 2022, 57, 166-179.e6.	3.1	25

#	ARTICLE	IF	CITATIONS
4613	Patterning the embryonic pulmonary mesenchyme. <i>IScience</i> , 2022, 25, 103838.	1.9	13
4614	Selective translation of epigenetic modifiers affects the temporal pattern and differentiation of neural stem cells. <i>Nature Communications</i> , 2022, 13, 470.	5.8	20
4615	Vec2image: an explainable artificial intelligence model for the feature representation and classification of high-dimensional biological data by vector-to-image conversion. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	9
4616	Dysregulation of interaction between LOX ^{high} fibroblast and smooth muscle cells contributes to the pathogenesis of aortic dissection. <i>Theranostics</i> , 2022, 12, 910-928.	4.6	17
4617	Robust Transcriptional Profiling and Identification of Differentially Expressed Genes With Low Input RNA Sequencing of Adult Hippocampal Neural Stem and Progenitor Populations. <i>Frontiers in Molecular Neuroscience</i> , 2022, 15, 810722.	1.4	9
4618	Colonic healing requires Wnt produced by epithelium as well as Tagln+ and Acta2+ stromal cells. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	9
4619	baredSC: Bayesian approach to retrieve expression distribution of single-cell data. <i>BMC Bioinformatics</i> , 2022, 23, 36.	1.2	3
4620	Single-cell chromatin accessibility landscape in kidney identifies additional cell-of-origin in heterogenous papillary renal cell carcinoma. <i>Nature Communications</i> , 2022, 13, 31.	5.8	20
4621	Dynamic transcriptome and chromatin architecture in granulosa cells during chicken folliculogenesis. <i>Nature Communications</i> , 2022, 13, 131.	5.8	24
4623	scPretrain: multi-task self-supervised learning for cell-type classification. <i>Bioinformatics</i> , 2022, 38, 1607-1614.	1.8	5
4624	Identification of a regulatory pathway inhibiting adipogenesis via RSPO2. <i>Nature Metabolism</i> , 2022, 4, 90-105.	5.1	39
4625	Generation of cDC-like cells from human induced pluripotent stem cells via Notch signaling. , 2022, 10, e003827.		14
4630	FSCAM: CAM-Based Feature Selection for Clustering scRNA-seq. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2022, , 1.	2.2	1
4633	Dissecting the heterogeneity of the microenvironment in primary and recurrent nasopharyngeal carcinomas using single-cell RNA sequencing. <i>Oncolmmunology</i> , 2022, 11, 2026583.	2.1	15
4634	Functional New Transcription Factors (TFs) Associated with Cervical Cancer. <i>Journal of Healthcare Engineering</i> , 2022, 2022, 1-11.	1.1	4
4635	Transmural pressure signals through retinoic acid to regulate lung branching. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	10
4636	Macrophages facilitate peripheral nerve regeneration by organizing regeneration tracks through Plexin-B2. <i>Genes and Development</i> , 2022, 36, 133-148.	2.7	9
4639	New horizons in the stormy sea of multimodal single-cell data integration. <i>Molecular Cell</i> , 2022, 82, 248-259.	4.5	9

#	ARTICLE	IF	CITATIONS
4640	TRAF6 functions as a tumor suppressor in myeloid malignancies by directly targeting MYC oncogenic activity. <i>Cell Stem Cell</i> , 2022, 29, 298-314.e9.	5.2	23
4642	Quiescent human glioblastoma cancer stem cells drive tumor initiation, expansion, and recurrence following chemotherapy. <i>Developmental Cell</i> , 2022, 57, 32-46.e8.	3.1	71
4643	Zero-preserving imputation of single-cell RNA-seq data. <i>Nature Communications</i> , 2022, 13, 192.	5.8	93
4644	Characterization of transcript enrichment and detection bias in single-nucleus RNA-seq for mapping of distinct human adipocyte lineages. <i>Genome Research</i> , 2022, 32, 242-257.	2.4	39
4645	Developmental single-cell transcriptomics of hypothalamic POMC neurons reveal the genetic trajectories of multiple neuropeptidergic phenotypes. <i>ELife</i> , 2022, 11, .	2.8	16
4648	JEBIN: analyzing gene co-expressions across multiple datasets by joint network embedding. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	1
4649	Single-cell RNA-seq sequencing of <i>Nicotiana attenuata</i> corolla cells reveals the biosynthetic pathway of a floral scent. <i>New Phytologist</i> , 2022, 234, 527-544.	3.5	34
4650	Single cell transcriptomic landscape of diabetic foot ulcers. <i>Nature Communications</i> , 2022, 13, 181.	5.8	111
4652	Correcting Differential Gene Expression Analysis for Cytoarchitectural Alterations in Substantia Nigra of Parkinson's Disease Patients Reveals Known and Potential Novel Disease-Associated Genes and Pathways. <i>Cells</i> , 2022, 11, 198.	1.8	0
4655	TNFR2 pathways are fully active in cancer regulatory T cells. <i>Bioscience, Biotechnology and Biochemistry</i> , 2022, , .	0.6	4
4656	Midbrain organoids mimic early embryonic neurodevelopment and recapitulate LRRK2-p.Gly2019Ser-associated gene expression. <i>American Journal of Human Genetics</i> , 2022, 109, 311-327.	2.6	24
4657	Single-Cell RNA-Seq Technologies and Computational Analysis Tools: Application in Cancer Research. <i>Methods in Molecular Biology</i> , 2022, 2413, 245-255.	0.4	2
4658	Comprehensive Analysis of Immune-Related Prognosis of TK1 in Hepatocellular Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 786873.	1.3	9
4659	Characterization of Pipefish Immune Cell Populations Through Single-Cell Transcriptomics. <i>Frontiers in Immunology</i> , 2022, 13, 820152.	2.2	11
4660	Single-cell transcriptomic analysis reveals a novel cell state and switching genes during hepatic stellate cell activation in vitro. <i>Journal of Translational Medicine</i> , 2022, 20, 53.	1.8	3
4661	Myeloid-Biased HSC Require Semaphorin 4A From the Bone Marrow Niche for Self-Renewal Under Stress and Life-Long Persistence. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4665	Coal dust exposure triggers heterogeneity of transcriptional profiles in mouse pneumoconiosis and Vitamin D remedies. <i>Particle and Fibre Toxicology</i> , 2022, 19, 7.	2.8	14
4666	Epigenomic priming of immune genes implicates oligodendroglia in multiple sclerosis susceptibility. <i>Neuron</i> , 2022, 110, 1193-1210.e13.	3.8	36

#	ARTICLE	IF	CITATIONS
4668	Single-cell analysis of early chick hypothalamic development reveals that hypothalamic cells are induced from prethalamalike progenitors. <i>Cell Reports</i> , 2022, 38, 110251.	2.9	19
4669	Single-cell analysis of gastric pre-cancerous and cancer lesions reveals cell lineage diversity and intratumoral heterogeneity. <i>Npj Precision Oncology</i> , 2022, 6, 9.	2.3	48
4672	SkewC: Identifying cells with skewed gene body coverage in single-cell RNA sequencing data. <i>IScience</i> , 2022, 25, 103777.	1.9	4
4673	Development of human alveolar epithelial cell models to study distal lung biology and disease. <i>IScience</i> , 2022, 25, 103780.	1.9	15
4674	Randomized trial of neoadjuvant vaccination with tumor-cell lysate induces T cell response in low-grade gliomas. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	32
4676	Single-Cell Technologies to Decipher the Immune Microenvironment in Myeloid Neoplasms: Perspectives and Opportunities. <i>Frontiers in Oncology</i> , 2021, 11, 796477.	1.3	0
4677	IL10 trains macrophage profibrotic function after lung injury. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2022, 322, L495-L502.	1.3	14
4679	Clonally Expanded Virus-Specific CD8 T Cells Acquire Diverse Transcriptional Phenotypes During Acute, Chronic, and Latent Infections. <i>Frontiers in Immunology</i> , 2022, 13, 782441.	2.2	7
4680	Galectin-3 promotes the adipogenic differentiation of PDGFR α ⁺ cells and ectopic fat formation in regenerating muscle. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	5
4681	Correlation between circulating innate lymphoid cell precursors and thymic function. <i>IScience</i> , 2022, 25, 103732.	1.9	6
4682	Decade-long leukaemia remissions with persistence of CD4 ⁺ CAR T cells. <i>Nature</i> , 2022, 602, 503-509.	13.7	369
4683	Convergent clonal selection of donor- and recipient-derived CMV-specific T cells in hematopoietic stem cell transplant patients. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	2
4684	Upregulation of CD14 in mesenchymal stromal cells accelerates lipopolysaccharide-induced response and enhances antibacterial properties. <i>IScience</i> , 2022, 25, 103759.	1.9	5
4685	Cross-species metabolomic analysis identifies uridine as a potent regeneration promoting factor. <i>Cell Discovery</i> , 2022, 8, 6.	3.1	50
4686	Single-cell transcriptomic landscape identifies the expansion of peripheral blood monocytes as an indicator of HIV-1-TB co-infection. , 2022, 1, 100005.		5
4687	Dissecting the cellular landscape and transcriptome network in viral myocarditis by single-cell RNA sequencing. <i>IScience</i> , 2022, 25, 103865.	1.9	12
4688	A Comprehensive Immune Cell Atlas of Cystic Kidney Disease Reveals the Involvement of Adaptive Immune Cells in Injury-Mediated Cyst Progression in Mice. <i>Journal of the American Society of Nephrology: JASN</i> , 2022, 33, 747-768.	3.0	8
4689	Single-cell resolution of MET- and EMT-like programs in osteoblasts during zebrafish fin regeneration. <i>IScience</i> , 2022, 25, 103784.	1.9	10

#	ARTICLE	IF	CITATIONS
4690	Diagnostic Evidence GAUGE of Single cells (DEGAS): a flexible deep transfer learning framework for prioritizing cells in relation to disease. <i>Genome Medicine</i> , 2022, 14, 11.	3.6	10
4692	A cell atlas of microbe-responsive processes in the zebrafish intestine. <i>Cell Reports</i> , 2022, 38, 110311.	2.9	31
4693	Generation of the organotypic kidney structure by integrating pluripotent stem cell-derived renal stroma. <i>Nature Communications</i> , 2022, 13, 611.	5.8	29
4694	Lung cancer scRNA-seq and lipidomics reveal aberrant lipid metabolism for early-stage diagnosis. <i>Science Translational Medicine</i> , 2022, 14, eabk2756.	5.8	57
4696	Calcium Signaling Is Impaired in PTEN-Deficient T Cell Acute Lymphoblastic Leukemia. <i>Frontiers in Immunology</i> , 2022, 13, 797244.	2.2	4
4697	A protocol to extract cell-type-specific signatures from differentially expressed genes in bulk-tissue RNA-seq. <i>STAR Protocols</i> , 2022, 3, 101121.	0.5	10
4698	Reproducibility of 10x Genomics single cell RNA sequencing method in the immune cell environment. <i>Journal of Immunological Methods</i> , 2022, 502, 113227.	0.6	3
4699	Recent advances in T-cell receptor repertoire analysis: Bridging the gap with multimodal single-cell RNA sequencing. <i>Immunoinformatics</i> , 2022, 5, 100009.	1.2	27
4700	Integrated hepatic single-cell RNA sequencing and untargeted metabolomics reveals the immune and metabolic modulation of Qing-Fei-Pai-Du decoction in mice with coronavirus-induced pneumonia. <i>Phytomedicine</i> , 2022, 97, 153922.	2.3	13
4701	Data harmonisation for information fusion in digital healthcare: A state-of-the-art systematic review, meta-analysis and future research directions. <i>Information Fusion</i> , 2022, 82, 99-122.	11.7	62
4702	SLRRSC: Single-Cell Type Recognition Method Based on Similarity and Graph Regularization Constraints. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2022, 26, 3556-3566.	3.9	8
4703	Choroidal endothelial and macrophage gene expression in atrophic and neovascular macular degeneration. <i>Human Molecular Genetics</i> , 2022, 31, 2406-2423.	1.4	26
4704	A high-throughput single cell-based antibody discovery approach against the full-length SARS-CoV-2 spike protein suggests a lack of neutralizing antibodies targeting the highly conserved S2 domain. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	2
4705	A blood atlas of COVID-19 defines hallmarks of disease severity and specificity. <i>Cell</i> , 2022, 185, 916-938.e58.	13.5	164
4706	The maize single-nucleus transcriptome comprehensively describes signaling networks governing movement and development of grass stomata. <i>Plant Cell</i> , 2022, , .	3.1	8
4707	<i>Csf1r</i> ⁺ <i>Cd68</i> ⁺ Macrophages Uniquely Express <i>Lactotransferrin</i> and <i>Vegfc</i> During Complex Tissue Regeneration in Spiny Mice. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4708	CITEMOXMBD: A flexible single-cell multimodal omics analysis framework to reveal the heterogeneity of immune cells. <i>RNA Biology</i> , 2022, 19, 290-304.	1.5	10
4709	Single-cell isoform analysis in human immune cells. <i>Genome Biology</i> , 2022, 23, 47.	3.8	35

#	ARTICLE	IF	CITATIONS
4710	GPR35 promotes neutrophil recruitment in response to serotonin metabolite 5-HIAA. <i>Cell</i> , 2022, 185, 815-830.e19.	13.5	52
4711	Human embryoid bodies as a novel system for genomic studies of functionally diverse cell types. <i>ELife</i> , 2022, 11, .	2.8	7
4712	The P522R protective variant of PLCC2 promotes the expression of antigen presentation genes by human microglia in an Alzheimer's disease mouse model. <i>Alzheimer's and Dementia</i> , 2022, 18, 1765-1778.	0.4	19
4713	Tryptophan-derived microbial metabolites activate the aryl hydrocarbon receptor in tumor-associated macrophages to suppress anti-tumor immunity. <i>Immunity</i> , 2022, 55, 324-340.e8.	6.6	179
4714	A single-cell Arabidopsis root atlas reveals developmental trajectories in wild-type and cell identity mutants. <i>Developmental Cell</i> , 2022, 57, 543-560.e9.	3.1	106
4717	A SIMPLI (Single-cell Identification from MultiPLexed Images) approach for spatially-resolved tissue phenotyping at single-cell resolution. <i>Nature Communications</i> , 2022, 13, 781.	5.8	19
4718	Temporal analyses of postnatal liver development and maturation by single-cell transcriptomics. <i>Developmental Cell</i> , 2022, 57, 398-414.e5.	3.1	30
4719	Spatial components of molecular tissue biology. <i>Nature Biotechnology</i> , 2022, 40, 308-318.	9.4	148
4720	EMBEDR: Distinguishing signal from noise in single-cell omics data. <i>Patterns</i> , 2022, 3, 100443.	3.1	13
4721	SARS-CoV-2 infects the human kidney and drives fibrosis in kidney organoids. <i>Cell Stem Cell</i> , 2022, 29, 217-231.e8.	5.2	146
4722	Cellular Phenotypic Transformation in Heart Failure Caused by Coronary Heart Disease and Dilated Cardiomyopathy: Delineating at Single-Cell Level. <i>Biomedicines</i> , 2022, 10, 402.	1.4	2
4723	Targeting an alternate Wilms's tumor antigen 1 peptide bypasses immunoproteasome dependency. <i>Science Translational Medicine</i> , 2022, 14, eabg8070.	5.8	12
4725	Deep Immune Phenotyping and Single-Cell Transcriptomics Allow Identification of Circulating TRM-Like Cells Which Correlate With Liver-Stage Immunity and Vaccine-Induced Protection From Malaria. <i>Frontiers in Immunology</i> , 2022, 13, 795463.	2.2	6
4727	Evidence of islet CADM1-mediated immune cell interactions during human type 1 diabetes. <i>JCI Insight</i> , 2022, 7, .	2.3	7
4728	Single-Cell Sequencing Unveils the Heterogeneity of Nonimmune Cells in Chronic Apical Periodontitis. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 820274.	1.8	9
4729	Cellular diversity and gene expression profiles in the male and female brain of <i>Aedes aegypti</i> . <i>BMC Genomics</i> , 2022, 23, 119.	1.2	7
4730	A Pilot Single Cell Analysis of the Zebrafish Embryo Cellular Responses to Uropathogenic <i>Escherichia coli</i> Infection. <i>Pathogens and Immunity</i> , 2022, 7, 1-18.	1.4	1
4731	Spatially resolved isotope tracing reveals tissue metabolic activity. <i>Nature Methods</i> , 2022, 19, 223-230.	9.0	67

#	ARTICLE	IF	CITATIONS
4732	Single-cell transcriptional analysis of human endothelial colony-forming cells from patients with low VWF levels. <i>Blood</i> , 2022, 139, 2240-2251.	0.6	9
4733	Spatial-CUT&Tag: Spatially resolved chromatin modification profiling at the cellular level. <i>Science</i> , 2022, 375, 681-686.	6.0	138
4734	MYCL-mediated reprogramming expands pancreatic insulin-producing cells. <i>Nature Metabolism</i> , 2022, 4, 254-268.	5.1	7
4735	Integrated Analysis of Single-Cell and Spatial Transcriptomics in Keloids: Highlights on Fibrovascular Interactions in Keloid Pathogenesis. <i>Journal of Investigative Dermatology</i> , 2022, 142, 2128-2139.e11.	0.3	24
4736	Single Cell RNA Sequencing Reveals Critical Functions of Mlx in Periodontal Ligament Homeostasis. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 795441.	1.8	8
4739	Single-cell RNA sequencing identifies an Il1rn+/Trem1+ macrophage subpopulation as a cellular target for mitigating the progression of thoracic aortic aneurysm and dissection. <i>Cell Discovery</i> , 2022, 8, 11.	3.1	30
4740	Deciphering spatial genomic heterogeneity at a single cell resolution in multiple myeloma. <i>Nature Communications</i> , 2022, 13, 807.	5.8	29
4745	Dimensionality Reduction and Louvain Agglomerative Hierarchical Clustering for Cluster-Specified Frequent Biomarker Discovery in Single-Cell Sequencing Data. <i>Frontiers in Genetics</i> , 2022, 13, 828479.	1.1	10
4746	DAISM-DNNXMBD: Highly accurate cell type proportion estimation with in silico data augmentation and deep neural networks. <i>Patterns</i> , 2022, 3, 100440.	3.1	10
4748	Complement activation induces excessive T cell cytotoxicity in severe COVID-19. <i>Cell</i> , 2022, 185, 493-512.e25.	13.5	122
4749	Deciphering the spatial-temporal transcriptional landscape of human hypothalamus development. <i>Cell Stem Cell</i> , 2022, 29, 328-343.e5.	5.2	15
4750	Single-cell transcriptomics uncovers an instructive T cell receptor role in adult T cell lineage commitment. <i>EMBO Journal</i> , 2022, 41, e110023.	3.5	7
4751	Systemic Influences of Mammary Cancer on Monocytes in Mice. <i>Cancers</i> , 2022, 14, 833.	1.7	5
4756	Second Heart Field-Derived Cells Contribute to Angiotensin II-Mediated Ascending Aortopathies. <i>Circulation</i> , 2022, 145, 987-1001.	1.6	18
4758	Single-cell RNA sequencing reveals time- and sex-specific responses of mouse spinal cord microglia to peripheral nerve injury and links ApoE to chronic pain. <i>Nature Communications</i> , 2022, 13, 843.	5.8	62
4760	UINMF performs mosaic integration of single-cell multi-omic datasets using nonnegative matrix factorization. <i>Nature Communications</i> , 2022, 13, 780.	5.8	35
4761	SLAMF7 engagement superactivates macrophages in acute and chronic inflammation. <i>Science Immunology</i> , 2022, 7, eabf2846.	5.6	31
4762	Fatty acid-binding proteins and fatty acid synthase influence glial reactivity and promote the formation of Müller glia-derived progenitor cells in the chick retina. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	11

#	ARTICLE	IF	CITATIONS
4763	Generation of a recessive dystrophic epidermolysis bullosa mouse model with patient-derived compound heterozygous mutations. <i>Laboratory Investigation</i> , 2022, , .	1.7	4
4765	Induction of Rosette-to-Lumen stage embryoids using reprogramming paradigms in ESCs. <i>Nature Communications</i> , 2021, 12, 7322.	5.8	6
4767	From nasal to basal: single-cell sequencing of the bursa of Fabricius highlights the IBDV infection mechanism in chickens. <i>Cell and Bioscience</i> , 2021, 11, 212.	2.1	12
4768	TIPE polarity proteins are required for mucosal deployment of T lymphocytes and mucosal defense against bacterial infection. <i>Molecular Biomedicine</i> , 2021, 2, 41.	1.7	1
4769	Interleukin-10 receptor signaling promotes the maintenance of a PD-1int TCF-1+ CD8+ TÂcell population that sustains anti-tumor immunity. <i>Immunity</i> , 2021, 54, 2825-2841.e10.	6.6	57
4770	Hedgehog Signaling in Papillary Fibroblasts Is Essential for Hair Follicle Regeneration during Wound Healing. <i>Journal of Investigative Dermatology</i> , 2022, 142, 1737-1748.e5.	0.3	9
4771	Single cell atlas for 11 non-model mammals, reptiles and birds. <i>Nature Communications</i> , 2021, 12, 7083.	5.8	32
4772	Single-cell analysis identifies a key role for Hhip in murine coronal suture development. <i>Nature Communications</i> , 2021, 12, 7132.	5.8	14
4773	A single-cell transcriptomic landscape of the lungs of patients with COVID-19. <i>Nature Cell Biology</i> , 2021, 23, 1314-1328.	4.6	91
4774	Non-genetic determinants of malignant clonal fitness at single-cell resolution. <i>Nature</i> , 2022, 601, 125-131.	13.7	71
4775	Lineage recording in human cerebral organoids. <i>Nature Methods</i> , 2022, 19, 90-99.	9.0	93
4780	Mouse and human share conserved transcriptional programs for interneuron development. <i>Science</i> , 2021, 374, eabj6641.	6.0	75
4781	Kidney-Targeted Renalase Agonist Prevents Cisplatin-Induced Chronic Kidney Disease by Inhibiting Regulated Necrosis and Inflammation. <i>Journal of the American Society of Nephrology: JASN</i> , 2022, 33, 342-356.	3.0	26
4782	SARS-CoV-2 Entry Genes Are Most Highly Expressed in Nasal Goblet and Ciliated Cells within Human Airways. <i>ArXiv Org</i> , 2020, , .	1.2	1
4783	YY1 safeguard multidimensional epigenetic landscape associated with extended pluripotency. <i>Nucleic Acids Research</i> , 2022, 50, 12019-12038.	6.5	14
4784	Pan-Cancer Indicators of Long-Term Survival Benefits After Immune Checkpoint Inhibitor Therapy. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4785	Single-Cell Atlas of Epithelial and Stromal Cell Heterogeneity by Lobe and Strain in the Mouse Prostate. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4786	Cervical lymph nodes and ovarian teratomas as germinal centres in NMDA receptor-antibody encephalitis. <i>Brain</i> , 2022, 145, 2742-2754.	3.7	33

#	ARTICLE	IF	CITATIONS
4787	CD36 &sup>+</sup> Cancer-Associated Fibroblasts Provide Immunosuppressive Microenvironment for Hepatocellular Carcinoma via Secretion of Macrophage Migration Inhibitory Factor. SSRN Electronic Journal, 0, , .	0.4	0
4788	Single-Cell in Research. <i>Methods in Molecular Biology</i> , 2022, 2419, 765-778.	0.4	4
4789	Big data: Historic advances and emerging trends in biomedical research. <i>Current Research in Biotechnology</i> , 2022, 4, 138-151.	1.9	12
4790	An analysis of classical multidimensional scaling with applications to clustering. <i>Information and Inference</i> , 2023, 12, 72-112.	0.9	7
4791	MarcoPolo: a method to discover differentially expressed genes in single-cell RNA-seq data without depending on prior clustering. <i>Nucleic Acids Research</i> , 2022, 50, e71-e71.	6.5	8
4792	Multi-scale integrative analyses identify THBS2⁺ cancer-associated fibroblasts as a key orchestrator promoting aggressiveness in early-stage lung adenocarcinoma. <i>Theranostics</i> , 2022, 12, 3104-3130.	4.6	23
4793	Unbiased integration of single cell transcriptome replicates. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac022.	1.5	8
4794	Multi-Omics Profiling of the Tumor Microenvironment. <i>Advances in Experimental Medicine and Biology</i> , 2022, 1361, 283-326.	0.8	6
4795	Emerging Bioinformatics Methods and Resources in Drug Toxicology. <i>Methods in Molecular Biology</i> , 2022, 2425, 133-146.	0.4	3
4796	Novel epigenetic network biomarkers for early detection of esophageal cancer. <i>Clinical Epigenetics</i> , 2022, 14, 23.	1.8	11
4798	A human brain vascular atlas reveals diverse mediators of Alzheimerâ€™s risk. <i>Nature</i> , 2022, 603, 885-892.	13.7	294
4799	Identification of bipotent progenitors that give rise to myogenic and connective tissues in mouse. <i>ELife</i> , 2022, 11, .	2.8	11
4800	Revealing the transcriptional heterogeneity of organâ€™specific metastasis in human gastric cancer using singleâ€™cell RNA Sequencing. <i>Clinical and Translational Medicine</i> , 2022, 12, e730.	1.7	59
4802	Single-Cell RNA Sequencing of the Nucleus Pulposus Reveals Chondrocyte Differentiation and Regulation in Intervertebral Disc Degeneration. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 824771.	1.8	24
4805	Single-cell profiling of human subventricular zone progenitors identifies SFRP1 as a target to re-activate progenitors. <i>Nature Communications</i> , 2022, 13, 1036.	5.8	19
4806	Tumor Treating Fields dually activate STING and AIM2 inflammasomes to induce adjuvant immunity in glioblastoma. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	45
4807	Normality sensing licenses local T cells for innate-like tissue surveillance. <i>Nature Immunology</i> , 2022, 23, 411-422.	7.0	30
4809	Single-cell dissection of the human brain vasculature. <i>Nature</i> , 2022, 603, 893-899.	13.7	135

#	ARTICLE	IF	CITATIONS
4810	Hypertrophic chondrocytes serve as a reservoir for marrow-associated skeletal stem and progenitor cells, osteoblasts, and adipocytes during skeletal development. <i>ELife</i> , 2022, 11, .	2.8	28
4811	Metalloproteinase inhibition reduces AML growth, prevents stem cell loss, and improves chemotherapy effectiveness. <i>Blood Advances</i> , 2022, 6, 3126-3141.	2.5	12
4813	Cell-Cell Communication Alterations via Intercellular Signaling Pathways in Substantia Nigra of Parkinson's Disease. <i>Frontiers in Aging Neuroscience</i> , 2022, 14, 828457.	1.7	4
4814	A non-catalytic scaffolding activity of hexokinase 2 contributes to EMT and metastasis. <i>Nature Communications</i> , 2022, 13, 899.	5.8	29
4815	Increased Expression of Tim-3 Is Associated With Depletion of NKT Cells In SARS-CoV-2 Infection. <i>Frontiers in Immunology</i> , 2022, 13, 796682.	2.2	8
4816	A global timing mechanism regulates cell-type-specific wiring programmes. <i>Nature</i> , 2022, 603, 112-118.	13.7	22
4817	HOTTIP-dependent R-loop formation regulates CTCF boundary activity and TAD integrity in leukemia. <i>Molecular Cell</i> , 2022, 82, 833-851.e11.	4.5	48
4818	Single-cell transcriptomic profiling unravels the adenoma-initiation role of protein tyrosine kinases during colorectal tumorigenesis. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 60.	7.1	31
4819	Organoids from human tooth showing epithelial stemness phenotype and differentiation potential. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 153.	2.4	12
4820	Aberrant translation regulated by METTL1/WDR4-mediated tRNA N7-methylguanosine modification drives head and neck squamous cell carcinoma progression. <i>Cancer Communications</i> , 2022, 42, 223-244.	3.7	75
4821	Endothelial Phospholipase C β 2 Improves Outcomes of Diabetic Ischemic Limb Rescue Following VEGF Therapy. <i>Diabetes</i> , 2022, 71, 1149-1165.	0.3	14
4822	Stromal HIF2 Regulates Immune Suppression in the Pancreatic Cancer Microenvironment. <i>Gastroenterology</i> , 2022, 162, 2018-2031.	0.6	62
4823	Signature-scoring methods developed for bulk samples are not adequate for cancer single-cell RNA sequencing data. <i>ELife</i> , 2022, 11, .	2.8	22
4824	Single-cell gene fusion detection by scFusion. <i>Nature Communications</i> , 2022, 13, 1084.	5.8	8
4825	DevKidCC allows for robust classification and direct comparisons of kidney organoid datasets. <i>Genome Medicine</i> , 2022, 14, 19.	3.6	23
4828	Exome-wide Analysis of De Novo and Rare Genetic Variants in Patients With Brain Arteriovenous Malformation. <i>Neurology</i> , 2022, , 10.1212/WNL.0000000000200114.	1.5	2
4829	Isolating and cryopreserving pig skin cells for single-cell RNA sequencing study. <i>PLoS ONE</i> , 2022, 17, e0263869.	1.1	6
4830	Comparative analysis of antibody- and lipid-based multiplexing methods for single-cell RNA-seq. <i>Genome Biology</i> , 2022, 23, 55.	3.8	17

#	ARTICLE	IF	CITATIONS
4832	In heart failure reactivation of RNA-binding proteins is associated with the expression of 1,523 fetal-specific isoforms. <i>PLoS Computational Biology</i> , 2022, 18, e1009918.	1.5	19
4834	Transcriptional landscapes of de novo root regeneration from detached Arabidopsis leaves revealed by time-lapse and single-cell RNA sequencing analyses. <i>Plant Communications</i> , 2022, 3, 100306.	3.6	29
4835	IQCELL: A platform for predicting the effect of gene perturbations on developmental trajectories using single-cell RNA-seq data. <i>PLoS Computational Biology</i> , 2022, 18, e1009907.	1.5	13
4836	RAGE Inhibitors as Alternatives to Dexamethasone for Managing Cerebral Edema Following Brain Tumor Surgery. <i>Neurotherapeutics</i> , 2022, 19, 635-648.	2.1	4
4837	Single-cell transcriptomics analysis reveals intratumoral heterogeneity and identifies a gene signature associated with prognosis of hepatocellular carcinoma. <i>Bioscience Reports</i> , 2022, 42, .	1.1	8
4839	Genetic resiliency associated with dominant lethal TPM1 mutation causing atrial septal defect with high heritability. <i>Cell Reports Medicine</i> , 2022, 3, 100501.	3.3	0
4841	ETV2 regulates PARP-1 binding protein to induce ER stress-mediated death in tuberin-deficient cells. <i>Life Science Alliance</i> , 2022, 5, e202201369.	1.3	2
4844	Single-cell multi-omics analysis of human pancreatic islets reveals novel cellular states in type 1 diabetes. <i>Nature Metabolism</i> , 2022, 4, 284-299.	5.1	52
4845	HIV-1 provirus transcription and translation in macrophages differs from pre-integrated cDNA complexes and requires E2F transcriptional programs. <i>Virulence</i> , 2022, 13, 386-413.	1.8	3
4846	Mapping the biogenesis of forward programmed megakaryocytes from induced pluripotent stem cells. <i>Science Advances</i> , 2022, 8, eabj8618.	4.7	4
4848	Global Characterization of Peripheral B Cells in Parkinson's Disease by Single-Cell RNA and BCR Sequencing. <i>Frontiers in Immunology</i> , 2022, 13, 814239.	2.2	22
4849	²²³ Ra Induces Transient Functional Bone Marrow Toxicity. <i>Journal of Nuclear Medicine</i> , 2022, 63, 1544-1550.	2.8	2
4850	The Lineage Differentiation and Dynamic Heterogeneity of Thymic Epithelial Cells During Thymus Organogenesis. <i>Frontiers in Immunology</i> , 2022, 13, 805451.	2.2	7
4851	Effects of hyperinsulinemia on pancreatic cancer development and the immune microenvironment revealed through single-cell transcriptomics. <i>Cancer & Metabolism</i> , 2022, 10, 5.	2.4	11
4852	The histone demethylase Kdm6b regulates subtype diversification of mouse spinal motor neurons during development. <i>Nature Communications</i> , 2022, 13, 958.	5.8	9
4853	Kidney Organoids Are Capable of Forming Tumors, but Not Teratomas. <i>Stem Cells</i> , 2022, 40, 577-591.	1.4	3
4855	Understanding the Transcriptomic Landscape to Drive New Innovations in Musculoskeletal Regenerative Medicine. <i>Current Osteoporosis Reports</i> , 2022, 20, 141-152.	1.5	3
4856	Protective immune trajectories in early viral containment of non-pneumonic SARS-CoV-2 infection. <i>Nature Communications</i> , 2022, 13, 1018.	5.8	16

#	ARTICLE	IF	CITATIONS
4859	Single-cell RNA sequencing reveals the multi-cellular ecosystem in different radiological components of pulmonary part-solid nodules. <i>Clinical and Translational Medicine</i> , 2022, 12, e723.	1.7	7
4860	An IL-9-pulmonary macrophage axis defines the allergic lung inflammatory environment. <i>Science Immunology</i> , 2022, 7, eabi9768.	5.6	29
4862	Regulatory network-based imputation of dropouts in single-cell RNA sequencing data. <i>PLoS Computational Biology</i> , 2022, 18, e1009849.	1.5	5
4863	Antimicrobial production by perifollicular dermal preadipocytes is essential to the pathophysiology of acne. <i>Science Translational Medicine</i> , 2022, 14, eabh1478.	5.8	19
4864	Integrating single-cell sequencing data with GWAS summary statistics reveals CD16+monocytes and memory CD8+T cells involved in severe COVID-19. <i>Genome Medicine</i> , 2022, 14, 16.	3.6	25
4865	A human breast cancer-derived xenograft and organoid platform for drug discovery and precision oncology. <i>Nature Cancer</i> , 2022, 3, 232-250.	5.7	133
4866	Patient-Derived Triple-Negative Breast Cancer Organoids Provide Robust Model Systems That Recapitulate Tumor Intrinsic Characteristics. <i>Cancer Research</i> , 2022, 82, 1174-1192.	0.4	21
4869	Trophoblast Cell Subtypes and Dysfunction in the Placenta of Individuals with Preeclampsia Revealed by Single-Cell RNA Sequencing. <i>Molecules and Cells</i> , 2022, 45, 317-328.	1.0	24
4870	A novel unconventional T cell population enriched in Crohn's disease. <i>Gut</i> , 2022, 71, 2194-2204.	6.1	22
4871	Prevention of Tumor Growth and Dissemination by In Situ Vaccination with Mitochondria-Targeted Atovaquone. <i>Advanced Science</i> , 2022, 9, e2101267.	5.6	17
4874	A human pluripotent stem cell-based model of SARS-CoV-2 infection reveals an ACE2-independent inflammatory activation of vascular endothelial cells through TLR4. <i>Stem Cell Reports</i> , 2022, 17, 538-555.	2.3	22
4875	Uncovering the molecular identity of cardiosphere-derived cells (CDCs) by single-cell RNA sequencing. <i>Basic Research in Cardiology</i> , 2022, 117, 11.	2.5	7
4876	Decoding the multicellular ecosystem of vena caval tumor thrombus in clear cell renal cell carcinoma by single-cell RNA sequencing. <i>Genome Biology</i> , 2022, 23, 87.	3.8	24
4877	Cell Type-Specific Induction of Inflammation-Associated Genes in Crohn's Disease and Colorectal Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3082.	1.8	7
4878	scINSIGHT for interpreting single-cell gene expression from biologically heterogeneous data. <i>Genome Biology</i> , 2022, 23, 82.	3.8	8
4881	Guidelines for bioinformatics of single-cell sequencing data analysis in Alzheimer's disease: review, recommendation, implementation and application. <i>Molecular Neurodegeneration</i> , 2022, 17, 17.	4.4	40
4882	Spatial and transcriptional heterogeneity of pancreatic beta cell neogenesis revealed by a time-resolved reporter system. <i>Diabetologia</i> , 2022, 65, 811-828.	2.9	7
4883	Loss of the intracellular enzyme QPCTL limits chemokine function and reshapes myeloid infiltration to augment tumor immunity. <i>Nature Immunology</i> , 2022, 23, 568-580.	7.0	18

#	ARTICLE	IF	CITATIONS
4884	Bacterial infection disrupts established germinal center reactions through monocyte recruitment and impaired metabolic adaptation. <i>Immunity</i> , 2022, 55, 442-458.e8.	6.6	12
4885	Single-cell immunology: Past, present, and future. <i>Immunity</i> , 2022, 55, 393-404.	6.6	47
4886	Allergic airway recall responses require IL-9 from resident memory CD4 ⁺ T cells. <i>Science Immunology</i> , 2022, 7, eabg9296.	5.6	22
4889	Myoepithelial progenitors as founder cells of hyperplastic human breast lesions upon PIK3CA transformation. <i>Communications Biology</i> , 2022, 5, 219.	2.0	2
4891	Human and mouse trigeminal ganglia cell atlas implicates multiple cell types in migraine. <i>Neuron</i> , 2022, 110, 1806-1821.e8.	3.8	61
4894	Single-cell transcriptome profile of mouse skin undergoing antigen-driven allergic inflammation recapitulates findings in atopic dermatitis skin lesions. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 150, 373-384.	1.5	14
4895	Linking the genotypes and phenotypes of cancer cells in heterogenous populations via real-time optical tagging and image analysis. <i>Nature Biomedical Engineering</i> , 2022, 6, 667-675.	11.6	12
4896	Targeting the PSGL-1 Immune Checkpoint Promotes Immunity to PD-1 ^{hi} Resistant Melanoma. <i>Cancer Immunology Research</i> , 2022, 10, 612-625.	1.6	12
4897	Single nucleus transcriptome and chromatin accessibility of postmortem human pituitaries reveal diverse stem cell regulatory mechanisms. <i>Cell Reports</i> , 2022, 38, 110467.	2.9	27
4899	Tig1 regulates proximo-distal identity during salamander limb regeneration. <i>Nature Communications</i> , 2022, 13, 1141.	5.8	7
4900	Cell-cell communication analysis for single-cell RNA sequencing and its applications in carcinogenesis and COVID-19. <i>Biosafety and Health</i> , 2022, 4, 220-227.	1.2	1
4901	A mouse model of the LEAP study reveals a role for CTLA-4 in preventing peanut allergy induced by environmental peanut exposure. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 150, 425-439.e3.	1.5	16
4903	A comprehensive temporal patterning gene network in <i>Drosophila</i> medulla neuroblasts revealed by single-cell RNA sequencing. <i>Nature Communications</i> , 2022, 13, 1247.	5.8	30
4906	Production of human spinal-cord organoids recapitulating neural-tube morphogenesis. <i>Nature Biomedical Engineering</i> , 2022, 6, 435-448.	11.6	40
4908	Single-cell transcriptomics reveals expression profiles of <i>Trypanosoma brucei</i> sexual stages. <i>PLoS Pathogens</i> , 2022, 18, e1010346.	2.1	12
4909	Integrated Analysis Highlights the Immunosuppressive Role of TREM2 ⁺ Macrophages in Hepatocellular Carcinoma. <i>Frontiers in Immunology</i> , 2022, 13, 848367.	2.2	28
4916	A novel high throughput screen to identify candidate molecular networks that regulate spermatogenic stem cell functions. <i>Biology of Reproduction</i> , 2022, 106, 1175-1190.	1.2	4
4917	Abnormal Changes of Monocyte Subsets in Patients With Sjögren's Syndrome. <i>Frontiers in Immunology</i> , 2022, 13, 864920.	2.2	10

#	ARTICLE	IF	CITATIONS
4918	Fate mapping and scRNA sequencing reveal origin and diversity of lymph node stromal precursors. <i>Immunity</i> , 2022, 55, 606-622.e6.	6.6	8
4919	Induction of an immortalized songbird cell line allows for gene characterization and knockout by CRISPR-Cas9. <i>Scientific Reports</i> , 2022, 12, 4369.	1.6	5
4920	A single-cell atlas of non-haematopoietic cells in human lymph nodes and lymphoma reveals a landscape of stromal remodelling. <i>Nature Cell Biology</i> , 2022, 24, 565-578.	4.6	42
4921	A single-cell analysis of breast cancer cell lines to study tumour heterogeneity and drug response. <i>Nature Communications</i> , 2022, 13, 1714.	5.8	65
4924	Limited extent and consequences of pancreatic SARS-CoV-2 infection. <i>Cell Reports</i> , 2022, 38, 110508.	2.9	36
4927	Chronic stress disrupts the homeostasis and progeny progression of oligodendroglial lineage cells, associating immune oligodendrocytes with prefrontal cortex hypomyelination. <i>Molecular Psychiatry</i> , 2022, 27, 2833-2848.	4.1	22
4929	Non-negative Independent Factor Analysis disentangles discrete and continuous sources of variation in scRNA-seq data. <i>Bioinformatics</i> , 2022, 38, 2749-2756.	1.8	1
4932	Single-cell RNA sequencing reveals intrahepatic and peripheral immune characteristics related to disease phases in HBV-infected patients. <i>Gut</i> , 2023, 72, 153-167.	6.1	42
4933	Intratumoral plasma cells predict outcomes to PD-L1 blockade in non-small cell lung cancer. <i>Cancer Cell</i> , 2022, 40, 289-300.e4.	7.7	148
4934	Single-cell transcriptomics reveals distinct effector profiles of infiltrating T cells in lupus skin and kidney. <i>JCI Insight</i> , 2022, 7, .	2.3	20
4936	Tissue-resident FOLR2+ macrophages associate with CD8+ T cell infiltration in human breast cancer. <i>Cell</i> , 2022, 185, 1189-1207.e25.	13.5	166
4937	HDAC11 activity contributes to MEK inhibitor escape in uveal melanoma. <i>Cancer Gene Therapy</i> , 2022, 29, 1840-1846.	2.2	3
4938	Circulating immune cell landscape in patients who had mild ischaemic stroke. <i>Stroke and Vascular Neurology</i> , 2022, 7, 319-327.	1.5	7
4940	EDClust: an EM-MM hybrid method for cell clustering in multiple-subject single-cell RNA sequencing. <i>Bioinformatics</i> , 2022, 38, 2692-2699.	1.8	4
4943	Chicken Peripheral Blood Mononuclear Cells Response to Avian Leukosis Virus Subgroup J Infection Assessed by Single-Cell RNA Sequencing. <i>Frontiers in Microbiology</i> , 2022, 13, 800618.	1.5	8
4944	Human distal airways contain a multipotent secretory cell that can regenerate alveoli. <i>Nature</i> , 2022, 604, 120-126.	13.7	128
4945	Construction and Validation of a Ferroptosis-Related Prognostic Signature for Melanoma Based on Single-Cell RNA Sequencing. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 818457.	1.8	14
4948	Functional and Phenotypic Characterization of Siglec-6 on Human Mast Cells. <i>Cells</i> , 2022, 11, 1138.	1.8	18

#	ARTICLE	IF	CITATIONS
4950	Deficiency of N-glycanase 1 perturbs neurogenesis and cerebral development modeled by human organoids. <i>Cell Death and Disease</i> , 2022, 13, 262.	2.7	4
4951	A copula based topology preserving graph convolution network for clustering of single-cell RNA-seq data. <i>PLoS Computational Biology</i> , 2022, 18, e1009600.	1.5	3
4952	PHGDH is required for germinal center formation and is a therapeutic target in MYC-driven lymphoma. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	14
4955	Single-cell RNA-seq reveals clonal diversity and prognostic genes of relapsed multiple myeloma. <i>Clinical and Translational Medicine</i> , 2022, 12, e757.	1.7	15
4956	Single nucleus multi-omics identifies human cortical cell regulatory genome diversity. <i>Cell Genomics</i> , 2022, 2, 100107.	3.0	58
4957	Evolutionary insights into primate skeletal gene regulation using a comparative cell culture model. <i>PLoS Genetics</i> , 2022, 18, e1010073.	1.5	10
4960	Characterization of Pyroptosis-Related Subtypes via RNA-Seq and ScRNA-Seq to Predict Chemo-Immunotherapy Response in Triple-Negative Breast Cancer. <i>Frontiers in Genetics</i> , 2022, 13, 788670.	1.1	1
4961	Transcriptional kinetics and molecular functions of long noncoding RNAs. <i>Nature Genetics</i> , 2022, 54, 306-317.	9.4	29
4962	Identification of Prognosis Biomarkers for High-Grade Serous Ovarian Cancer Based on Stemness. <i>Frontiers in Genetics</i> , 2022, 13, 861954.	1.1	5
4963	Impact of proinflammatory epicardial adipose tissue and differentially enhanced autonomic remodeling on human atrial fibrillation. <i>Journal of Thoracic and Cardiovascular Surgery</i> , 2023, 165, e158-e174.	0.4	11
4964	KIR ⁺ CD8 ⁺ T cells suppress pathogenic T cells and are active in autoimmune diseases and COVID-19. <i>Science</i> , 2022, 376, eabi9591.	6.0	113
4965	Characterizing gene expression in an in vitro biomechanical strain model of joint health. <i>F1000Research</i> , 0, 11, 296.	0.8	1
4967	Heterogeneity and clonality of kidney-infiltrating T cells in murine lupus nephritis. <i>JCI Insight</i> , 2022, 7, .	2.3	6
4968	ADAP1 promotes latent HIV-1 reactivation by selectively tuning KRAS-ERK-AP-1 T cell signaling-transcriptional axis. <i>Nature Communications</i> , 2022, 13, 1109.	5.8	2
4969	Keratin filaments mediate the expansion of extra-embryonic membranes in the post-gastrulation mouse embryo. <i>EMBO Journal</i> , 2022, 41, e108747.	3.5	6
4970	Ovarian cancer-specific dysregulated genes with prognostic significance: scRNA-seq with bulk RNA-seq data and experimental validation. <i>Annals of the New York Academy of Sciences</i> , 2022, 1512, 154-173.	1.8	10
4972	Behavioral Neuroscience in the Era of Genomics: Tools and Lessons for Analyzing High-Dimensional Datasets. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3811.	1.8	2
4973	MBNL1 drives dynamic transitions between fibroblasts and myofibroblasts in cardiac wound healing. <i>Cell Stem Cell</i> , 2022, 29, 419-433.e10.	5.2	25

#	ARTICLE	IF	CITATIONS
4974	Immunosuppressive TREM2(+) macrophages are associated with undesirable prognosis and responses to anti-PD-1 immunotherapy in non-small cell lung cancer. <i>Cancer Immunology, Immunotherapy</i> , 2022, 71, 2511-2522.	2.0	43
4976	Homeostatic serum IgE is secreted by plasma cells in the thymus and enhances mast cell survival. <i>Nature Communications</i> , 2022, 13, 1418.	5.8	11
4977	Single-Cell Sequencing of Immune Cells in Human Aortic Dissection Tissue Provides Insights Into Immune Cell Heterogeneity. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 791875.	1.1	9
4978	Spatiotemporal reprogramming of differentiated cells underlies regeneration and neoplasia in the intestinal epithelium. <i>Nature Communications</i> , 2022, 13, 1500.	5.8	17
4982	Identification of new marker genes from plant single-cell RNA-seq data using interpretable machine learning methods. <i>New Phytologist</i> , 2022, 234, 1507-1520.	3.5	11
4983	Dietary Fiber as a Counterbalance to Age-Related Microglial Cell Dysfunction. <i>Frontiers in Nutrition</i> , 2022, 9, 835824.	1.6	8
4985	Single-Cell RNA-seq Reveals a Developmental Hierarchy Superimposed Over Subclonal Evolution in the Cellular Ecosystem of Prostate Cancer. <i>Advanced Science</i> , 2022, 9, e2105530.	5.6	14
4986	B lymphocyte-derived acetylcholine limits steady-state and emergency hematopoiesis. <i>Nature Immunology</i> , 2022, 23, 605-618.	7.0	33
4987	Single-cell RNA sequencing of mast cells in eosinophilic esophagitis reveals heterogeneity, local proliferation, and activation that persists in remission. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 149, 2062-2077.	1.5	37
4988	Inhibiting USP16 rescues stem cell aging and memory in an Alzheimer's model. <i>ELife</i> , 2022, 11, .	2.8	6
4989	Single-cell transcriptomics of popliteal lymphatic vessels and peripheral veins reveals altered lymphatic muscle and immune cell populations in the TNF-Tg arthritis model. <i>Arthritis Research and Therapy</i> , 2022, 24, 64.	1.6	9
4990	m ⁶ A mRNA modification maintains colonic epithelial cell homeostasis via NF- κ B-mediated antiapoptotic pathway. <i>Science Advances</i> , 2022, 8, eabl5723.	4.7	31
4991	Global transcriptomic characterization of T cells in individuals with chronic HIV-1 infection. <i>Cell Discovery</i> , 2022, 8, 29.	3.1	18
4994	Comprehensive generation, visualization, and reporting of quality control metrics for single-cell RNA sequencing data. <i>Nature Communications</i> , 2022, 13, 1688.	5.8	23
4995	Characterization and reduction of non-endocrine cells accompanying islet-like endocrine cells differentiated from human iPSC. <i>Scientific Reports</i> , 2022, 12, 4740.	1.6	6
4996	Joint dimension reduction and clustering analysis of single-cell RNA-seq and spatial transcriptomics data. <i>Nucleic Acids Research</i> , 2022, 50, e72-e72.	6.5	26
4997	Single-Cell Analysis of Refractory Celiac Disease Demonstrates Inter- and Intra-Patient Aberrant Cell Heterogeneity. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2022, , .	2.3	3
4998	Functional, metabolic and transcriptional maturation of human pancreatic islets derived from stem cells. <i>Nature Biotechnology</i> , 2022, 40, 1042-1055.	9.4	135

#	ARTICLE	IF	CITATIONS
4999	Altered intercellular communication and extracellular matrix signaling as a potential disease mechanism in human hypertrophic cardiomyopathy. <i>Scientific Reports</i> , 2022, 12, 5211.	1.6	10
5000	Are batch effects still relevant in the age of big data?. <i>Trends in Biotechnology</i> , 2022, 40, 1029-1040.	4.9	10
5002	Quantitative transportomics identifies Kif5a as a major regulator of neurodegeneration. <i>ELife</i> , 2022, 11, .	2.8	10
5005	Single-cell transcriptome analysis reveals three sequential phases of gene expression during zebrafish sensory hair cell regeneration. <i>Developmental Cell</i> , 2022, 57, 799-819.e6.	3.1	34
5006	IFN- β is critical for normal wound repair and is decreased in diabetic wounds. <i>JCI Insight</i> , 2022, 7, .	2.3	5
5007	Cure of syngeneic carcinomas with targeted IL-12 through obligate reprogramming of lymphoid and myeloid immunity. <i>JCI Insight</i> , 2022, 7, .	2.3	5
5011	Ly49E separates liver ILC1s into embryo-derived and postnatal subsets with different functions. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	25
5012	Rod genesis driven by mafba in an nrl knockout zebrafish model with altered photoreceptor composition and progressive retinal degeneration. <i>PLoS Genetics</i> , 2022, 18, e1009841.	1.5	8
5013	Dissection of artifactual and confounding glial signatures by single-cell sequencing of mouse and human brain. <i>Nature Neuroscience</i> , 2022, 25, 306-316.	7.1	166
5015	Extrinsic KRAS Signaling Shapes the Pancreatic Microenvironment Through Fibroblast Reprogramming. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2022, 13, 1673-1699.	2.3	36
5016	Single-Cell RNA-Seq Analysis of Cells from Degenerating and Non-Degenerating Intervertebral Discs from the Same Individual Reveals New Biomarkers for Intervertebral Disc Degeneration. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3993.	1.8	39
5017	BFF and cellhashR: analysis tools for accurate demultiplexing of cell hashing data. <i>Bioinformatics</i> , 2022, 38, 2791-2801.	1.8	8
5018	Computational integration of renal histology and urinary proteomics using neural networks. , 2022, , .		0
5020	Transcriptome analysis revealed a two-step transformation of vascular smooth muscle cells to macrophage-like cells. <i>Atherosclerosis</i> , 2022, 346, 26-35.	0.4	13
5021	Concurrent delivery of immune checkpoint blockade modulates T cell dynamics to enhance neoantigen vaccine-generated antitumor immunity. <i>Nature Cancer</i> , 2022, 3, 437-452.	5.7	19
5022	Deep neural network modeling identifies biomarkers of response to immune-checkpoint therapy. <i>IScience</i> , 2022, 25, 104228.	1.9	4
5023	Cell Type Diversity Statistic: An Entropy-Based Metric to Compare Overall Cell Type Composition Across Samples. <i>Frontiers in Genetics</i> , 2022, 13, 855076.	1.1	7
5024	$\text{NF-}\kappa\text{B}$ signaling promotes glial reactivity and suppresses Müller glia-mediated neuron regeneration in the mammalian retina. <i>Glia</i> , 2022, 70, 1380-1401.	2.5	28

#	ARTICLE	IF	CITATIONS
5025	Human pluripotent stem cell-derived myogenic progenitors undergo maturation to quiescent satellite cells upon engraftment. <i>Cell Stem Cell</i> , 2022, 29, 610-619.e5.	5.2	10
5027	A rare frameshift mutation in <i>SYCP1</i> is associated with human male infertility. <i>Molecular Human Reproduction</i> , 2022, 28, .	1.3	9
5028	Molecular insights into the early stage of glomerular injury in IgA nephropathy using single-cell RNA sequencing. <i>Kidney International</i> , 2022, 101, 752-765.	2.6	23
5029	Glomerular endothelial cell-podocyte stresses and crosstalk in structurally normal kidney transplants. <i>Kidney International</i> , 2022, 101, 779-792.	2.6	11
5030	Dirichlet process mixture models for single-cell RNA-seq clustering. <i>Biology Open</i> , 2022, 11, .	0.6	4
5031	Neutrophil and natural killer cell imbalances prevent muscle stem cell-mediated regeneration following murine volumetric muscle loss. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2111445119.	3.3	24
5032	Recessive PRDM13 mutations cause fatal perinatal brainstem dysfunction with cerebellar hypoplasia and disrupt Purkinje cell differentiation. <i>American Journal of Human Genetics</i> , 2022, 109, 909-927.	2.6	10
5033	Glutathione-dependent redox balance characterizes the distinct metabolic properties of follicular and marginal zone B cells. <i>Nature Communications</i> , 2022, 13, 1789.	5.8	18
5035	ZNF384 Fusion Oncoproteins Drive Lineage Aberrancy in Acute Leukemia. <i>Blood Cancer Discovery</i> , 2022, 3, 240-263.	2.6	11
5037	Large-Scale Single-Cell and Bulk Sequencing Analyses Reveal the Prognostic Value and Immune Aspects of CD147 in Pan-Cancer. <i>Frontiers in Immunology</i> , 2022, 13, 810471.	2.2	16
5038	A small-molecule cocktail promotes mammalian cardiomyocyte proliferation and heart regeneration. <i>Cell Stem Cell</i> , 2022, 29, 545-558.e13.	5.2	32
5039	Specification of fetal liver endothelial progenitors to functional zoned adult sinusoids requires c-Maf induction. <i>Cell Stem Cell</i> , 2022, 29, 593-609.e7.	5.2	32
5040	A dual SHOX2:GFP; MYH6:mCherry knockin hESC reporter line for derivation of human SAN-like cells. <i>iScience</i> , 2022, 25, 104153.	1.9	1
5042	Multiscale Transcriptomic Integration Reveals B-Cell Depletion and T-Cell Mistrafficking in Nasopharyngeal Carcinoma Progression. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 857137.	1.8	4
5043	A scRNA-seq Approach to Identifying Changes in Spermatogonial Stem Cell Gene Expression Following in vitro Culture. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 782996.	1.8	2
5044	Integrative molecular roadmap for direct conversion of fibroblasts into myocytes and myogenic progenitor cells. <i>Science Advances</i> , 2022, 8, eabj4928.	4.7	10
5045	Replicative history marks transcriptional and functional disparity in the CD8+ T cell memory pool. <i>Nature Immunology</i> , 2022, 23, 791-801.	7.0	30
5046	Tumor-resident intracellular microbiota promotes metastatic colonization in breast cancer. <i>Cell</i> , 2022, 185, 1356-1372.e26.	13.5	287

#	ARTICLE	IF	CITATIONS
5047	Single-cell analysis of SÅ©zary syndrome reveals novel markers andÂshifting gene profiles associated with treatment. <i>Blood Advances</i> , 2023, 7, 321-335.	2.5	7
5048	Uncompensated mitochondrial oxidative stress underlies heart failure in an iPSC-derived model of congenital heart disease. <i>Cell Stem Cell</i> , 2022, 29, 840-855.e7.	5.2	18
5049	Current progress and open challenges for applying deep learning across the biosciences. <i>Nature Communications</i> , 2022, 13, 1728.	5.8	105
5052	Single cell enhancer activity distinguishes GABAergic and cholinergic lineages in embryonic mouse basal ganglia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2108760119.	3.3	15
5053	Capybara: A computational tool to measure cell identity and fate transitions. <i>Cell Stem Cell</i> , 2022, 29, 635-649.e11.	5.2	24
5054	Postnatal state transition of cardiomyocyte as a primary step in heart maturation. <i>Protein and Cell</i> , 2022, 13, 842-862.	4.8	5
5055	An atlas of transcriptionally defined cell populations in the rat ventral tegmental area. <i>Cell Reports</i> , 2022, 39, 110616.	2.9	43
5056	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. <i>Nature Genetics</i> , 2022, 54, 412-436.	9.4	700
5057	<i>trans</i> -2-Enoyl-CoA Reductase Tecr-Driven Lipid Metabolism in Endothelial Cells Protects against Transcytosis to Maintain Blood-Brain Barrier Homeostasis. <i>Research</i> , 2022, 2022, 9839368.	2.8	4
5058	Stromal oncostatin M cytokine promotes breast cancer progression by reprogramming the tumor microenvironment. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	21
5059	Chaperone-mediated autophagy plays an important role in regulating retinal progenitor cell homeostasis. <i>Stem Cell Research and Therapy</i> , 2022, 13, 136.	2.4	3
5060	Novel STAG3 variant associated with primary ovarian insufficiency and non-obstructive azoospermia in an Iranian consanguineous family. <i>Gene</i> , 2022, 821, 146281.	1.0	7
5061	Intranasal delivery of SARS-CoV-2 spike protein is sufficient to cause olfactory damage, inflammation and olfactory dysfunction in zebrafish. <i>Brain, Behavior, and Immunity</i> , 2022, 102, 341-359.	2.0	27
5062	Analyses of murine lymph node endothelial cell subsets using single-cell RNA sequencing and spectral flow cytometry. <i>STAR Protocols</i> , 2022, 3, 101267.	0.5	1
5063	Poly C Binding Protein 2 dependent nuclear retention of the utrophin-A mRNA in C2C12 cells. <i>RNA Biology</i> , 2021, 18, 612-622.	1.5	2
5065	eNOS controls angiogenic sprouting and retinal neovascularization through the regulation of endothelial cell polarity. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 1.	2.4	25
5066	Cytokine and Nitric Oxide-Dependent Gene Regulation in Islet Endocrine and Nonendocrine Cells. <i>Function</i> , 2021, 3, zqab063.	1.1	5
5067	Dysregulated coordination of MAPT exon 2 and exon 10 splicing underlies different tau pathologies in PSP and AD. <i>Acta Neuropathologica</i> , 2022, 143, 225-243.	3.9	10

#	ARTICLE	IF	CITATIONS
5069	Class Ib MHCâ€‘Mediated Immune Interactions Play a Critical Role in Maintaining Mucosal Homeostasis in the Mammalian Large Intestine. <i>ImmunoHorizons</i> , 2021, 5, 953-971.	0.8	0
5071	CCPE: cell cycle pseudotime estimation for single cell RNA-seq data. <i>Nucleic Acids Research</i> , 2022, 50, 704-716.	6.5	11
5072	Evolutionary assembly of cooperating cell types in an animal chemical defense system. <i>Cell</i> , 2021, 184, 6138-6156.e28.	13.5	13
5074	nSeP: immune and metabolic biomarkers for early detection of neonatal sepsisâ€‘protocol for a prospective multicohort study. <i>BMJ Open</i> , 2021, 11, e050100.	0.8	3
5075	Therapeutic Effect of IL-38 on Experimental Autoimmune Uveitis: Reprogrammed Immune Cell Landscape and Reduced Th17 Cell Pathogenicity. , 2021, 62, 31.		11
5078	Patientâ€‘Derived Upper Tract Urothelial Carcinoma Organoids as a Platform for Drug Screening. <i>Advanced Science</i> , 2022, 9, e2103999.	5.6	12
5080	Integration of Multiple scRNA-Seq Datasets on the Autoencoder Latent Space. , 2021, , .		4
5081	Pyruvate metabolism guides definitive lineage specification during hematopoietic emergence. <i>EMBO Reports</i> , 2022, 23, e54384.	2.0	9
5082	Stress ball morphogenesis: How the lizard builds its lung. <i>Science Advances</i> , 2021, 7, eabk0161.	4.7	11
5083	Bulk and Single-Cell Profiling of Breast Tumors Identifies TREM-1 as a Dominant Immune Suppressive Marker Associated With Poor Outcomes. <i>Frontiers in Oncology</i> , 2021, 11, 734959.	1.3	8
5084	Singleâ€‘cell RNA sequencing predicts motility networks in purified human gastric interstitial cells of Cajal. <i>Neurogastroenterology and Motility</i> , 2022, 34, e14303.	1.6	5
5087	Cluster learning-assisted directed evolution. <i>Nature Computational Science</i> , 2021, 1, 809-818.	3.8	30
5088	CTLA4-Mediated Immunosuppression in Glioblastoma is Associated with the Infiltration of Macrophages in the Tumor Microenvironment. <i>Journal of Inflammation Research</i> , 2021, Volume 14, 7315-7329.	1.6	15
5089	Metabolic detection and systems analyses of pancreatic ductal adenocarcinoma through machine learning, lipidomics, and multi-omics. <i>Science Advances</i> , 2021, 7, eabh2724.	4.7	27
5090	Inflammatory Cells Accelerated Carotid Artery Calcification via MMP9: Evidences From Single-Cell Analysis. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 766613.	1.1	2
5091	HDMC: a novel deep learning-based framework for removing batch effects in single-cell RNA-seq data. <i>Bioinformatics</i> , 2022, 38, 1295-1303.	1.8	8
5092	Cell type identification for single cell RNA data by bulk data reference projection. , 2021, , .		0
5094	Reinvestigation of Classic T Cell Subsets and Identification of Novel Cell Subpopulations by Single-Cell RNA Sequencing. <i>Journal of Immunology</i> , 2022, 208, 396-406.	0.4	34

#	ARTICLE	IF	CITATIONS
5096	Cross-Tissue Characterization of Heterogeneities of Mesenchymal Stem Cells and Their Differentiation Potentials. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 781021.	1.8	13
5097	MAL2 mediates the formation of stable HER2 signaling complexes within lipid raft-rich membrane protrusions in breast cancer cells. <i>Cell Reports</i> , 2021, 37, 110160.	2.9	12
5098	CellDepot: A Unified Repository for scRNA-seq Data and Visual Exploration. <i>Journal of Molecular Biology</i> , 2022, 434, 167425.	2.0	6
5099	Heterologous prime-boost immunizations with chimpanzee adenoviral vectors elicit potent and protective immunity against SARS-CoV-2 infection. <i>Cell Discovery</i> , 2021, 7, 123.	3.1	10
5100	Single-cell transcriptome analysis identifies a unique tumor cell type producing multiple hormones in ectopic ACTH and CRH secreting pheochromocytoma. <i>ELife</i> , 2021, 10, .	2.8	9
5101	Dissecting the Landscape of Activated CMV-Stimulated CD4+ T Cells in Humans by Linking Single-Cell RNA-Seq With T-Cell Receptor Sequencing. <i>Frontiers in Immunology</i> , 2021, 12, 779961.	2.2	12
5103	Predicting heterogeneity in clone-specific therapeutic vulnerabilities using single-cell transcriptomic signatures. <i>Genome Medicine</i> , 2021, 13, 189.	3.6	20
5104	Deep learning tackles single-cell analysis—a survey of deep learning for scRNA-seq analysis. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	19
5105	YAP1 Is a Potential Predictive Molecular Biomarker for Response to SMO Inhibitor in Medulloblastoma Cells. <i>Cancers</i> , 2021, 13, 6249.	1.7	1
5108	Single-cell RNA sequencing reveals B cell-related molecular biomarkers for Alzheimer's disease. <i>Experimental and Molecular Medicine</i> , 2021, 53, 1888-1901.	3.2	32
5109	A Pan-Cancer Immunogenomic Atlas for Immune Checkpoint Blockade Immunotherapy. <i>Cancer Research</i> , 2022, 82, 539-542.	0.4	9
5112	Single cell sequencing analysis identifies genetics-modulated ORMDL3+ cholangiocytes having higher metabolic effects on primary biliary cholangitis. <i>Journal of Nanobiotechnology</i> , 2021, 19, 406.	4.2	16
5113	Single Cell RNA-Seq: Cell Isolation and Data Analysis. <i>Methods in Molecular Biology</i> , 2022, 2403, 81-89.	0.4	1
5114	The onset of circulation triggers a metabolic switch required for endothelial to hematopoietic transition. <i>Cell Reports</i> , 2021, 37, 110103.	2.9	17
5115	NKG7 Is a T-cell-Intrinsic Therapeutic Target for Improving Antitumor Cytotoxicity and Cancer Immunotherapy. <i>Cancer Immunology Research</i> , 2022, 10, 162-181.	1.6	26
5117	MACA: marker-based automatic cell-type annotation for single-cell expression data. <i>Bioinformatics</i> , 2022, 38, 1756-1760.	1.8	14
5119	Single-cell transcriptome atlas of human mesenchymal stem cells exploring cellular heterogeneity. <i>Clinical and Translational Medicine</i> , 2021, 11, e650.	1.7	49
5121	A Single-Cell Transcriptome Profiling of Anterior Kidney Leukocytes From Nile Tilapia (<i>Oreochromis Tj</i>) ETQq1 1 0.784314 rgBT/Overl	2.2	14

#	ARTICLE	IF	CITATIONS
5122	Adaptive total-variation joint learning model for analyzing single cell RNA seq data. , 2021, , .		0
5123	Combinatorial immunotherapy induces tumor-infiltrating CD8 ⁺ T cells with distinct functional, migratory, and stem-like properties. , 2021, 9, e003614.		11
5124	Single-cell RNA-sequencing reveals distinct immune cell subsets and signaling pathways in IgA nephropathy. Cell and Bioscience, 2021, 11, 203.	2.1	11
5127	Molecular Subtypes Based on Cell Differentiation Trajectories in Head and Neck Squamous Cell Carcinoma: Differential Prognosis and Immunotherapeutic Responses. Frontiers in Immunology, 2021, 12, 791621.	2.2	2
5128	Effective and scalable single-cell data alignment with non-linear canonical correlation analysis. Nucleic Acids Research, 2022, 50, e21-e21.	6.5	13
5130	Profiling senescent cells in human brains reveals neurons with CDKN2D/p19 and tau neuropathology. Nature Aging, 2021, 1, 1107-1116.	5.3	45
5134	CellMeSH: probabilistic cell-type identification using indexed literature. Bioinformatics, 2022, 38, 1393-1402.	1.8	7
5135	Construction and Validation of Prognostic Regulation Network Based on RNA-Binding Protein Genes in Lung Squamous Cell Carcinoma. DNA and Cell Biology, 2021, 40, 1563-1583.	0.9	6
5137	GDPLichi: a DNA Damage Repair-Related Gene Classifier for Predicting Lung Adenocarcinoma Immune Checkpoint Inhibitors Response. Frontiers in Oncology, 2021, 11, 733533.	1.3	4
5139	MarkovHC: Markov hierarchical clustering for the topological structure of high-dimensional single-cell omics data with transition pathway and critical point detection. Nucleic Acids Research, 2022, 50, 46-56.	6.5	9
5140	Allosteric inhibition of SHP2 uncovers aberrant TLR7 trafficking in aggravating psoriasis. EMBO Molecular Medicine, 2022, 14, e14455.	3.3	29
5141	CoRE-ATAC: A deep learning model for the functional classification of regulatory elements from single cell and bulk ATAC-seq data. PLoS Computational Biology, 2021, 17, e1009670.	1.5	7
5145	Targeting metabotropic glutamate receptor 4 for cancer immunotherapy. Science Advances, 2021, 7, eabj4226.	4.7	11
5148	LKB1 deficiency upregulates RELM β to drive airway goblet cell metaplasia. Cellular and Molecular Life Sciences, 2022, 79, 1.	2.4	32
5149	Single-cell transcriptional profiling of splenic fibroblasts reveals subset-specific innate immune signatures in homeostasis and during viral infection. Communications Biology, 2021, 4, 1355.	2.0	12
5151	DeepCl: a deep learning based clustering method for single cell RNA-seq data. , 2021, , .		3
5152	EASI-FISH for thick tissue defines lateral hypothalamus spatio-molecular organization. Cell, 2021, 184, 6361-6377.e24.	13.5	72
5153	Mutant glucocerebrosidase impairs α -synuclein degradation by blockade of chaperone-mediated autophagy. Science Advances, 2022, 8, eabm6393.	4.7	63

#	ARTICLE	IF	CITATIONS
5154	MOJITOO: a fast and universal method for integration of multimodal single-cell data. <i>Bioinformatics</i> , 2022, 38, i282-i289.	1.8	6
5155	psupertime: supervised pseudotime analysis for time-series single-cell RNA-seq data. <i>Bioinformatics</i> , 2022, 38, i290-i298.	1.8	10
5156	scESI: evolutionary sparse imputation for single-cell transcriptomes from nearest neighbor cells. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	4
5157	Gene expression changes following chronic antipsychotic exposure in single cells from mouse striatum. <i>Molecular Psychiatry</i> , 2022, 27, 2803-2812.	4.1	10
5158	EP3 enhances adhesion and cytotoxicity of NK cells toward hepatic stellate cells in a murine liver fibrosis model. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	13
5159	A single-cell atlas of diffuse large B cell lymphoma. <i>Cell Reports</i> , 2022, 39, 110713.	2.9	33
5160	Androgen conspires with the CD8 ⁺ T cell exhaustion program and contributes to sex bias in cancer. <i>Science Immunology</i> , 2022, 7, .	5.6	74
5161	RNA polymerase II pausing factor NELF in CD8 ⁺ T cells promotes antitumor immunity. <i>Nature Communications</i> , 2022, 13, 2155.	5.8	7
5162	Identification of Transcription Factors Regulating SARS-CoV-2 Tropism Factor Expression by Inferring Cell-Type-Specific Transcriptional Regulatory Networks in Human Lungs. <i>Viruses</i> , 2022, 14, 837.	1.5	3
5163	Nasal symbiont <i>Staphylococcus epidermidis</i> restricts the cellular entry of influenza virus into the nasal epithelium. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, 26.	2.9	5
5164	Single-cell transcriptomic analysis reveals circadian rhythm disruption associated with poor prognosis and drug resistance in lung adenocarcinoma. <i>Journal of Pineal Research</i> , 2022, 73, .	3.4	21
5165	Multi-omics Profiling Shows BAP1 Loss Is Associated with Upregulated Cell Adhesion Molecules in Uveal Melanoma. <i>Molecular Cancer Research</i> , 2022, 20, 1260-1271.	1.5	9
5166	Microglial NF- κ B drives tau spreading and toxicity in a mouse model of tauopathy. <i>Nature Communications</i> , 2022, 13, 1969.	5.8	103
5167	Heparanase Blockade as a Novel Dual-Targeting Therapy for COVID-19. <i>Journal of Virology</i> , 2022, 96, e0005722.	1.5	14
5168	Single-Cell RNA Sequencing Unveils the Clonal and Transcriptional Landscape of Cutaneous T-Cell Lymphomas. <i>Clinical Cancer Research</i> , 2022, 28, 2610-2622.	3.2	9
5169	Integrating human brain proteomes with genome-wide association data implicates novel proteins in post-traumatic stress disorder. <i>Molecular Psychiatry</i> , 2022, 27, 3075-3084.	4.1	13
5170	Generation of resolving memory neutrophils through pharmacological training with 4-PBA or genetic deletion of TRAM. <i>Cell Death and Disease</i> , 2022, 13, 345.	2.7	3
5171	Single-cell RNA sequencing coupled to TCR profiling of large granular lymphocyte leukemia T cells. <i>Nature Communications</i> , 2022, 13, 1982.	5.8	23

#	ARTICLE	IF	CITATIONS
5172	Distinct phases of adult microglia proliferation: a Myc-mediated early phase and a Tnfaip3-mediated late phase. <i>Cell Discovery</i> , 2022, 8, 34.	3.1	11
5173	Decomposing a deterministic path to mesenchymal niche formation by two intersecting morphogen gradients. <i>Developmental Cell</i> , 2022, 57, 1053-1067.e5.	3.1	16
5174	Glioblastoma scRNA-seq shows treatment-induced, immune-dependent increase in mesenchymal cancer cells and structural variants in distal neural stem cells. <i>Neuro-Oncology</i> , 2022, 24, 1494-1508.	0.6	11
5176	Advances and applications of single-cell omics technologies in plant research. <i>Plant Journal</i> , 2022, 110, 1551-1563.	2.8	27
5177	An estrogen-sensitive fibroblast population drives abdominal muscle fibrosis in an inguinal hernia mouse model. <i>JCI Insight</i> , 2022, 7, .	2.3	2
5178	A mesenchymal to epithelial switch in Fgf10 expression specifies an evolutionary-conserved population of ionocytes in salivary glands. <i>Cell Reports</i> , 2022, 39, 110663.	2.9	15
5179	LINC00355 regulates p27KIP expression by binding to MENIN to induce proliferation in late-stage relapse breast cancer. <i>Npj Breast Cancer</i> , 2022, 8, 49.	2.3	4
5181	Identify the Prognostic and Immune Profile of VSIR in the Tumor Microenvironment: A Pan-Cancer Analysis. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 821649.	1.8	4
5183	Pyroptosis-Related Signature Predicts Prognosis and Immunotherapy Efficacy in Muscle-Invasive Bladder Cancer. <i>Frontiers in Immunology</i> , 2022, 13, 782982.	2.2	19
5184	Inflammatory responses in the placenta upon SARS-CoV-2 infection late in pregnancy. <i>IScience</i> , 2022, 25, 104223.	1.9	58
5185	Differential effects of macrophage subtypes on SARS-CoV-2 infection in a human pluripotent stem cell-derived model. <i>Nature Communications</i> , 2022, 13, 2028.	5.8	34
5186	Normalizing and denoising protein expression data from droplet-based single cell profiling. <i>Nature Communications</i> , 2022, 13, 2099.	5.8	63
5187	Generation of human islet cell type-specific identity genesets. <i>Nature Communications</i> , 2022, 13, 2020.	5.8	25
5188	Single-cell transcriptomics identifies Mcl-1 as a target for senolytic therapy in cancer. <i>Nature Communications</i> , 2022, 13, 2177.	5.8	35
5190	DGCyTOF: Deep learning with graphic cluster visualization to predict cell types of single cell mass cytometry data. <i>PLoS Computational Biology</i> , 2022, 18, e1008885.	1.5	9
5191	IFN γ Potentiates Anti-PD-1 Efficacy by Remodeling Glucose Metabolism in the Hepatocellular Carcinoma Microenvironment. <i>Cancer Discovery</i> , 2022, 12, 1718-1741.	7.7	66
5192	Programme of self-reactive innate-like T cell-mediated cancer immunity. <i>Nature</i> , 2022, 605, 139-145.	13.7	38
5193	Characterization of HIV-1 Infection in Microglia-Containing Human Cerebral Organoids. <i>Viruses</i> , 2022, 14, 829.	1.5	24

#	ARTICLE	IF	CITATIONS
5194	Single-cell RNA sequencing of the retina in a model of retinitis pigmentosa reveals early responses to degeneration in rods and cones. <i>BMC Biology</i> , 2022, 20, 86.	1.7	12
5195	G-Protein Subunit Gamma 4 as a Potential Biomarker for Predicting the Response of Chemotherapy and Immunotherapy in Bladder Cancer. <i>Genes</i> , 2022, 13, 693.	1.0	4
5197	Specification of CNS macrophage subsets occurs postnatally in defined niches. <i>Nature</i> , 2022, 604, 740-748.	13.7	107
5198	Single-nucleus RNA sequencing identified cells with ependymal cell-like features enriched in neonatal mice after spinal cord injury. <i>Neuroscience Research</i> , 2022, 181, 22-38.	1.0	2
5199	Single-Cell RNA Sequencing of Human Corpus Cavernosum Reveals Cellular Heterogeneity Landscapes in Erectile Dysfunction. <i>Frontiers in Endocrinology</i> , 2022, 13, 874915.	1.5	9
5200	Oncogenic Vav1-Myo1f induces therapeutically targetable macrophage-rich tumor microenvironment in peripheral T cell lymphoma. <i>Cell Reports</i> , 2022, 39, 110695.	2.9	13
5201	Semantic clustering analysis of E3-ubiquitin ligases in gastrointestinal tract defines genes ontology clusters with tissue expression patterns. <i>BMC Gastroenterology</i> , 2022, 22, 186.	0.8	0
5391	Single-Cell RNA Sequencing Reveals Heterogeneity of Myf5-Derived Cells and Altered Myogenic Fate in the Absence of SRSF2. <i>Advanced Science</i> , 2022, , 2105775.	5.6	3
5392	Simultaneous brain cell type and lineage determined by scRNA-seq reveals stereotyped cortical development. <i>Cell Systems</i> , 2022, 13, 438-453.e5.	2.9	2
5393	IFN- γ ³ + cytotoxic CD4 ⁺ T lymphocytes are involved in the pathogenesis of colitis induced by IL-23 and the food colorant Red 40. , 2022, 19, 777-790.		16
5394	Reduced chromatin accessibility correlates with resistance to Notch activation. <i>Nature Communications</i> , 2022, 13, 2210.	5.8	5
5395	Human pluripotent stem cell-derived cells endogenously expressing follicle-stimulating hormone receptors: modeling the function of an inactivating receptor mutation. <i>Molecular Human Reproduction</i> , 2022, 28, .	1.3	1
5396	Single-cell Characterization of the Cellular Landscape of Acral Melanoma Identifies Novel Targets for Immunotherapy. <i>Clinical Cancer Research</i> , 2022, 28, 2131-2146.	3.2	36
5397	Multiplatform Single-Cell Analysis Identifies Immune Cell Types Enhanced in Pulmonary Fibrosis. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2022, 67, 50-60.	1.4	22
5399	Astrogenesis in the murine dentate gyrus is a life-long and dynamic process. <i>EMBO Journal</i> , 2022, 41, e110409.	3.5	10
5400	Single-cell RNA-seq reveals heterogeneity in hiPSC-derived muscle progenitors and E2F family as a key regulator of proliferation. <i>Life Science Alliance</i> , 2022, 5, e202101312.	1.3	1
5401	Reorganization of postmitotic neuronal chromatin accessibility for maturation of serotonergic identity. <i>ELife</i> , 2022, 11, .	2.8	5
5402	Dissection of the Differentiation of Human Monocyte Subtypes to Osteoclasts at Single-Cell Resolution. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0

#	ARTICLE	IF	CITATIONS
5403	scTSSR2: Imputing Dropout Events for Single-Cell RNA Sequencing Using Fast Two-Side Self-Representation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 1445-1456.	1.9	0
5404	Machine Learning Approaches to Single-Cell Data Integration and Translation. <i>Proceedings of the IEEE</i> , 2022, 110, 557-576.	16.4	2
5405	Langerhans Cells are an Essential Component of the Angiogenic Niche During Skin Repair. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
5406	Insight into the potential pathogenesis of human osteoarthritis via single-cell RNA sequencing data on osteoblasts. <i>Mathematical Biosciences and Engineering</i> , 2022, 19, 6344-6361.	1.0	2
5407	Semi-Supervised Deep Learning for Cell Type Identification From Single-Cell Transcriptomic Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 1492-1505.	1.9	4
5408	Organization of gene programs revealed by unsupervised analysis of diverse gene-trait associations. <i>Nucleic Acids Research</i> , 2022, 50, e87-e87.	6.5	5
5410	Identification of Alzheimer's Disease Molecular Subtypes Based on Parallel Large-Scale Sequencing. <i>Frontiers in Aging Neuroscience</i> , 2022, 14, 770136.	1.7	9
5411	Cyromazine Effects the Reproduction of <i>Drosophila</i> by Decreasing the Number of Germ Cells in the Female Adult Ovary. <i>Insects</i> , 2022, 13, 414.	1.0	4
5412	CD66 ⁺ CD64 ^{dim} CD115 ⁺ cells in the human bone marrow represent neutrophil-committed progenitors. <i>Nature Immunology</i> , 2022, 23, 679-691.	7.0	28
5414	Single-cell and spatial RNA sequencing identify perturbators of microglial functions with aging. <i>Nature Aging</i> , 2022, 2, 508-525.	5.3	11
5416	Distinct Inflammatory Macrophage Populations Sequentially Infiltrate Bone-Tendon Interface Tissue After Anterior Cruciate Ligament (ACL) Reconstruction Surgery in Mice. <i>JBMR Plus</i> , 2022, 6, .	1.3	9
5417	The myogenesis program drives clonal selection and drug resistance in rhabdomyosarcoma. <i>Developmental Cell</i> , 2022, 57, 1226-1240.e8.	3.1	24
5418	Molecular Characterization of Membranous Nephropathy. <i>Journal of the American Society of Nephrology: JASN</i> , 2022, 33, 1208-1221.	3.0	12
5422	Decoding the PITX2-controlled genetic network in atrial fibrillation. <i>JCI Insight</i> , 2022, 7, .	2.3	5
5423	A Brain Region-Specific Expression Profile for Genes Within Large Introgression Deserts and Under Positive Selection in <i>Homo sapiens</i> . <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 824740.	1.8	5
5425	Imputing dropouts for single-cell RNA sequencing based on multi-objective optimization. <i>Bioinformatics</i> , 2022, 38, 3222-3230.	1.8	5
5427	circMbl functions in cis and in trans to regulate gene expression and physiology in a tissue-specific fashion. <i>Cell Reports</i> , 2022, 39, 110740.	2.9	19
5428	Establishment of a lncRNA-Based Prognostic Gene Signature Associated With Altered Immune Responses in HCC. <i>Frontiers in Immunology</i> , 2022, 13, 880288.	2.2	9

#	ARTICLE	IF	CITATIONS
5429	A Cd9+Cd271+ stem/progenitor population and the SHP2 pathway contribute to neonatal-to-adult switching that regulates tendon maturation. <i>Cell Reports</i> , 2022, 39, 110762.	2.9	3
5432	Human branching cholangiocyte organoids recapitulate functional bile duct formation. <i>Cell Stem Cell</i> , 2022, 29, 776-794.e13.	5.2	17
5434	Nonlesional lupus skin contributes to inflammatory education of myeloid cells and primes for cutaneous inflammation. <i>Science Translational Medicine</i> , 2022, 14, eabn2263.	5.8	52
5435	Revealing the Immune Heterogeneity between Systemic Lupus Erythematosus and Rheumatoid Arthritis Based on Multi-Omics Data Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5166.	1.8	18
5437	Single Cell Multiomic Approaches to Disentangle T Cell Heterogeneity. <i>Immunology Letters</i> , 2022, 246, 37-51.	1.1	1
5438	Reestablishment of spermatogenesis after more than 20 years of cryopreservation of rat spermatogonial stem cells reveals an important impact in differentiation capacity. <i>PLoS Biology</i> , 2022, 20, e3001618.	2.6	5
5439	Cancer-Associated Fibroblasts and Squamous Epithelial Cells Constitute a Unique Microenvironment in a Mouse Model of Inflammation-Induced Colon Cancer. <i>Frontiers in Oncology</i> , 2022, 12, .	1.3	6
5440	Single-Cell RNA-Seq and Bulk RNA-Seq Reveal Intratumoral Heterogeneity and Tumor Microenvironment Characteristics in Diffuse Large B-Cell Lymphoma. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	2
5441	YTHDF2 suppresses the plasmablast genetic program and promotes germinal center formation. <i>Cell Reports</i> , 2022, 39, 110778.	2.9	11
5442	Single-cell RNA-seq of UVB-radiated skin reveals landscape of photoaging-related inflammation and protection by vitamin D. <i>Gene</i> , 2022, 831, 146563.	1.0	10
5443	Integrated Single Cell and Bulk RNA-Seq Analysis Revealed Immunomodulatory Effects of Ulinastatin in Sepsis: A Multicenter Cohort Study. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	5
5444	Epicardium-derived cells organize through tight junctions to replenish cardiac muscle in salamanders. <i>Nature Cell Biology</i> , 2022, 24, 645-658.	4.6	12
5445	Meningioma DNA methylation groups identify biological drivers and therapeutic vulnerabilities. <i>Nature Genetics</i> , 2022, 54, 649-659.	9.4	93
5446	Dual functions of microRNA-17 in maintaining cartilage homeostasis and protection against osteoarthritis. <i>Nature Communications</i> , 2022, 13, 2447.	5.8	42
5447	Single-cell transcriptomic profiling of lung endothelial cells identifies dynamic inflammatory and regenerative subpopulations. <i>JCI Insight</i> , 2022, 7, .	2.3	21
5449	Shared and Cell-Type-Specific Gene Expression Patterns Associated With Autism Revealed by Integrative Regularized Non-Negative Matrix Factorization. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	0
5450	Mesothelial cell-derived antigen-presenting cancer-associated fibroblasts induce expansion of regulatory T cells in pancreatic cancer. <i>Cancer Cell</i> , 2022, 40, 656-673.e7.	7.7	155
5451	A common epigenetic mechanism across different cellular origins underlies systemic immune dysregulation in an idiopathic autism mouse model. <i>Molecular Psychiatry</i> , 2022, 27, 3343-3354.	4.1	4

#	ARTICLE	IF	CITATIONS
5452	Bringing machine learning to research on intellectual and developmental disabilities: taking inspiration from neurological diseases. <i>Journal of Neurodevelopmental Disorders</i> , 2022, 14, 28.	1.5	9
5453	Conservation and divergence of myelin proteome and oligodendrocyte transcriptome profiles between humans and mice. <i>ELife</i> , 2022, 11, .	2.8	24
5454	Single-nucleus transcriptome analysis reveals disease- and regeneration-associated endothelial cells in white matter vascular dementia. <i>Journal of Cellular and Molecular Medicine</i> , 2022, 26, 3183-3195.	1.6	11
5455	Multi-omics single-cell data integration and regulatory inference with graph-linked embedding. <i>Nature Biotechnology</i> , 2022, 40, 1458-1466.	9.4	153
5456	Single-cell landscape of immunocytes in patients with extrahepatic cholangiocarcinoma. <i>Journal of Translational Medicine</i> , 2022, 20, 210.	1.8	7
5457	Rare variants implicate NMDA receptor signaling and cerebellar gene networks in risk for bipolar disorder. <i>Molecular Psychiatry</i> , 2022, 27, 3842-3856.	4.1	5
5458	The Tabula Sapiens: A multiple-organ, single-cell transcriptomic atlas of humans. <i>Science</i> , 2022, 376, eabl4896.	6.0	289
5459	A downsampling method enables robust clustering and integration of single-cell transcriptome data. <i>Journal of Biomedical Informatics</i> , 2022, 130, 104093.	2.5	2
5460	A Markov random field model-based approach for differentially expressed gene detection from single-cell RNA-seq data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	3
5461	p57Kip2 imposes the reserve stem cell state of gastric chief cells. <i>Cell Stem Cell</i> , 2022, 29, 826-839.e9.	5.2	17
5462	Lymph node colonization induces tumor-immune tolerance to promote distant metastasis. <i>Cell</i> , 2022, 185, 1924-1942.e23.	13.5	111
5463	Single-cell transcriptome analysis reveals the immune heterogeneity and the repopulation of microglia by Hif1 α in mice after spinal cord injury. <i>Cell Death and Disease</i> , 2022, 13, 432.	2.7	18
5464	Cross-species single-cell transcriptomic analysis reveals divergence of cell composition and functions in mammalian ileum epithelium. <i>Cell Regeneration</i> , 2022, 11, 19.	1.1	13
5466	IRF4 drives clonal evolution and lineage choice in a zebrafish model of T-cell lymphoma. <i>Nature Communications</i> , 2022, 13, 2420.	5.8	5
5467	Single-Cell Transcriptomics Uncovers Cellular Heterogeneity, Mechanisms, and Therapeutic Targets for Parkinson's Disease. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	3
5468	Sequential Single-Cell Transcriptional and Protein Marker Profiling Reveals TIGIT as a Marker of CD19 CAR-T Cell Dysfunction in Patients with Non-Hodgkin Lymphoma. <i>Cancer Discovery</i> , 2022, 12, 1886-1903.	7.7	31
5469	Defining the Skeletal Myogenic Lineage in Human Pluripotent Stem Cell-Derived Teratomas. <i>Cells</i> , 2022, 11, 1589.	1.8	4
5470	NanoDam identifies Homeobrain (ARX) and Scarecrow (NKX2.1) as conserved temporal factors in the <i>Drosophila</i> central brain and visual system. <i>Developmental Cell</i> , 2022, 57, 1193-1207.e7.	3.1	14

#	ARTICLE	IF	CITATIONS
5471	Peripheral Blood Monocyte Abundance Predicts Outcomes in Patients with Breast Cancer. <i>Cancer Research Communications</i> , 2022, 2, 286-292.	0.7	2
5474	Decoding the pathogenesis of Diamond-Blackfan anemia using single-cell RNA-seq. <i>Cell Discovery</i> , 2022, 8, 41.	3.1	14
5477	Single-cell genomic profiling of human dopamine neurons identifies a population that selectively degenerates in Parkinson's disease. <i>Nature Neuroscience</i> , 2022, 25, 588-595.	7.1	155
5478	Distinctive molecular features of regenerative stem cells in the damaged male germline. <i>Nature Communications</i> , 2022, 13, 2500.	5.8	9
5480	Interplay Between GH-regulated, Sex-biased Liver Transcriptome and Hepatic Zonation Revealed by Single-Nucleus RNA Sequencing. <i>Endocrinology</i> , 2022, 163, .	1.4	22
5481	Extricating human tumour immune alterations from tissue inflammation. <i>Nature</i> , 2022, 605, 728-735.	13.7	56
5482	ICARUS, an interactive web server for single cell RNA-seq analysis. <i>Nucleic Acids Research</i> , 2022, 50, W427-W433.	6.5	20
5483	Transcriptomic mapping uncovers Purkinje neuron plasticity driving learning. <i>Nature</i> , 2022, 605, 722-727.	13.7	24
5484	Dynamic spectrum of ectopic lymphoid B cell activation and hypermutation in the RA synovium characterized by NR4A nuclear receptor expression. <i>Cell Reports</i> , 2022, 39, 110766.	2.9	20
5485	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
5486	An activation to memory differentiation trajectory of tumor-infiltrating lymphocytes informs metastatic melanoma outcomes. <i>Cancer Cell</i> , 2022, 40, 524-544.e5.	7.7	23
5487	Computational Identification of Preneoplastic Cells Displaying High Stemness and Risk of Cancer Progression. <i>Cancer Research</i> , 2022, 82, 2520-2537.	0.4	9
5488	DAE-TPGM: A deep autoencoder network based on a two-part-gamma model for analyzing single-cell RNA-seq data. <i>Computers in Biology and Medicine</i> , 2022, 146, 105578.	3.9	1
5489	DDX24 is required for muscle fiber organization and the suppression of wound-induced Wnt activity necessary for pole re-establishment during planarian regeneration. <i>Developmental Biology</i> , 2022, 488, 11-29.	0.9	5
5490	Single-cell transcriptomic analysis revealing changes in retinal cell subpopulation levels and the pathways involved in diabetic retinopathy. <i>Annals of Translational Medicine</i> , 2022, 10, 562-562.	0.7	4
5491	EBAG9 controls CD8+ T cell memory formation responding to tumor challenge in mice. <i>JCI Insight</i> , 2022, , .	2.3	2
5492	A CRISPR view on autophagy. <i>Trends in Cell Biology</i> , 2022, , .	3.6	2
5493	MYC drives aggressive prostate cancer by disrupting transcriptional pause release at androgen receptor targets. <i>Nature Communications</i> , 2022, 13, 2559.	5.8	56

#	ARTICLE	IF	CITATIONS
5494	Pan-Cancer Single-Cell Analysis Reveals the Core Factors and Pathway in Specific Cancer Stem Cells of Upper Gastrointestinal Cancer. <i>Frontiers in Bioengineering and Biotechnology</i> , 2022, 10, .	2.0	2
5495	Endothelial ETS1 inhibition exacerbate bloodâ€‘brain barrier dysfunction in multiple sclerosis through inducing endothelial-to-mesenchymal transition. <i>Cell Death and Disease</i> , 2022, 13, 462.	2.7	7
5496	Single-cell analysis of transcription factor regulatory networks reveals molecular basis for subtype-specific dysregulation in acute myeloid leukemia. <i>Blood Science</i> , 2022, 4, 65-75.	0.4	4
5497	Benchmarking spatial and single-cell transcriptomics integration methods for transcript distribution prediction and cell type deconvolution. <i>Nature Methods</i> , 2022, 19, 662-670.	9.0	130
5498	Integrative analysis of scRNA-seq and scATAC-seq revealed transit-amplifying thymic epithelial cells expressing autoimmune regulator. <i>ELife</i> , 2022, 11, .	2.8	10
5499	Temporal perturbation of histone deacetylase activity reveals a requirement for HDAC1â€‘3 in mesendoderm cell differentiation. <i>Cell Reports</i> , 2022, 39, 110818.	2.9	0
5500	Single-Cell RNA-seq Analysis Reveals Cellular Functional Heterogeneity in Dermis Between Fibrotic and Regenerative Wound Healing Fates. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	8
5501	Human liver single nucleus and single-Cell RNA sequencing identify a hepatocellular carcinoma-associated cell-type affecting survival. <i>Genome Medicine</i> , 2022, 14, 50.	3.6	27
5502	Distinguishing cellâ€‘cell complexes from dual lineage cells using single-Cell transcriptomics is not trivial. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2022, 101, 547-551.	1.1	0
5503	Integrating single-cell RNA sequencing with spatial transcriptomics reveals immune landscape for interstitial cystitis. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 161.	7.1	19
5504	The use of single-cell multi-omics in immuno-oncology. <i>Nature Communications</i> , 2022, 13, 2728.	5.8	13
5505	Integrated analysis of an in vivo model of intra-nasal exposure to instilled air pollutants reveals cell-type specific responses in the placenta. <i>Scientific Reports</i> , 2022, 12, 8438.	1.6	6
5506	Disrupting mechanotransduction decreases fibrosis and contracture in split-thickness skin grafting. <i>Science Translational Medicine</i> , 2022, 14, eabj9152.	5.8	31
5507	Single cell transcriptomic analysis of human amnion identifies cell-specific signatures associated with membrane rupture and parturition. <i>Cell and Bioscience</i> , 2022, 12, 64.	2.1	7
5508	Embryonic vascular establishment requires protein C receptor-expressing endothelial progenitors. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	4
5509	TFAP2 paralogs facilitate chromatin access for MITF at pigmentation and cell proliferation genes. <i>PLoS Genetics</i> , 2022, 18, e1010207.	1.5	13
5510	Molecular Characterization of Membranous Nephropathy: <i>Quo Vadis?</i> <i>Journal of the American Society of Nephrology: JASN</i> , 2022, 33, 1057-1059.	3.0	0
5511	Lupus Susceptibility Loci Predispose Mice to Clonal Lymphocytic Responses and Myeloid Expansion. <i>Journal of Immunology</i> , 2022, 208, 2403-2424.	0.4	5

#	ARTICLE	IF	CITATIONS
5512	Single-cell landscape reveals active cell subtypes and their interaction in the tumor microenvironment of gastric cancer. <i>Theranostics</i> , 2022, 12, 3818-3833.	4.6	40
5513	Single-Cell Analysis of the Transcriptome and Epigenome. <i>Methods in Molecular Biology</i> , 2022, , 21-60.	0.4	5
5514	Lactate metabolism coordinates macrophage response and regeneration in zebrafish. <i>Theranostics</i> , 2022, 12, 3995-4009.	4.6	4
5527	Single-cell transcriptomic classification of rabies-infected cortical neurons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	19
5528	Single-cell analysis reveals X upregulation is not global in pre-gastrulation embryos. <i>IScience</i> , 2022, 25, 104465.	1.9	9
5530	Chemoprevention of Lung Cancer with a Combination of Mitochondria-Targeted Compounds. <i>Cancers</i> , 2022, 14, 2538.	1.7	6
5531	Robust differential abundance test in compositional data. <i>Biometrika</i> , 2023, 110, 169-185.	1.3	5
5532	Large-scale chromatin reorganization reactivates placenta-specific genes that drive cellular aging. <i>Developmental Cell</i> , 2022, 57, 1347-1368.e12.	3.1	32
5533	Mast cell marker gene signature in head and neck squamous cell carcinoma. <i>BMC Cancer</i> , 2022, 22, .	1.1	14
5535	Single-cell transcriptomics provides insights into the origin and microenvironment of human oesophageal high-grade intraepithelial neoplasia. <i>Clinical and Translational Medicine</i> , 2022, 12, .	1.7	5
5537	Tumor-induced erythroid precursor-differentiated myeloid cells mediate immunosuppression and curtail anti-PD-1/PD-L1 treatment efficacy. <i>Cancer Cell</i> , 2022, 40, 674-693.e7.	7.7	41
5540	Transcription factor GATA2 may potentiate follicle-stimulating hormone production in mice via induction of the BMP antagonist gremlin in gonadotrope cells. <i>Journal of Biological Chemistry</i> , 2022, 298, 102072.	1.6	5
5541	Astrocyte-targeted gene delivery of interleukin 2 specifically increases brain-resident regulatory T cell numbers and protects against pathological neuroinflammation. <i>Nature Immunology</i> , 2022, 23, 878-891.	7.0	59
5542	A human breast atlas integrating single-cell proteomics and transcriptomics. <i>Developmental Cell</i> , 2022, 57, 1400-1420.e7.	3.1	50
5546	Single-cell deletion analyses show control of pro-T cell developmental speed and pathways by Tcf7, Spi1, Gata3, Bcl11a, Erg, and Bcl11b. <i>Science Immunology</i> , 2022, 7, .	5.6	20
5547	Specific Microglial Subtypes and Inflammatory Mechanisms in Early Diabetic Retinopathy. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
5549	A Global Regulatory Network for Dysregulated Gene Expression and Abnormal Metabolic Signaling in Immune Cells in the Microenvironment of Graves' Disease and Hashimoto's Thyroiditis. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	5
5551	Mapping the cardiac vascular niche in heart failure. <i>Nature Communications</i> , 2022, 13, .	5.8	31

#	ARTICLE	IF	CITATIONS
5554	Cross-tissue, single-cell stromal atlas identifies shared pathological fibroblast phenotypes in four chronic inflammatory diseases. <i>Med</i> , 2022, 3, 481-518.e14.	2.2	51
5555	Constitutive loss of DNMT3A causes morbid obesity through misregulation of adipogenesis. <i>ELife</i> , 0, 11, .	2.8	12
5559	Altered patterning of trisomy 21 interneuron progenitors. <i>Stem Cell Reports</i> , 2022, 17, 1366-1379.	2.3	11
5561	Hormone sensitive lipase ablation promotes bone regeneration. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2022, 1868, 166449.	1.8	1
5564	AP-1 activation mediates post-natal cardiomyocyte maturation. <i>Cardiovascular Research</i> , 2023, 119, 536-550.	1.8	8
5566	Single-Cell Transcriptomics-Based Study of Transcriptional Regulatory Features in the Non-Obstructive Azoospermia Testis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
5570	Evolution and developmental expression of the sodium-iodide symporter (<i>NIS</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 15, 1079-1098.	1.5	4
5573	Identification of two cancer stem cell-like populations in triple-negative breast cancer xenografts. <i>DMM Disease Models and Mechanisms</i> , 2022, 15, .	1.2	7
5574	Transcriptional adaptation of olfactory sensory neurons to GPCR identity and activity. <i>Nature Communications</i> , 2022, 13, .	5.8	13
5575	Transcriptional profiling of human VÎ1 TÎcells reveals a pathogen-driven adaptive differentiation program. <i>Cell Reports</i> , 2022, 39, 110858.	2.9	13
5582	IL-13-programmed airway tuft cells produce PGE2, which promotes CFTR-dependent mucociliary function. <i>JCI Insight</i> , 2022, 7, .	2.3	19
5583	Interspecies commensal interactions have nonlinear impacts on host immunity. <i>Cell Host and Microbe</i> , 2022, 30, 988-1002.e6.	5.1	23
5584	Ileum tissue single-cell mRNA sequencing elucidates the cellular architecture of pathophysiological changes associated with weaning in piglets. <i>BMC Biology</i> , 2022, 20, .	1.7	4
5585	Brain motor and fear circuits regulate leukocytes during acute stress. <i>Nature</i> , 2022, 607, 578-584.	13.7	69
5586	Identification of cell types in multiplexed in situ images by combining protein expression and spatial information using CELESTA. <i>Nature Methods</i> , 2022, 19, 759-769.	9.0	42
5587	Comparative analysis of the testes from wild-type and <i>Alkbh5</i> -knockout mice using single-cell RNA sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	5
5588	A phenotypic spectrum of autism is attributable to the combined effects of rare variants, polygenic risk and sex. <i>Nature Genetics</i> , 2022, 54, 1284-1292.	9.4	66
5592	The spatiotemporal program of zonal liver regeneration following acute injury. <i>Cell Stem Cell</i> , 2022, 29, 973-989.e10.	5.2	60

#	ARTICLE	IF	CITATIONS
5594	± Cell dysfunction in islets from nondiabetic, glutamic acid decarboxylase autoantibody± positive individuals. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	24
5595	Enhanced transcriptional heterogeneity mediated by NF-±B super-enhancers. <i>PLoS Genetics</i> , 2022, 18, e1010235.	1.5	7
5598	Reversal of synapse loss in Alzheimer mouse models by targeting mGluR5 to prevent synaptic tagging by C1Q. <i>Science Translational Medicine</i> , 2022, 14, .	5.8	38
5599	Single-Cell Transcriptomic Analysis of the Mouse Pancreas: Characteristic Features of Pancreatic Ductal Cells in Chronic Pancreatitis. <i>Genes</i> , 2022, 13, 1015.	1.0	3
5600	Single-Cell Sequencing Analysis of the db/db Mouse Hippocampus Reveals Cell-Type-Specific Insights Into the Pathobiology of Diabetes-Associated Cognitive Dysfunction. <i>Frontiers in Endocrinology</i> , 2022, 13, .	1.5	11
5601	Inherent constraints on a polyfunctional tissue lead to a reproduction-immunity tradeoff. <i>BMC Biology</i> , 2022, 20, .	1.7	13
5603	Single-cell atlas unveils cellular heterogeneity and novel markers in human neonatal and adult intervertebral discs. <i>IScience</i> , 2022, 25, 104504.	1.9	11
5604	mRNA-1273 vaccination protects against SARS-CoV-2± elicited lung inflammation in nonhuman primates. <i>JCI Insight</i> , 2022, 7, .	2.3	3
5605	A stromal Integrated Stress Response activates perivascular cancer-associated fibroblasts to drive angiogenesis and tumour progression. <i>Nature Cell Biology</i> , 2022, 24, 940-953.	4.6	52
5606	Recombinant multimeric dog allergen prevents airway hyperresponsiveness in a model of asthma marked by vigorous <sc>T_H2</sc> and <sc>T_H17</sc> cell responses. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2022, 77, 2987-3001.	2.7	4
5607	Development of an Improved in vitro Model of Bovine Trophectoderm Differentiation. <i>Frontiers in Animal Science</i> , 0, 3, .	0.8	1
5608	scAmp± A versatile pipeline for single-cell RNA-seq analysis from basics to clinics. <i>PLoS Computational Biology</i> , 2022, 18, e1010097.	1.5	8
5610	Applying transcriptomics to study glycosylation at the cell type level. <i>IScience</i> , 2022, 25, 104419.	1.9	20
5611	Population-scale analysis of common and rare genetic variation associated with hearing loss in adults. <i>Communications Biology</i> , 2022, 5, .	2.0	12
5612	Gene Coexpression Network Characterizing Microenvironmental Heterogeneity and Intercellular Communication in Pancreatic Ductal Adenocarcinoma: Implications of Prognostic Significance and Therapeutic Target. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	1
5613	Skeletal Stem/Progenitor Cells in Periosteum and Skeletal Muscle Share a Common Molecular Response to Bone Injury. <i>Journal of Bone and Mineral Research</i> , 2020, 37, 1545-1561.	3.1	17
5614	The secretome of irradiated peripheral blood mononuclear cells attenuates activation of mast cells and basophils. <i>EBioMedicine</i> , 2022, 81, 104093.	2.7	7
5619	Nonparametric Bayesian Two-Level Clustering for Subject-Level Single-Cell Expression Data. <i>Statistica Sinica</i> , 2023, , .	0.2	2

#	ARTICLE	IF	CITATIONS
5620	From single-omics to interactomics: How can ligand-induced perturbations modulate single-cell phenotypes?. <i>Advances in Protein Chemistry and Structural Biology</i> , 2022, , .	1.0	1
5621	Approaches of Single-Cell Analysis in Crop Improvement. <i>Springer Protocols</i> , 2022, , 271-294.	0.1	1
5622	<i>Xist</i>-Dependent Impaired Lymphopoiesis in Male Offspring is a Unique Hallmark of X-chromosome Imprinting During Maternal Schistosomiasis. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
5623	Single-cell transcriptome profiling of the immune space-time landscape reveals dendritic cell regulatory program in polymicrobial sepsis. <i>Theranostics</i> , 2022, 12, 4606-4628.	4.6	17
5624	Plasticity in Airway Smooth Muscle Differentiation During Mouse Lung Development. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
5627	Identification of early neurodegenerative pathways in progressive multiple sclerosis. <i>Nature Neuroscience</i> , 2022, 25, 944-955.	7.1	55
5628	Single-cell transcriptomic analysis of honeybee brains identifies vitellogenin as caste differentiation-related factor. <i>IScience</i> , 2022, 25, 104643.	1.9	15
5629	A single-cell transcriptomic atlas characterizes the silk-producing organ in the silkworm. <i>Nature Communications</i> , 2022, 13, .	5.8	13
5630	Comparison of methods and resources for cell-cell communication inference from single-cell RNA-Seq data. <i>Nature Communications</i> , 2022, 13, .	5.8	143
5634	Complementary brains. <i>Nature Ecology and Evolution</i> , 0, , .	3.4	0
5636	Single-cell RNA-seq-based proteogenomics identifies glioblastoma-specific transposable elements encoding HLA-I-presented peptides. <i>Cell Reports</i> , 2022, 39, 110916.	2.9	28
5639	c-Rel-dependent monocytes are potent immune suppressor cells in cancer. <i>Journal of Leukocyte Biology</i> , 2022, 112, 845-859.	1.5	2
5640	Transcriptional and functional motifs defining renal function revealed by single-nucleus RNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	22
5641	Comprehensive RNA Expression Analysis Revealed Biological Functions of Key Gene Sets and Identified Disease-Associated Cell Types Involved in Rat Traumatic Brain Injury. <i>Journal of Clinical Medicine</i> , 2022, 11, 3437.	1.0	2
5642	Microglial amyloid beta clearance is driven by PIEZO1 channels. <i>Journal of Neuroinflammation</i> , 2022, 19, .	3.1	45
5643	Integration of Single-Cell Transcriptomics With a High Throughput Functional Screening Assay to Resolve Cell Type, Growth Kinetics, and Stemness Heterogeneity Within the Comma-1D Cell Line. <i>Frontiers in Genetics</i> , 0, , .	1.1	0
5644	Interleukin-17 governs hypoxic adaptation of injured epithelium. <i>Science</i> , 2022, 377, .	6.0	75
5645	Secretory Cells Are the Primary Source of pIgR in Small Airways. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2022, 67, 334-345.	1.4	7

#	ARTICLE	IF	CITATIONS
5646	NuRD complex recruitment to Thpok mediates CD4 ⁺ T cell lineage differentiation. <i>Science Immunology</i> , 2022, 7, .	5.6	11
5647	Discovering Immune-Mediated Mechanisms of Gastric Carcinogenesis Through Single-Cell RNA Sequencing. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	6
5648	Single-Cell Landscape of Mouse Islet Allograft and Syngeneic Graft. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
5649	Identification of the central intermediate in the extra-embryonic to embryonic endoderm transition through single-cell transcriptomics. <i>Nature Cell Biology</i> , 2022, 24, 833-844.	4.6	15
5650	A single-cell transcriptomic atlas tracking the neural basis of division of labour in an ant superorganism. <i>Nature Ecology and Evolution</i> , 2022, 6, 1191-1204.	3.4	15
5652	Embigin is a fibronectin receptor that affects sebaceous gland differentiation and metabolism. <i>Developmental Cell</i> , 2022, 57, 1453-1465.e7.	3.1	6
5654	Mass Cytometry and Single-Cell Transcriptome Analyses Reveal the Immune Cell Characteristics of Ulcerative Colitis. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	2
5655	Altered differentiation of endometrial mesenchymal stromal fibroblasts is associated with endometriosis susceptibility. <i>Communications Biology</i> , 2022, 5, .	2.0	4
5658	Identification of Highly Cross-Reactive Mimotopes for a Public T Cell Response in Murine Melanoma. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
5659	Absence of microglia promotes diverse pathologies and early lethality in Alzheimer's disease mice. <i>Cell Reports</i> , 2022, 39, 110961.	2.9	48
5660	Computational Methods for Single-cell DNA Methylome Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 48-66.	3.0	4
5662	Inference of age-associated transcription factor regulatory activity changes in single cells. <i>Nature Aging</i> , 2022, 2, 548-561.	5.3	15
5663	Deep Learning Framework for Integrating Multibatch Calibration, Classification, and Pathway Activities. <i>Analytical Chemistry</i> , 0, , .	3.2	3
5664	Integrated analysis reveals the pivotal interactions between immune cells in the melanoma tumor microenvironment. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
5665	DJ-1 governs airway progenitor cell/eosinophil interactions to promote allergic inflammation. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 150, 1178-1193.e13.	1.5	4
5666	Modulation of <i>Atg</i> genes expression in aged rat liver, brain, and kidney by caloric restriction analyzed via single-nucleus/cell RNA sequencing. <i>Autophagy</i> , 2023, 19, 706-715.	4.3	5
5667	Cochlear Development; New Tools and Approaches. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	7
5668	Joint profiling of gene expression and chromatin accessibility during amphioxus development at single-cell resolution. <i>Cell Reports</i> , 2022, 39, 110979.	2.9	12

#	ARTICLE	IF	CITATIONS
5669	Single-cell transcriptomics and surface epitope detection in human brain epileptic lesions identifies pro-inflammatory signaling. <i>Nature Neuroscience</i> , 2022, 25, 956-966.	7.1	29
5670	Advancements in Genomic and Behavioral Neuroscience Analysis for the Study of Normal and Pathological Brain Function. <i>Frontiers in Molecular Neuroscience</i> , 0, 15, .	1.4	0
5671	Viral coinfection promotes tuberculosis immunopathogenesis by type I IFN signaling-dependent impediment of Th1 cell pulmonary influx. <i>Nature Communications</i> , 2022, 13, .	5.8	11
5672	LSH-GAN enables in-silico generation of cells for small sample high dimensional scRNA-seq data. <i>Communications Biology</i> , 2022, 5, .	2.0	3
5673	Exploring the cellular landscape of circular RNAs using full-length single-cell RNA sequencing. <i>Nature Communications</i> , 2022, 13, .	5.8	25
5675	Nephrin expression in human epidermal keratinocytes and its implication in poor wound closure. <i>FASEB Journal</i> , 2022, 36, .	0.2	2
5676	Inflammatory adipose activates a nutritional immunity pathway leading to retinal dysfunction. <i>Cell Reports</i> , 2022, 39, 110942.	2.9	9
5680	A preoptic neuronal population controls fever and appetite during sickness. <i>Nature</i> , 2022, 606, 937-944.	13.7	52
5681	Therapeutic inhibition of the SRC-kinase HCK facilitates T cell tumor infiltration and improves response to immunotherapy. <i>Science Advances</i> , 2022, 8, .	4.7	16
5682	RNA-binding proteins direct myogenic cell fate decisions. <i>ELife</i> , 0, 11, .	2.8	7
5683	Occult polyclonality of preclinical pancreatic cancer models drives in vitro evolution. <i>Nature Communications</i> , 2022, 13, .	5.8	13
5686	MNK2 deficiency potentiates \hat{I}^2 -cell regeneration via translational regulation. <i>Nature Chemical Biology</i> , 2022, 18, 942-953.	3.9	9
5688	Unravelling the sex-specific diversity and functions of adrenal gland macrophages. <i>Cell Reports</i> , 2022, 39, 110949.	2.9	13
5689	Single-cell RNA-sequencing of peripheral blood mononuclear cells reveals widespread, context-specific gene expression regulation upon pathogenic exposure. <i>Nature Communications</i> , 2022, 13, .	5.8	39
5690	Multi-omics profiling of single nuclei from frozen archived postmortem human pituitary tissue. <i>STAR Protocols</i> , 2022, 3, 101446.	0.5	7
5691	MicroRNA $\hat{e}202$ safeguards meiotic progression by $\hat{e}9$ preventing premature SEPARASE \hat{e} mediated REC8 cleavage. <i>EMBO Reports</i> , 2022, 23, .	2.0	8
5692	BCG hydrogel promotes CTSS-mediated antigen processing and presentation, thereby suppressing metastasis and prolonging survival in melanoma. , 2022, 10, e004133.		8
5693	Characterization of naked mole \hat{e} rat hematopoiesis reveals unique stem and progenitor cell patterns and neotenic traits. <i>EMBO Journal</i> , 2022, 41, .	3.5	12

#	ARTICLE	IF	CITATIONS
5694	Dissecting the Single-Cell Transcriptome Network of Immune Environment Underlying Cervical Premalignant Lesion, Cervical Cancer and Metastatic Lymph Nodes. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	24
5695	Decoding lymphomyeloid divergence and immune hyporesponsiveness in G-CSF-primed human bone marrow by single-cell RNA-seq. <i>Cell Discovery</i> , 2022, 8, .	3.1	5
5696	Marsupials and Multi-Omics: Establishing New Comparative Models of Neural Crest Patterning and Craniofacial Development. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	0
5698	Decoding the activated stem cell phenotype of the neonatally maturing pituitary. <i>ELife</i> , 0, 11, .	2.8	10
5699	An armed oncolytic virus enhances the efficacy of tumor-infiltrating lymphocyte therapy by converting tumors to artificial antigen-presenting cells in situ. <i>Molecular Therapy</i> , 2022, 30, 3658-3676.	3.7	13
5700	GPR15L is an epithelial inflammation-derived pruritogen. <i>Science Advances</i> , 2022, 8, .	4.7	5
5704	Gene expression profiles of ischemic stroke clots retrieved by mechanical thrombectomy are associated with disease etiology. <i>Journal of NeuroInterventional Surgery</i> , 2023, 15, e33-e40.	2.0	4
5705	Immune landscape of a genetically engineered murine model of glioma compared with human glioma. <i>JCI Insight</i> , 2022, 7, .	2.3	10
5706	Single-cell RNA-seq reveals the genesis and heterogeneity of tumor microenvironment in pancreatic undifferentiated carcinoma with osteoclast-like giant-cells. <i>Molecular Cancer</i> , 2022, 21, .	7.9	16
5707	Foxa2 and Pet1 Direct and Indirect Synergy Drive Serotonergic Neuronal Differentiation. <i>Frontiers in Neuroscience</i> , 0, 16, .	1.4	1
5709	Elucidation of the genetic causes of bicuspid aortic valve disease. <i>Cardiovascular Research</i> , 2023, 119, 857-866.	1.8	11
5710	Dissecting the Heterogeneity of Human Thoracic Aortic Aneurysms Using Single-Cell Transcriptomics. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2022, 42, 919-930.	1.1	12
5711	Significance of Liver Zonation in Hepatocellular Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	0
5714	Single-cell antigen-specific landscape of CAR T infusion product identifies determinants of CD19-positive relapse in patients with ALL. <i>Science Advances</i> , 2022, 8, .	4.7	63
5715	A Single-Cell Characterization of Human Post-implantation Embryos Cultured In Vitro Delineates Morphogenesis in Primary Syncytialization. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	3
5716	A Tead1-Apelin axis directs paracrine communication from myogenic to endothelial cells in skeletal muscle. <i>iScience</i> , 2022, 25, 104589.	1.9	6
5717	Modeling Susceptibility to Cardiotoxicity in Cancer Therapy Using Human iPSC-Derived Cardiac Cells and Systems Biology. <i>Heart Failure Clinics</i> , 2022, 18, 335-347.	1.0	1
5718	Single-cell entropy network detects the activity of immune cells based on ribosomal protein genes. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3556-3566.	1.9	2

#	ARTICLE	IF	CITATIONS
5719	Delineation and Birth of a Layered Intestinal Stem Cell Niche. SSRN Electronic Journal, 0, , .	0.4	3
5720	MSPJ: Discovering potential biomarkers in small gene expression datasets via ensemble learning. Computational and Structural Biotechnology Journal, 2022, 20, 3783-3795.	1.9	1
5721	Tracing the cell-type-specific modules of immune responses during COVID-19 progression using scDisProcema. Computational and Structural Biotechnology Journal, 2022, 20, 3545-3555.	1.9	1
5722	A Retro-Inverso Modified Peptide Alleviated Ovalbumin-Induced Asthma Model by Affecting Glycerophospholipid and Purine Metabolism of Immune Cells. SSRN Electronic Journal, 0, , .	0.4	0
5723	A transcriptome atlas and interactive analysis platform for autoimmune disease. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	2
5724	Gastric stem cells promote inflammation and gland remodeling in response to <i>Helicobacter pylori</i> via <i>Rspo3</i> - <i>Lgr4</i> axis. EMBO Journal, 2022, 41, .	3.5	13
5725	Dynamic immune ecosystem of dengue infection revealed by single-cell sequencing. Journal of Leukocyte Biology, 2022, 112, 1621-1631.	1.5	2
5726	GREM1 is required to maintain cellular heterogeneity in pancreatic cancer. Nature, 2022, 607, 163-168.	13.7	31
5727	Mapping developmental paths of monkey primordial germ-like cells differentiation from pluripotent stem cells by single cell ribonucleic acid sequencing analysis. Biology of Reproduction, 2022, 107, 237-249.	1.2	2
5729	Retinal ganglion cell-specific genetic regulation in primary open-angle glaucoma. Cell Genomics, 2022, 2, 100142.	3.0	9
5731	Regulatory Programs of B-cell Activation and Germinal Center Reaction Allow B-ALL Escape from CD19 CAR T-cell Therapy. Cancer Immunology Research, 2022, 10, 1055-1068.	1.6	3
5732	Cell fate determining molecular switches and signaling pathways in Pax7-expressing somitic mesoderm. Cell Discovery, 2022, 8, .	3.1	3
5735	Molecular Characterization of the Tumor Microenvironment in Renal Medullary Carcinoma. Frontiers in Oncology, 0, 12, .	1.3	4
5736	Single-cell transcriptomic analysis identifies an immune-prone population in erythroid precursors during human ontogenesis. Nature Immunology, 2022, 23, 1109-1120.	7.0	30
5737	Prognostic Ability of Enhancer RNAs in Metastasis of Non-Small Cell Lung Cancer. Molecules, 2022, 27, 4108.	1.7	2
5738	Vascular Regulation by Super Enhancer-Derived LINC00607. Frontiers in Cardiovascular Medicine, 0, 9, .	1.1	4
5741	Proinflammatory signaling in islet β^2 cells propagates invasion of pathogenic immune cells in autoimmune diabetes. Cell Reports, 2022, 39, 111011.	2.9	11
5742	Bulk RNA Sequencing With Integrated Single-Cell RNA Sequencing Identifies BCL2A1 as a Potential Diagnostic and Prognostic Biomarker for Sepsis. Frontiers in Public Health, 0, 10, .	1.3	2

#	ARTICLE	IF	CITATIONS
5743	Revealing the Key MSCs Niches and Pathogenic Genes in Influencing CEP Homeostasis: A Conjoint Analysis of Single-Cell and WGCNA. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	8
5747	A single-cell map of dynamic chromatin landscapes of immune cells in renal cell carcinoma. <i>Nature Cancer</i> , 2022, 3, 885-898.	5.7	20
5748	Clonal structure, stability and dynamics of human memory B cells and circulating plasmablasts. <i>Nature Immunology</i> , 2022, 23, 1076-1085.	7.0	39
5749	G1/S restriction point coordinates phasic gene expression and cell differentiation. <i>Nature Communications</i> , 2022, 13, .	5.8	6
5754	In vivo multidimensional CRISPR screens identify <i>Lgals2</i> as an immunotherapy target in triple-negative breast cancer. <i>Science Advances</i> , 2022, 8, .	4.7	26
5758	Mucosal viral infection induces a regulatory T cell activation phenotype distinct from tissue residency in mouse and human tissues. <i>Mucosal Immunology</i> , 2022, 15, 1012-1027.	2.7	3
5759	Gut microbe-derived metabolite trimethylamine N-oxide activates PERK to drive fibrogenic mesenchymal differentiation. <i>IScience</i> , 2022, 25, 104669.	1.9	8
5761	Single-cell RNA sequencing reveals localized tumour ablation and intratumoural immunostimulant delivery potentiate T cell mediated tumour killing. <i>Clinical and Translational Medicine</i> , 2022, 12, .	1.7	9
5762	DC ENaC-Dependent Inflammasome Activation Contributes to Salt-Sensitive Hypertension. <i>Circulation Research</i> , 2022, 131, 328-344.	2.0	31
5764	Cell Trajectory-Related Genes of Lung Adenocarcinoma Predict Tumor Immune Microenvironment and Prognosis of Patients. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	8
5765	Innate immune regulation in HIV latency models. <i>Retrovirology</i> , 2022, 19, .	0.9	3
5766	Single-cell transcriptomics reveals a senescence-associated <i>IL6</i> / <i>CCR6</i> axis driving radiodermatitis. <i>EMBO Molecular Medicine</i> , 2022, 14, .	3.3	9
5771	Synthesizing genome regulation data with vote-counting. <i>Trends in Genetics</i> , 2022, 38, 1208-1216.	2.9	5
5772	ZnT8 loss-of-function accelerates functional maturation of hESC-derived β^2 cells and resists metabolic stress in diabetes. <i>Nature Communications</i> , 2022, 13, .	5.8	17
5773	Inhibition of immunoglobulin E attenuates pulmonary hypertension. , 2022, 1, 665-678.		3
5774	Non-heat-stressed method to isolate hepatic stellate cells from highly steatotic tumor-bearing liver using CD49a. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2022, , .	2.3	0
5775	Spatially Resolved Transcriptomes of Mammalian Kidneys Illustrate the Molecular Complexity and Interactions of Functional Nephron Segments. <i>Frontiers in Medicine</i> , 0, 9, .	1.2	6
5777	Durable response in a patient with recurrent respiratory papillomatosis treated with immune checkpoint blockade. <i>Head and Neck</i> , 2022, 44, .	0.9	2

#	ARTICLE	IF	CITATIONS
5778	SYK Is Associated With Malignant Phenotype and Immune Checkpoints in Diffuse Glioma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
5780	Insulin-Like Growth Factor 1 Attenuates the Pro-Inflammatory Phenotype of Neutrophils in Myocardial Infarction. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	11
5781	CTSB+ macrophage repress memory immune hub in the liver metastasis site of colorectal cancer patient revealed by multi-omics analysis. <i>Biochemical and Biophysical Research Communications</i> , 2022, 626, 8-14.	1.0	6
5784	Patient-derived renal cell carcinoma organoids for personalized cancer therapy. <i>Clinical and Translational Medicine</i> , 2022, 12, .	1.7	24
5785	Vasculature atrophy causes a stiffened microenvironment that augments epidermal stem cell differentiation in aged skin. <i>Nature Aging</i> , 2022, 2, 592-600.	5.3	12
5787	CProtMEDIAS: clustering of amino acid sequences encoded by gene families by MErging and Dlgitizing Aligned Sequences. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	2
5788	An integrated atlas of human placental development delineates essential regulators of trophoblast stem cells. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	14
5789	Genome-wide DNA hypermethylation opposes healing in patients with chronic wounds by impairing epithelial-mesenchymal transition. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	20
5790	Lymphocyte subsets in Atlantic cod (<i>Gadus morhua</i>) interrogated by single-cell sequencing. <i>Communications Biology</i> , 2022, 5, .	2.0	4
5791	Hematopoietic transcription factor GFI1 promotes anchorage independence by sustaining ERK activity in cancer cells. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	1
5792	FMO2 (Flavin Containing Monooxygenase 2) Prevents Cardiac Fibrosis via CYP2J3-SMURF2 Axis. <i>Circulation Research</i> , 2022, 131, 189-206.	2.0	10
5793	Repopulated microglia induce expression of Cxcl13 with differential changes in Tau phosphorylation but do not impact amyloid pathology. <i>Journal of Neuroinflammation</i> , 2022, 19, .	3.1	7
5794	Single-cell transcriptomic signatures and gene regulatory networks modulated by WIs in mammalian midline facial formation and clefts. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	6
5795	Mouse pulmonary interstitial macrophages mediate the pro-tumorigenic effects of IL-9. <i>Nature Communications</i> , 2022, 13, .	5.8	11
5797	Orexin neurons inhibit sleep to promote arousal. <i>Nature Communications</i> , 2022, 13, .	5.8	27
5798	17q21.31 sub-haplotypes underlying H1-associated risk for Parkinson's disease are associated with LRR37A/2 expression in astrocytes. <i>Molecular Neurodegeneration</i> , 2022, 17, .	4.4	15
5799	Systemic gene therapy with thymosin β 4 alleviates glomerular injury in mice. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
5800	Dissecting the treatment-naive ecosystem of human melanoma brain metastasis. <i>Cell</i> , 2022, 185, 2591-2608.e30.	13.5	62

#	ARTICLE	IF	CITATIONS
5801	Mechanical checkpoint regulates monocyte differentiation in fibrotic niches. <i>Nature Materials</i> , 2022, 21, 939-950.	13.3	22
5802	ZBTB46 defines and regulates ILC3s that protect the intestine. <i>Nature</i> , 2022, 609, 159-165.	13.7	33
5803	Resolving SARS-CoV-2 CD4+ T _H cell specificity via reverse epitope discovery. <i>Cell Reports Medicine</i> , 2022, 3, 100697.	3.3	25
5804	Multi-Omics Uncover Neonatal Cecal Cell Development Potentials. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	0
5805	In vivo transcriptional analysis of mice infected with <i>Leishmania major</i> unveils cellular heterogeneity and altered transcriptomic profiling at single-cell resolution. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010518.	1.3	9
5806	A hypometabolic defense strategy against malaria. <i>Cell Metabolism</i> , 2022, 34, 1183-1200.e12.	7.2	10
5807	Integrated single cell and spatial transcriptomics reveal autoreactive differentiated B cells in joints of early rheumatoid arthritis. <i>Scientific Reports</i> , 2022, 12, .	1.6	18
5808	Enhancing PD-L1 Degradation by ITCH during MAPK Inhibitor Therapy Suppresses Acquired Resistance. <i>Cancer Discovery</i> , 2022, 12, 1942-1959.	7.7	15
5809	Cerebral organoids containing an <i>AUTS2</i> missense variant model microcephaly. <i>Brain</i> , 2023, 146, 387-404.	3.7	11
5810	Molecular landscapes of human hippocampal immature neurons across lifespan. <i>Nature</i> , 2022, 607, 527-533.	13.7	116
5811	A reference single-cell regulomic and transcriptomic map of cynomolgus monkeys. <i>Nature Communications</i> , 2022, 13, .	5.8	20
5812	A Novel Type I Interferon Primed Dendritic Cell Subpopulation in TREX1 Mutant Chilblain Lupus Patients. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
5816	Increased H3K27 trimethylation contributes to cone survival in a mouse model of cone dystrophy. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, .	2.4	3
5818	Single-cell transcriptome analysis of embryonic and adult endothelial cells allows to rank the hemogenic potential of post-natal endothelium. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
5821	<i>Cebpb</i> Regulates Skeletal Stem Cell Osteogenic Differentiation and Fracture Healing via the WNT/ β -Catenin Pathway. <i>Stem Cells International</i> , 2022, 2022, 1-16.	1.2	2
5822	Bacteria reduce flagellin synthesis to evade microglia-astrocyte-driven immunity in the brain. <i>Cell Reports</i> , 2022, 40, 111033.	2.9	7
5825	Single-nucleus chromatin accessibility and RNA sequencing reveal impaired brain development in prenatally e-cigarette exposed neonatal rats. <i>iScience</i> , 2022, 25, 104686.	1.9	3
5826	Multiomic analyses reveal enriched glycolytic processes in β -myosin heavy chain-expressed cardiomyocytes in early cardiac hypertrophy. , 2022, 1, 100011.		0

#	ARTICLE	IF	CITATIONS
5827	A deep matrix factorization based approach for single-cell RNA-seq data clustering. <i>Methods</i> , 2022, 205, 114-122.	1.9	4
5828	Nox4 promotes endothelial differentiation through chromatin remodeling. <i>Redox Biology</i> , 2022, 55, 102381.	3.9	5
5829	Single-cell RNA sequencing analysis of T helper cell differentiation and heterogeneity. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2022, 1869, 119321.	1.9	2
5830	Mapping hormone-regulated cell-cell interaction networks in the human breast at single-cell resolution. <i>Cell Systems</i> , 2022, 13, 644-664.e8.	2.9	13
5831	Follicular Lymphoma Microenvironment Characteristics Associated with Tumor Cell Mutations and MHC Class II Expression. <i>Blood Cancer Discovery</i> , 2022, 3, 428-443.	2.6	35
5832	Microglia-derived PDGFB promotes neuronal potassium currents to suppress basal sympathetic tonicity and limit hypertension. <i>Immunity</i> , 2022, 55, 1466-1482.e9.	6.6	20
5834	Noncanonical activation of GLI signaling in SOX2 ⁺ cells drives medulloblastoma relapse. <i>Science Advances</i> , 2022, 8, .	4.7	8
5835	Identifying potential signatures for atherosclerosis in the context of predictive, preventive, and personalized medicine using integrative bioinformatics approaches and machine-learning strategies. <i>EPMA Journal</i> , 2022, 13, 433-449.	3.3	5
5839	Epigenetic Regulation of Profibrotic Macrophages in Systemic Sclerosisâ€‘Associated Interstitial Lung Disease. <i>Arthritis and Rheumatology</i> , 2022, 74, 2003-2014.	2.9	12
5840	ARHGEF39, a Gene Implicated in Developmental Language Disorder, Activates RHOA and Is Involved in Cell De-Adhesion and Neural Progenitor Cell Proliferation. <i>Frontiers in Molecular Neuroscience</i> , 0, 15, .	1.4	1
5841	Unfolding the genotype-to-phenotype black box of cardiovascular diseases through cross-scale modeling. <i>IScience</i> , 2022, 25, 104790.	1.9	1
5842	Transplanted organoids empower human preclinical assessment of drug candidate for the clinic. <i>Science Advances</i> , 2022, 8, .	4.7	11
5843	CD8+ T cell trajectory subtypes decode tumor heterogeneity and provide treatment recommendations for hepatocellular carcinoma. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	14
5845	TREM2 macrophages induced by human lipids drive inflammation in acne lesions. <i>Science Immunology</i> , 2022, 7, .	5.6	37
5846	Identification and Characterization of Cancer-Associated Fibroblast Subpopulations in Lung Adenocarcinoma. <i>Cancers</i> , 2022, 14, 3486.	1.7	5
5848	The molecular mechanisms of CTHRC1 in gastric cancer by integrating TCGA, GEO and GSA datasets. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
5849	Cell-type specific changes in PKC-delta neurons of the central amygdala during alcohol withdrawal. <i>Translational Psychiatry</i> , 2022, 12, .	2.4	17
5852	A brain precursor atlas reveals the acquisition of developmental-like states in adult cerebral tumours. <i>Nature Communications</i> , 2022, 13, .	5.8	11

#	ARTICLE	IF	CITATIONS
5854	Benchmarking methods for detecting differential states between conditions from multi-subject single-cell RNA-seq data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	19
5856	Alveolar macrophages in early stage COPD show functional deviations with properties of impaired immune activation. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	12
5857	Molecular signatures underlying neurofibrillary tangle susceptibility in Alzheimer's disease. <i>Neuron</i> , 2022, 110, 2929-2948.e8.	3.8	48
5860	Detecting retinal neural and stromal cell classes and ganglion cell subtypes based on transcriptome data with deep transfer learning. <i>Bioinformatics</i> , 2022, 38, 4321-4329.	1.8	1
5862	Coupled Analysis of Single-Cell Transcriptome and TCR Sequencing Uncovers the Role of TRAV1-2 <sup>+</sup> MAIT Cells in Immune Reconstitution of HIV-Infected Patients Under Antiretroviral Therapy. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
5863	Single-cell analysis reveals an Angpt4-initiated EPDC-EC-CM cellular coordination cascade during heart regeneration. <i>Protein and Cell</i> , 0, , .	4.8	0
5864	Impact of single-cell RNA sequencing on understanding immune regulation. <i>Journal of Cellular and Molecular Medicine</i> , 2022, 26, 4645-4657.	1.6	6
5867	Joint analysis of scATAC-seq datasets using epiConv. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	1
5868	BAP1 Loss Promotes Suppressive Tumor Immune Microenvironment via Upregulation of PROS1 in Class 2 Uveal Melanomas. <i>Cancers</i> , 2022, 14, 3678.	1.7	13
5869	Functional neuronal circuitry and oscillatory dynamics in human brain organoids. <i>Nature Communications</i> , 2022, 13, .	5.8	57
5870	Evidence for oligodendrocyte progenitor cell heterogeneity in the adult mouse brain. <i>Scientific Reports</i> , 2022, 12, .	1.6	18
5872	Association of a common genetic variant with Parkinson's disease is mediated by microglia. <i>Science Translational Medicine</i> , 2022, 14, .	5.8	40
5874	Single-cell RNA-Seq reveals changes in immune landscape in post-traumatic osteoarthritis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	20
5875	Single-cell multimodal analysis identifies common regulatory programs in synovial fibroblasts of rheumatoid arthritis patients and modeled TNF-driven arthritis. <i>Genome Medicine</i> , 2022, 14, .	3.6	23
5876	Shared mechanisms across the major psychiatric and neurodegenerative diseases. <i>Nature Communications</i> , 2022, 13, .	5.8	48
5877	A Study on the Radiosensitivity of Radiation-Induced Lung Injury at the Acute Phase Based on Single-Cell Transcriptomics. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4
5878	CXCR4 ^{high} megakaryocytes regulate host-defense immunity against bacterial pathogens. <i>ELife</i> , 0, 11, .	2.8	10
5880	Panoramic comparison between NK cells in healthy and cancerous liver through single-cell RNA sequencing. <i>Cancer Biology and Medicine</i> , 0, , 1-18.	1.4	2

#	ARTICLE	IF	CITATIONS
5881	Polarization disorder of decidual NK cells in unexplained recurrent spontaneous abortion revealed by single-cell transcriptome analysis. <i>Reproductive Biology and Endocrinology</i> , 2022, 20, .	1.4	6
5882	Immunosuppressive landscape in hepatocellular carcinoma revealed by single-cell sequencing. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	15
5883	Mouse fetal growth restriction through parental and fetal immune gene variation and intercellular communications cascade. <i>Nature Communications</i> , 2022, 13, .	5.8	4
5886	Genomic landscapes of canine splenic angiosarcoma (hemangiosarcoma) contain extensive heterogeneity within and between patients. <i>PLoS ONE</i> , 2022, 17, e0264986.	1.1	10
5889	Identification of a Gene Signature of Cancer-Associated Fibroblasts to Predict Prognosis in Ovarian Cancer. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	8
5891	Identification of Malignant Cell Populations Associated with Poor Prognosis in High-Grade Serous Ovarian Cancer Using Single-Cell RNA Sequencing. <i>Cancers</i> , 2022, 14, 3580.	1.7	5
5892	FitDevo: accurate inference of single-cell developmental potential using sample-specific gene weight. <i>Briefings in Bioinformatics</i> , 0, , .	3.2	1
5893	SMGR: a joint statistical method for integrative analysis of single-cell multi-omics data. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, .	1.5	24
5895	Dynamic plasticity of prostate cancer intermediate cells during androgen receptor-targeted therapy. <i>Cell Reports</i> , 2022, 40, 111123.	2.9	6
5897	Systems spatiotemporal dynamics of traumatic brain injury at single-cell resolution reveals humanin as a therapeutic target. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, .	2.4	6
5898	Single cell spatial analysis reveals the topology of immunomodulatory purinergic signaling in glioblastoma. <i>Nature Communications</i> , 2022, 13, .	5.8	27
5900	Contrastive learning enables rapid mapping to multimodal single-cell atlas of multimillion scale. <i>Nature Machine Intelligence</i> , 2022, 4, 696-709.	8.3	14
5901	Anti-COX-2 autoantibody is a novel biomarker of immune aplastic anemia. <i>Leukemia</i> , 2022, 36, 2317-2327.	3.3	2
5902	Transcriptional variability accelerates preleukemia by cell diversification and perturbation of protein synthesis. <i>Science Advances</i> , 2022, 8, .	4.7	2
5903	Scarf enables a highly memory-efficient analysis of large-scale single-cell genomics data. <i>Nature Communications</i> , 2022, 13, .	5.8	11
5905	Nrf2 dictates the neuronal survival and differentiation of embryonic zebrafish harboring compromised alanyl-tRNA synthetase. <i>Development (Cambridge)</i> , 0, , .	1.2	1
5908	Limbal BCAM expression identifies a proliferative progenitor population capable of holoclone formation and corneal differentiation. <i>Cell Reports</i> , 2022, 40, 111166.	2.9	7
5909	Production of human entorhinal stellate cell-like cells by forward programming shows an important role of Foxp1 in reprogramming. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	2

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5910	Spatiotemporal single-cell regulatory atlas reveals neural crest lineage diversification and cellular function during tooth morphogenesis. <i>Nature Communications</i> , 2022, 13, .	5.8	24
5913	Selective Inference for Hierarchical Clustering. <i>Journal of the American Statistical Association</i> , 2024, 119, 332-342.	1.8	17
5914	Spatially restricted drivers and transitional cell populations cooperate with the microenvironment in untreated and chemo-resistant pancreatic cancer. <i>Nature Genetics</i> , 2022, 54, 1390-1405.	9.4	68
5915	Intestinal single-cell atlas reveals novel lymphocytes in pigs with similarities to human cells. <i>Life Science Alliance</i> , 2022, 5, e202201442.	1.3	12
5916	PlaqView 2.0: A comprehensive web portal for cardiovascular single-cell genomics. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	9
5917	Construction of a solid Cox model for AML patients based on multiomics bioinformatic analysis. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	4
5919	Differential requirement for DICER1 activity during the development of mitral and tricuspid valves. <i>Journal of Cell Science</i> , 2022, 135, .	1.2	1
5920	Single-Cell RNA Sequencing Reveals Smooth Muscle Cells Heterogeneity in Experimental Aortic Dissection. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
5922	The Impact of Inflammation-Induced Tumor Plasticity during Myeloid Transformation. <i>Cancer Discovery</i> , 2022, 12, 2392-2413.	7.7	28
5923	Single-cell transcriptomic profiling unveils dysregulation of cardiac progenitor cells and cardiomyocytes in a mouse model of maternal hyperglycemia. <i>Communications Biology</i> , 2022, 5, .	2.0	5
5924	Single-cell RNA-sequencing identifies anti-cancer immune phenotypes in the early lung metastatic niche during breast cancer. <i>Clinical and Experimental Metastasis</i> , 2022, 39, 865-881.	1.7	6
5926	Steroidogenic Factor 1 Regulates Transcription of the Inhibin B Coreceptor in Pituitary Gonadotrope Cells. <i>Endocrinology</i> , 2022, 163, .	1.4	1
5927	Pan-Cancer Analysis of the Immunological Role of PDIA5: A Potential Target for Immunotherapy. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
5928	Lymphangiocrine signals are required for proper intestinal repair after cytotoxic injury. <i>Cell Stem Cell</i> , 2022, 29, 1262-1272.e5.	5.2	24
5929	Modulation of macrophage inflammatory function through selective inhibition of the epigenetic reader protein SP140. <i>BMC Biology</i> , 2022, 20, .	1.7	4
5930	Transcriptomic heterogeneity of cultured ADSCs corresponds to embolic risk in the host. <i>IScience</i> , 2022, 25, 104822.	1.9	4
5931	DARPP32, a target of hyperactive mTORC1 in the retinal pigment epithelium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	5
5932	Integrating single cell transcriptomics and volume electron microscopy confirms the presence of pancreatic acinar-like cells in sea urchins. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	11

#	ARTICLE	IF	CITATIONS
5933	Systematic exploration of dynamic splicing networks reveals conserved multistage regulators of neurogenesis. <i>Molecular Cell</i> , 2022, 82, 2982-2999.e14.	4.5	10
5934	Single-cell transcriptome analysis of fractional CO ₂ laser efficiency in treating a mouse model of alopecia. <i>Lasers in Surgery and Medicine</i> , 2022, 54, 1167-1176.	1.1	3
5935	Single-cell RNA sequencing reveals distinct immunology profiles in human keloid. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	23
5937	Metacells untangle large and complex single-cell transcriptome networks. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	14
5938	Single-cell analysis reveals differences among iNKT cells colonizing peripheral organs and identifies Klf2 as a key gene for iNKT emigration. <i>Cell Discovery</i> , 2022, 8, .	3.1	5
5940	Single-cell sequencing reveals novel cellular heterogeneity in uterine leiomyomas. <i>Human Reproduction</i> , 2022, 37, 2334-2349.	0.4	19
5941	Postmitotic accumulation of histone variant H3.3 in new cortical neurons establishes neuronal chromatin, transcriptome, and identity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	6
5942	Single-cell analysis and functional characterization uncover the stem cell hierarchies and developmental origins of rhabdomyosarcoma. <i>Nature Cancer</i> , 2022, 3, 961-975.	5.7	16
5943	N6-adenomethylation of GsdmC is essential for Lgr5+ stem cell survival to maintain normal colonic epithelial morphogenesis. <i>Developmental Cell</i> , 2022, 57, 1976-1994.e8.	3.1	12
5944	Bioinformatics analysis of potential pathogenesis and risk genes of immunoinflammation-promoted renal injury in severe COVID-19. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4
5945	A Cell Differentiation Trajectory-Related Signature for Predicting the Prognosis of Lung Adenocarcinoma. <i>Genetical Research</i> , 2022, 2022, 1-11.	0.3	2
5949	Precise reconstruction of the TME using bulk RNA-seq and a machine learning algorithm trained on artificial transcriptomes. <i>Cancer Cell</i> , 2022, 40, 879-894.e16.	7.7	48
5950	Activation of the NF κ B signaling pathway in IL6+CSF3+ vascular endothelial cells promotes the formation of keloids. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 10, .	2.0	0
5952	STAG2 promotes the myelination transcriptional program in oligodendrocytes. <i>ELife</i> , 0, 11, .	2.8	7
5953	Early Deregulation Of Cholangiocyte NROB2 During Primary Sclerosing Cholangitis. , 2022, , .		1
5954	Gruffi: an algorithm for computational removal of stressed cells from brain organoid transcriptomic datasets. <i>EMBO Journal</i> , 2022, 41, .	3.5	19
5956	RB1 loss triggers dependence on ESRRG in retinoblastoma. <i>Science Advances</i> , 2022, 8, .	4.7	5
5957	Immune-mediated tubule atrophy promotes acute kidney injury to chronic kidney disease transition. <i>Nature Communications</i> , 2022, 13, .	5.8	24

#	ARTICLE	IF	CITATIONS
5958	A regulatory network of Sox and Six transcription factors initiate a cell fate transformation during hearing regeneration in adult zebrafish. <i>Cell Genomics</i> , 2022, 2, 100170.	3.0	13
5960	Helminth-induced reprogramming of the stem cell compartment inhibits type 2 immunity. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	10
5962	Intra-tumor heterogeneity and prognostic risk signature for hepatocellular carcinoma based on single-cell analysis. <i>Experimental Biology and Medicine</i> , 2022, 247, 1741-1751.	1.1	1
5963	Medulloblastoma group 3 and 4 tumors comprise a clinically and biologically significant expression continuum reflecting human cerebellar development. <i>Cell Reports</i> , 2022, 40, 111162.	2.9	21
5964	Single-cell RNA sequencing depicts the local cell landscape in thyroid-associated ophthalmopathy. <i>Cell Reports Medicine</i> , 2022, 3, 100699.	3.3	11
5965	Scalable batch-correction approach for integrating large-scale single-cell transcriptomes. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	0
5966	Cellular mechanisms of oligoclonal vascular smooth muscle cell expansion in cardiovascular disease. <i>Cardiovascular Research</i> , 2023, 119, 1279-1294.	1.8	12
5967	Binary organization of epidermal basal domains highlights robustness to environmental exposure. <i>EMBO Journal</i> , 2022, 41, .	3.5	10
5968	Identification of Quiescent LGR5+ Stem Cells in the Human Colon. <i>Gastroenterology</i> , 2022, 163, 1391-1406.e24.	0.6	14
5970	ASURAT: functional annotation-driven unsupervised clustering of single-cell transcriptomes. <i>Bioinformatics</i> , 2022, 38, 4330-4336.	1.8	2
5971	In vivo visualization and molecular targeting of the cardiac conduction system. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	10
5972	Large-scale multiplexed mosaic CRISPR perturbation in the whole organism. <i>Cell</i> , 2022, 185, 3008-3024.e16.	13.5	15
5974	Immune modulation by molecularly targeted photothermal ablation in a mouse model of advanced hepatocellular carcinoma and cirrhosis. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
5975	Single-cell transcriptomics of immune cells in lymph nodes reveals their composition and alterations in functional dynamics during the early stages of bubonic plague. <i>Science China Life Sciences</i> , 2023, 66, 110-126.	2.3	7
5976	Molecular and cellular evolution of the primate dorsolateral prefrontal cortex. <i>Science</i> , 2022, 377, .	6.0	61
5977	A Deep Learning Pipeline for the Automatic cell type Assignment of scRNA-seq Data. , 2022, , .		1
5979	Targeting <sc>YAP1</sc>/<sc>TAZ</sc> in nonsmallâ€cell lung carcinoma: From molecular mechanisms to precision medicine. <i>International Journal of Cancer</i> , 2023, 152, 558-571.	2.3	10
5980	Temporally restricted activation of IFNÎ² signaling underlies response to immune checkpoint therapy in mice. <i>Nature Communications</i> , 2022, 13, .	5.8	12

#	ARTICLE	IF	CITATIONS
5983	Transcriptomics, regulatory syntax, and enhancer identification in mesoderm-induced ESCs at single-cell resolution. <i>Cell Reports</i> , 2022, 40, 111219.	2.9	8
5984	DNGR-1-tracing marks an ependymal cell subset with damage-responsive neural stem cell potential. <i>Developmental Cell</i> , 2022, 57, 1957-1975.e9.	3.1	7
5985	Spatial profiling of chromatin accessibility in mouse and human tissues. <i>Nature</i> , 2022, 609, 375-383.	13.7	119
5986	Single-Cell and Bulk RNA Sequencing Reveal Malignant Epithelial Cell Heterogeneity and Prognosis Signatures in Gastric Carcinoma. <i>Cells</i> , 2022, 11, 2550.	1.8	3
5988	Single-cell RNA sequencing to decipher the immunogenicity of ChAdOx1 nCoV-19/AZD1222 and mRNA-1273 vaccines in patients with autoimmune rheumatic diseases. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
5989	Midkine expression by stem-like tumor cells drives persistence to mTOR inhibition and an immune-suppressive microenvironment. <i>Nature Communications</i> , 2022, 13, .	5.8	14
5990	Oncofetal reprogramming in tumour development and progression. <i>Nature Reviews Cancer</i> , 2022, 22, 593-602.	12.8	22
5991	Inhibition of mutant IDH1 promotes cycling of acute myeloid leukemia stem cells. <i>Cell Reports</i> , 2022, 40, 111182.	2.9	5
5993	Temporal profiling of the breast tumour microenvironment reveals collagen XII as a driver of metastasis. <i>Nature Communications</i> , 2022, 13, .	5.8	63
5994	Single-cell transcriptomics and cell-specific proteomics reveals molecular signatures of sleep. <i>Communications Biology</i> , 2022, 5, .	2.0	16
5995	Fc Fragment of <i>IgE</i> Receptor <i>Ig</i> (<i>FCER1G</i>) acts as a key gene involved in cancer immune infiltration and tumour microenvironment. <i>Immunology</i> , 2023, 168, 302-319.	2.0	7
5996	Single cell transcriptomic analysis of the immune cell compartment in the human small intestine and in Celiac disease. <i>Nature Communications</i> , 2022, 13, .	5.8	12
5998	Single-Cell Transcriptional Profiling and Gene Regulatory Network Modeling in Tg2576 Mice Reveal Gender-Dependent Molecular Features Preceding Alzheimer-Like Pathologies. <i>Molecular Neurobiology</i> , 2024, 61, 541-566.	1.9	5
6001	ABC portal: a single-cell database and web server for blood cells. <i>Nucleic Acids Research</i> , 2023, 51, D792-D804.	6.5	6
6002	ELF5 is a potential respiratory epithelial cell-specific risk gene for severe COVID-19. <i>Nature Communications</i> , 2022, 13, .	5.8	12
6003	Pyramidal neuron subtype diversity governs microglia states in the neocortex. <i>Nature</i> , 2022, 608, 750-756.	13.7	45
6004	Nonproductive exposure of <i>PBMCs</i> to <i>SARS-CoV-2</i> induces cell-intrinsic innate immune responses. <i>Molecular Systems Biology</i> , 2022, 18, .	3.2	7
6005	Drug resistance in NSCLC is associated with tumor micro-environment. <i>Reproductive Biology</i> , 2022, 22, 100680.	0.9	7

#	ARTICLE	IF	CITATIONS
6006	Deciphering the dynamic niches and regeneration-associated transcriptional program of motoneurons following peripheral nerve injury. <i>IScience</i> , 2022, 25, 104917.	1.9	2
6007	Protocol to estimate cell type proportions from bulk RNA-seq using DAISM-DNNXMBD. <i>STAR Protocols</i> , 2022, 3, 101587.	0.5	0
6008	Uncovering the dynamic effects of DEX treatment on lung cancer by integrating bioinformatic inference and multiscale modeling of scRNA-seq and proteomics data. <i>Computers in Biology and Medicine</i> , 2022, 149, 105999.	3.9	1
6011	devCellPy is a machine learning-enabled pipeline for automated annotation of complex multilayered single-cell transcriptomic data. <i>Nature Communications</i> , 2022, 13, .	5.8	16
6012	Cell type-specific inference of differential expression in spatial transcriptomics. <i>Nature Methods</i> , 2022, 19, 1076-1087.	9.0	40
6013	Identification of Human Global, Tissue and Within-Tissue Cell-Specific Stably Expressed Genes at Single-Cell Resolution. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10214.	1.8	0
6014	Single-cell transcriptome mapping identifies a local, innate B cell population driving chronic rejection after lung transplantation. <i>JCI Insight</i> , 2022, 7, .	2.3	2
6016	Executable models of immune signaling pathways in HIV-associated atherosclerosis. <i>Npj Systems Biology and Applications</i> , 2022, 8, .	1.4	3
6018	PD-1 expression on mouse intratumoral NK cells and its effects on NK cell phenotype. <i>IScience</i> , 2022, 25, 105137.	1.9	6
6019	SARS-CoV-2 infection of human pluripotent stem cell-derived liver organoids reveals potential mechanisms of liver pathology. <i>IScience</i> , 2022, 25, 105146.	1.9	8
6020	Human PSCs determine the competency of cerebral organoid differentiation via FGF signaling and epigenetic mechanisms. <i>IScience</i> , 2022, 25, 105140.	1.9	3
6021	Downregulation of zinc finger protein 71 expression in oral squamous cell carcinoma tissues and its underlying molecular mechanism. <i>Pathology Research and Practice</i> , 2022, 238, 154109.	1.0	1
6022	Single-cell RNA analysis of chemokine expression in heterogeneous CD14+ monocytes with lipopolysaccharide-induced bone resorption. <i>Experimental Cell Research</i> , 2022, 420, 113343.	1.2	0
6023	Cellular and molecular profiles of larval and adult <i>Xenopus</i> corneal epithelia resolved at the single-cell level. <i>Developmental Biology</i> , 2022, 491, 13-30.	0.9	4
6024	RNA-seq characterization of histamine-releasing mast cells as potential therapeutic target of osteoarthritis. <i>Clinical Immunology</i> , 2022, 244, 109117.	1.4	8
6025	Interferon $\hat{\pm}$ facilitates anti-HBV cellular immune response in a B cell-dependent manner. <i>Antiviral Research</i> , 2022, 207, 105420.	1.9	5
6026	A non-invasive piTreg-related gene signature for spontaneous tolerance in renal transplantation. <i>Gene</i> , 2023, 848, 146901.	1.0	0
6027	Cell Classification Based on Stacked Autoencoder for Single-Cell RNA Sequencing. <i>Lecture Notes in Computer Science</i> , 2022, , 245-259.	1.0	0

#	ARTICLE	IF	CITATIONS
6028	SCDF: A Novel Single-Cell Classification Method Based on Dimension-Reduced Data Fusion. Lecture Notes in Computer Science, 2022, , 196-206.	1.0	0
6029	Single Nucleus RNA-sequencing Reveals Altered Intercellular Communication and Dendritic Cell Activation in Nonobstructive Hypertrophic Cardiomyopathy. Cardiology and Cardiovascular Medicine, 2022, 06, .	0.1	4
6030	Colorectal Cancer Cell Differentiation Trajectory Predicts Patient Immunotherapy Response and Prognosis. Cancer Control, 2022, 29, 107327482211213.	0.7	1
6031	<i>Stardust</i>: improving spatial transcriptomics data analysis through space-aware modularity optimization-based clustering. GigaScience, 2022, 11, .	3.3	2
6032	Single-Cell RNA sequencing reveals immune cell dynamics and local intercellular communication in acute murine cardiac allograft rejection. Theranostics, 2022, 12, 6242-6257.	4.6	4
6033	A Clustering Method Unifying Cell-Type Recognition and Subtype Identification for Tumor Heterogeneity Analysis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, 20, 822-832.	1.9	2
6034	Human regulatory T cells locally differentiate and are functionally heterogeneous within the inflamed arthritic joint. Clinical and Translational Immunology, 2022, 11, .	1.7	9
6035	Single-Cell RNA Sequence Data Analysing Using Fuzzy de Based Clustering Technique. Lecture Notes in Networks and Systems, 2022, , 479-487.	0.5	1
6036	<P Class="Head">Multi-Organ Single Cell Analysis Reveals an On/Off Switch System with Potential for Personalized Treatment of Immunological Diseases<O:P><O:P><P>. SSRN Electronic Journal, 0, , .	0.4	0
6037	Stability of scRNA-Seq Analysis Workflows is Susceptible to Preprocessing and is Mitigated by Regularized or Supervised Approaches. Evolutionary Bioinformatics, 2022, 18, 117693432211230.	0.6	0
6038	Interactive Analysis of Single-Cell Data Using Flexible Workflows With SCTK2.0. SSRN Electronic Journal, 0, , .	0.4	0
6039	Cell Heterogeneity Uncovered by Single-Cell RNA Sequencing Offers Potential Therapeutic Targets for Ischemic Stroke. , 2022, 13, 1436.		11
6040	A novel cuproptosis-related lncRNA prognostic signature for predicting treatment and immune environment of head and neck squamous cell carcinoma. Mathematical Biosciences and Engineering, 2022, 19, 12127-12145.	1.0	0
6041	Single-cell transcriptomics reveals the regulative roles of cancer associated fibroblasts in tumor immune microenvironment of recurrent osteosarcoma. Theranostics, 2022, 12, 5877-5887.	4.6	21
6042	NLRP3-Mediated Glutaminolysis Regulates Microglia in Alzheimer's Disease. SSRN Electronic Journal, 0, , .	0.4	1
6043	scWizard: A web-based automated tool for classifying and annotating single cells and downstream analysis of single-cell RNA-seq data in cancers. Computational and Structural Biotechnology Journal, 2022, 20, 4902-4909.	1.9	0
6044	Computational solutions for spatial transcriptomics. Computational and Structural Biotechnology Journal, 2022, 20, 4870-4884.	1.9	30
6045	Current insights in mouse iNKT and MAIT cell development using single cell transcriptomics data. Seminars in Immunology, 2022, 60, 101658.	2.7	7

#	ARTICLE	IF	CITATIONS
6046	Efficient Matching of Single Cells and Cell Types. , 2022, , .		0
6047	Celda: a Bayesian model to perform co-clustering of genes into modules and cells into subpopulations using single-cell RNA-seq data. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, .	1.5	10
6048	Renewal of embryonic and neonatal-derived cardiac-resident macrophages in response to environmental cues abrogated their potential to promote cardiomyocyte proliferation via Jagged-1â€™Notch1. <i>Acta Pharmaceutica Sinica B</i> , 2023, 13, 128-141.	5.7	7
6049	Identification of a novel histone phosphorylation prognostic signature in hepatocellular carcinoma based on bulk and single-cell RNA sequencing. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	3
6050	TFAM Deficiencyâ€™Mediated Mitochondrial Disorder Affects Langerhans Cell Maintenance and Function. <i>Journal of Investigative Dermatology</i> , 2023, 143, 508-513.e2.	0.3	1
6051	Comprehensive Characterization of the Multiple Myeloma Immune Microenvironment Using Integrated scRNA-seq, CyTOF, and CITE-seq Analysis. <i>Cancer Research Communications</i> , 2022, 2, 1255-1265.	0.7	9
6052	Inflammatory perturbations in early life long-lastingly shape the transcriptome and TCR repertoire of the first wave of regulatory T cells. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
6054	A brainstem map for visceral sensations. <i>Nature</i> , 2022, 609, 320-326.	13.7	40
6055	A bifurcation concept for B-lymphoid/plasmacytoid dendritic cells with largely fluctuating transcriptome dynamics. <i>Cell Reports</i> , 2022, 40, 111260.	2.9	4
6056	Single Cell Sequencing Reveals Mechanisms of Persistent Truncus Arteriosus Formation after PDGFRÎ± and PDGFRÎ² Double Knockout in Cardiac Neural Crest Cells. <i>Genes</i> , 2022, 13, 1708.	1.0	1
6057	sciCAN: single-cell chromatin accessibility and gene expression data integration via cycle-consistent adversarial network. <i>Npj Systems Biology and Applications</i> , 2022, 8, .	1.4	10
6058	Tumor-Infiltrating Myeloid Cells Confer <i>De Novo</i> Resistance to PD-L1 Blockade through EMTâ€™Stromal and TgfÎ²-Dependent Mechanisms. <i>Molecular Cancer Therapeutics</i> , 2022, 21, 1729-1741.	1.9	0
6059	Elevating microglia TREM2 reduces amyloid seeding and suppresses disease-associated microglia. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	20
6060	Single-cell RNA sequencing combined with whole exome sequencing reveals the landscape of the immune pathogenic response to chronic mucocutaneous candidiasis with STAT1 GOF mutation. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	7
6061	Decoding brain memory formation by single-cell RNA sequencing. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	6
6062	Ensembles of endothelial and mural cells promote angiogenesis in prenatal human brain. <i>Cell</i> , 2022, 185, 3753-3769.e18.	13.5	28
6065	Synovial fibroblasts assume distinct functional identities and secrete R-spondin 2 in osteoarthritis. <i>Annals of the Rheumatic Diseases</i> , 2023, 82, 272-282.	0.5	33
6066	Transcriptional states of CAR-T infusion relate to neurotoxicity â€™ lessons from high-resolution single-cell SOM expression portraying. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4

#	ARTICLE	IF	CITATIONS
6067	In vitro propagation of XXY human Klinefelter spermatogonial stem cells: A step towards new fertility opportunities. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	3
6069	A glycan-based approach to cell characterization and isolation: Hematopoiesis as a paradigm. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	1
6070	Macrophage-specific inhibition of the histone demethylase JMJD3 decreases STING and pathologic inflammation in diabetic wound repair. , 2022, 19, 1251-1262.		19
6071	Transcriptomic architecture of nuclei in the marmoset CNS. <i>Nature Communications</i> , 2022, 13, .	5.8	4
6072	Single-cell sequencing reveals activation of core transcription factors in PRC2-deficient malignant peripheral nerve sheath tumor. <i>Cell Reports</i> , 2022, 40, 111363.	2.9	4
6073	Cell Taxonomy: a curated repository of cell types with multifaceted characterization. <i>Nucleic Acids Research</i> , 2023, 51, D853-D860.	6.5	12
6075	Fibronectin-1 is a dominant mechanism for rheumatoid arthritis via the mediation of synovial fibroblasts activity. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	2
6077	Modeling human extraembryonic mesoderm cells using naive pluripotent stem cells. <i>Cell Stem Cell</i> , 2022, 29, 1346-1365.e10.	5.2	35
6078	Heterogeneity and transcriptome changes of human CD8+ T cells across nine decades of life. <i>Nature Communications</i> , 2022, 13, .	5.8	14
6080	Systematic analysis of MCM3 in pediatric medulloblastoma via multi-omics analysis. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	3
6081	Murine fetal bone marrow does not support functional hematopoietic stem and progenitor cells until birth. <i>Nature Communications</i> , 2022, 13, .	5.8	13
6083	Human tau mutations in cerebral organoids induce a progressive dyshomeostasis of cholesterol. <i>Stem Cell Reports</i> , 2022, 17, 2127-2140.	2.3	16
6085	Critical role of guanylate binding protein 5 in tumor immune microenvironment and predictive value of immunotherapy response. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
6088	Progenitor Hierarchy of Chronic Myelomonocytic Leukemia Identifies Inflammatory Monocytic-Biased Trajectory Linked to Worse Outcomes. <i>Blood Cancer Discovery</i> , 2022, 3, 536-553.	2.6	3
6089	Identification of cellular heterogeneity and immunogenicity of chondrocytes via single-cell RNA sequencing technique in human osteoarthritis. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	7
6090	Single-Cell RNA Sequencing Reveals Molecular Features of Heterogeneity in the Murine Retinal Pigment Epithelium. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10419.	1.8	3
6093	Self-supervised contrastive learning for integrative single cell RNA-seq data analysis. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	23
6095	Development of Spondyloarthritis After COVID-19 in HLAB27-Positive Monozygotic Twins: Case Reports With Single Cell Transcriptome Profiling. <i>Journal of Rheumatic Diseases</i> , 2022, , .	0.4	0

#	ARTICLE	IF	CITATIONS
6099	Carbon ion irradiation plus CTLA4 blockade elicits therapeutic immune responses in a murine tumor model. <i>Cancer Letters</i> , 2022, 550, 215928.	3.2	8
6100	<i>S. mediterranea</i> ETS-1 regulates the function of cathepsin-positive cells and the epidermal lineage landscape via basement membrane remodeling. <i>Journal of Cell Science</i> , 2022, 135, .	1.2	7
6101	Phosphorylation status of B β subunit acts as a switch to regulate the function of phosphatase ζ in ethylene-mediated root growth inhibition. <i>New Phytologist</i> , 2022, 236, 1762-1778.	3.5	6
6103	A LILRB1 variant with a decreased ability to phosphorylate SHP-1 leads to autoimmune diseases. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
6104	Transcriptomics and RNA-Based Therapeutics as Potential Approaches to Manage SARS-CoV-2 Infection. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11058.	1.8	2
6105	The immune landscape of human thymic epithelial tumors. <i>Nature Communications</i> , 2022, 13, .	5.8	8
6107	Characterizing gene expression in an <i>in vitro</i> biomechanical strain model of joint health. <i>F1000Research</i> , 0, 11, 296.	0.8	1
6108	Reduced cell invasion may be a characteristic of placental defects in pregnant women of advanced maternal age at single-cell level. <i>Journal of Zhejiang University: Science B</i> , 2022, 23, 747-759.	1.3	3
6109	Polygenic enrichment distinguishes disease associations of individual cells in single-cell RNA-seq data. <i>Nature Genetics</i> , 2022, 54, 1572-1580.	9.4	42
6110	Single-cell multi-omics of human clonal hematopoiesis reveals that DNMT3A R882 mutations perturb early progenitor states through selective hypomethylation. <i>Nature Genetics</i> , 2022, 54, 1514-1526.	9.4	50
6112	Reduced SPAG17 Expression in Systemic Sclerosis Triggers Myofibroblast Transition and Drives Fibrosis. <i>Journal of Investigative Dermatology</i> , 2023, 143, 284-293.	0.3	6
6113	Selective Elimination of NRF2-Activated Cells by Competition With Neighboring Cells in the Esophageal Epithelium. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2023, 15, 153-178.	2.3	5
6114	Zebrafish <i>Danio rerio</i> myotomal muscle structure and growth from a spatial transcriptomics perspective. <i>Genomics</i> , 2022, 114, 110477.	1.3	3
6118	Deficiency of <i>Irx5</i> protects mice from obesity and associated metabolic abnormalities. <i>International Journal of Obesity</i> , 2022, 46, 2029-2039.	1.6	2
6119	Nemvaleukin alfa, a novel engineered IL-2 fusion protein, drives antitumor immunity and inhibits tumor growth in small cell lung cancer. , 2022, 10, e004913.		5
6120	Single-Cell Profiling of the Immune Atlas of Tumor-Infiltrating Lymphocytes in Endometrial Carcinoma. <i>Cancers</i> , 2022, 14, 4311.	1.7	3
6121	Single cell RNA-seq: A powerful yet still challenging technology to study cellular heterogeneity. <i>BioEssays</i> , 2022, 44, .	1.2	24
6122	Lactate increases stemness of CD8 α^+ T cells to augment anti-tumor immunity. <i>Nature Communications</i> , 2022, 13, .	5.8	88

#	ARTICLE	IF	CITATIONS
6124	Malignant clonal evolution drives multiple myeloma cellular ecological diversity and microenvironment reprogramming. <i>Molecular Cancer</i> , 2022, 21, .	7.9	12
6125	Clearance of small intestinal crypts involves goblet cell mucus secretion by intracellular granule rupture and enterocyte ion transport. <i>Science Signaling</i> , 2022, 15, .	1.6	15
6126	The whole-cell pertussis vaccine imposes a broad effector B cell response in mouse heterologous prime-boost settings. <i>JCI Insight</i> , 2022, 7, .	2.3	2
6127	Identification of spatially variable genes with graph cuts. <i>Nature Communications</i> , 2022, 13, .	5.8	12
6130	Delving into the Heterogeneity of Different Breast Cancer Subtypes and the Prognostic Models Utilizing scRNA-Seq and Bulk RNA-Seq. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9936.	1.8	8
6131	The Single-Cell Immunogenomic Landscape of B and Plasma Cells in Early-Stage Lung Adenocarcinoma. <i>Cancer Discovery</i> , 2022, 12, 2626-2645.	7.7	26
6132	Impaired expression of serine/arginine protein kinase 2 (SRPK2) affects melanoma progression. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
6134	Interleukin-1 receptor associated kinase 1 (IRAK1) is epigenetically activated in luminal epithelial cells in prostate cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	0
6135	Multi-species meta-analysis identifies transcriptional signatures associated with cardiac endothelial responses in the ischaemic heart. <i>Cardiovascular Research</i> , 2023, 119, 136-154.	1.8	6
6136	CEP192 is a novel prognostic marker and correlates with the immune microenvironment in hepatocellular carcinoma. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
6138	INSISTC: Incorporating network structure information for single-cell type classification. <i>Genomics</i> , 2022, 114, 110480.	1.3	1
6139	Single-cell transcriptome reveals cellular hierarchies and guides p-EMT-targeted trial in skull base chordoma. <i>Cell Discovery</i> , 2022, 8, .	3.1	12
6140	Single-cell analysis of embryoids reveals lineage diversification roadmaps of early human development. <i>Cell Stem Cell</i> , 2022, 29, 1402-1419.e8.	5.2	18
6142	Single-nuclei transcriptome analysis of the shoot apex vascular system differentiation in <i>Populus</i> . <i>Development (Cambridge)</i> , 2022, 149, .	1.2	22
6143	Dynamic <i>Ins2</i> Gene Activity Defines β -Cell Maturity States. <i>Diabetes</i> , 2022, 71, 2612-2631.	0.3	5
6145	ILC3s select microbiota-specific regulatory T cells to establish tolerance in the gut. <i>Nature</i> , 2022, 610, 744-751.	13.7	98
6147	Integrating Micro and Nano Technologies for Cell Engineering and Analysis: Toward the Next Generation of Cell Therapy Workflows. <i>ACS Nano</i> , 2022, 16, 15653-15680.	7.3	5
6148	Coupled myovascular expansion directs cardiac growth and regeneration. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	2

#	ARTICLE	IF	CITATIONS
6149	Single-cell analysis in endometrial research. <i>Reproductive and Developmental Medicine</i> , 0, Publish Ahead of Print, .	0.2	0
6150	Big data in basic and translational cancer research. <i>Nature Reviews Cancer</i> , 2022, 22, 625-639.	12.8	67
6152	A Novel MIP-1 Expressing Macrophage Subtype in Bronchoalveolar Lavage Fluid from Healthy Volunteers. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 0, , .	1.4	1
6153	Inhibition of the CtBP complex and FBXO11 enhances MHC class II expression and anti-cancer immune responses. <i>Cancer Cell</i> , 2022, 40, 1190-1206.e9.	7.7	7
6157	Identification of differentially expressed genes at the single-cell level and prognosis prediction through bulk RNA sequencing data in breast cancer. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
6160	Airway basal cells show a dedifferentiated KRT17 ^{high} Phenotype and promote fibrosis in idiopathic pulmonary fibrosis. <i>Nature Communications</i> , 2022, 13, .	5.8	36
6161	Liver group 2 innate lymphoid cells regulate blood glucose levels through IL-13 signaling and suppression of gluconeogenesis. <i>Nature Communications</i> , 2022, 13, .	5.8	10
6163	TGF- β 2 generates a population of cancer cells residing in G1 phase with high motility and metastatic potential via KRTAP2-3. <i>Cell Reports</i> , 2022, 40, 111411.	2.9	7
6165	Improved Muscle Regeneration into a Joint Prosthesis with Mechano-Growth Factor Loaded within Mesoporous Silica Combined with Carbon Nanotubes on a Porous Titanium Alloy. <i>ACS Nano</i> , 2022, 16, 14344-14361.	7.3	5
6167	Bone marrow-derived naïve B lymphocytes improve heart function after myocardial infarction: a novel cardioprotective mechanism for empagliflozin. <i>Basic Research in Cardiology</i> , 2022, 117, .	2.5	12
6168	Characterization of cancer-related fibroblasts (CAF) in hepatocellular carcinoma and construction of CAF-based risk signature based on single-cell RNA-seq and bulk RNA-seq data. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	28
6169	Dysfunctional purinergic signaling correlates with disease severity in COVID-19 patients. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	14
6172	The proprotein convertase furin regulates the development of thymic epithelial cells to ensure central immune tolerance. <i>IScience</i> , 2022, 25, 105233.	1.9	2
6173	Independent origins of fetal liver haematopoietic stem and progenitor cells. <i>Nature</i> , 2022, 609, 779-784.	13.7	56
6178	The impact of single-cell genomics on the field of mycobacterial infection. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
6179	Long read genome assemblies complemented by single cell RNA-sequencing reveal genetic and cellular mechanisms underlying the adaptive evolution of yak. <i>Nature Communications</i> , 2022, 13, .	5.8	11
6180	Resident macrophage subpopulations occupy distinct microenvironments in the kidney. <i>JCI Insight</i> , 2022, 7, .	2.3	15
6183	An Innovative Approach to Tissue Processing and Cell Sorting of Fixed Cells for Subsequent Single-Cell RNA Sequencing. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10233.	1.8	1

#	ARTICLE	IF	CITATIONS
6184	Single-cell profiling of peripheral neuroblastic tumors identifies an aggressive transitional state that bridges an adrenergic-mesenchymal trajectory. <i>Cell Reports</i> , 2022, 41, 111455.	2.9	15
6185	From multitude to singularity: An up-to-date overview of scRNA-seq data generation and analysis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	9
6186	Modeling human telencephalic development and autism-associated SHANK3 deficiency using organoids generated from single neural rosettes. <i>Nature Communications</i> , 2022, 13, .	5.8	30
6188	Single-cell transcriptome profiling reveals heterogeneous neutrophils with prognostic values in sepsis. <i>IScience</i> , 2022, 25, 105301.	1.9	10
6189	Integrative genomic analysis facilitates precision strategies for glioblastoma treatment. <i>IScience</i> , 2022, 25, 105276.	1.9	0
6190	Deeper insights into transcriptional features of cancer-associated fibroblasts: An integrated meta-analysis of single-cell and bulk RNA-sequencing data. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	1
6192	HAL-X: Scalable hierarchical clustering for rapid and tunable single-cell analysis. <i>PLoS Computational Biology</i> , 2022, 18, e1010349.	1.5	2
6193	Single-cell scRNA-seq reveals early heterogeneity during aging in yeast. <i>Aging Cell</i> , 2022, 21, .	3.0	6
6194	Muscle injury induces a transient senescence-like state that is required for myofiber growth during muscle regeneration. <i>FASEB Journal</i> , 2022, 36, .	0.2	15
6195	Distinct responses of newly identified monocyte subsets to advanced gastrointestinal cancer and COVID-19. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
6196	Single-cell sequencing resolves the landscape of immune cells and regulatory mechanisms in HIV-infected immune non-responders. <i>Cell Death and Disease</i> , 2022, 13, .	2.7	7
6197	Single Nuclei Analyses Reveal Transcriptional Profiles and Marker Genes for Diverse Supraspinal Populations. <i>Journal of Neuroscience</i> , 2022, 42, 8780-8794.	1.7	7
6198	Single-cell RNA sequencing analysis of shrimp immune cells identifies macrophage-like phagocytes. <i>ELife</i> , 0, 11, .	2.8	13
6199	A human iPSC-array-based GWAS identifies a virus susceptibility locus in the NDUF4A gene and functional variants. <i>Cell Stem Cell</i> , 2022, 29, 1475-1490.e6.	5.2	5
6200	Deciphering transcriptome alterations in bone marrow hematopoiesis at single-cell resolution in immune thrombocytopenia. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, .	7.1	6
6201	<i>Helicobacter pylori</i> shows tropism to gastric differentiated pit cells dependent on urea chemotaxis. <i>Nature Communications</i> , 2022, 13, .	5.8	14
6202	Cooperative ETS transcription factors enforce adult endothelial cell fate and cardiovascular homeostasis. , 2022, 1, 882-899.		5
6203	In vivo correction of cystic fibrosis mediated by PNA nanoparticles. <i>Science Advances</i> , 2022, 8, .	4.7	16

#	ARTICLE	IF	CITATIONS
6204	Leveraging the CSF proteome toward minimally-invasive diagnostics surveillance of brain malignancies. <i>Neuro-Oncology Advances</i> , 2022, 4, .	0.4	3
6206	Comprehensive single cell analysis of pandemic influenza A virus infection in the human airways uncovers cell-type specific host transcriptional signatures relevant for disease progression and pathogenesis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	9
6207	RNA-binding protein Elavl1/HuR is required for maintenance of cranial neural crest specification. <i>ELife</i> , 0, 11, .	2.8	2
6210	Cellular Landscapes of Nondiseased Human Cardiac Valves From End-Stage Heart Failure“Explanted Heart. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2022, 42, 1429-1446.	1.1	6
6211	A model-based constrained deep learning approach for clustering spatial-resolved single-cell data. <i>Genome Research</i> , 0, , gr.276477.121.	2.4	0
6214	Single-cell dissection of remodeled inflammatory ecosystem in primary and metastatic gallbladder carcinoma. <i>Cell Discovery</i> , 2022, 8, .	3.1	10
6215	Revealing the heterogeneity of CD4+ T cells through single-cell transcriptomics. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 150, 748-755.	1.5	5
6216	Single cell clonal analysis identifies an <scp>AID</scp> â€dependent pathway of plasma cell differentiation. <i>EMBO Reports</i> , 2022, 23, .	2.0	4
6217	The HASTER lncRNA promoter is a cis-acting transcriptional stabilizer of HNF1A. <i>Nature Cell Biology</i> , 2022, 24, 1528-1540.	4.6	18
6218	Single-cell transcriptomics reveals functionally specialized vascular endothelium in brain. <i>ELife</i> , 0, 11, .	2.8	32
6220	AgeAnno: a knowledgebase of single-cell annotation of aging in human. <i>Nucleic Acids Research</i> , 2023, 51, D805-D815.	6.5	13
6221	The Programmed Death-1 Signaling Axis Modulates Inflammation and LV Structure/Function in a“Stress-Induced Cardiomyopathy Model. <i>JACC Basic To Translational Science</i> , 2022, 7, 1120-1139.	1.9	8
6222	Conservation at the uterineâ€placental interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	8
6223	LncRNA TP53TG1 plays an anti-oncogenic role in cervical cancer by synthetically regulating transcriptome profile in HeLa cells. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
6226	Single-cell analysis reveals nanosecond pulsed electric field ablation induced myeloid cells remodeling in pancreatic cancer. <i>Bioelectrochemistry</i> , 2022, 148, 108266.	2.4	1
6227	Protocol for fast scRNA-seq raw data processing using scKB and non-arbitrary quality control with COPILOT. <i>STAR Protocols</i> , 2022, 3, 101729.	0.5	3
6228	The development of the amnion in mice and other amniotes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, .	1.8	9
6229	Single-cell transcriptomics of peripheral blood reveals anti-tumor systemic immunity induced by oncolytic virotherapy. <i>Theranostics</i> , 2022, 12, 7371-7389.	4.6	4

#	ARTICLE	IF	CITATIONS
6230	Comparison of Different in Vitro Models of Alzheimer's Disease Using Re-Analysis of Scrna-Seq Data. , 2022, , .		0
6231	IL-4-Induced Quiescence of Resting Naive B Cells Is Disrupted in Systemic Lupus Erythematosus. Journal of Immunology, 2022, 209, 1513-1522.	0.4	4
6232	Characterization of placental and decidual cell development in early pregnancy loss by single-cell RNA sequencing. Cell and Bioscience, 2022, 12, .	2.1	4
6233	Live slow-frozen human tumor tissues viable for 2D, 3D, ex vivo cultures and single-cell RNAseq. Communications Biology, 2022, 5, .	2.0	3
6234	Reemergence of pathogenic, autoantibody-producing B cell clones in myasthenia gravis following B cell depletion therapy. Acta Neuropathologica Communications, 2022, 10, .	2.4	5
6236	Targeting the Hippo Pathway in Gastric Cancer and Other Malignancies in the Digestive System: From Bench to Bedside. Biomedicines, 2022, 10, 2512.	1.4	9
6237	Exploration the global single-cell ecological landscape of adenomyosis-related cell clusters by single-cell RNA sequencing. Frontiers in Genetics, 0, 13, .	1.1	1
6238	Automatic Cell Type Annotation Using Marker Genes for Single-Cell RNA Sequencing Data. Biomolecules, 2022, 12, 1539.	1.8	5
6240	Characterizing the composition of iPSC derived cells from bulk transcriptomics data with CellMap. Scientific Reports, 2022, 12, .	1.6	1
6241	Statistical and functional convergence of common and rare genetic influences on autism at chromosome 16p. Nature Genetics, 2022, 54, 1630-1639.	9.4	14
6243	C9orf16 represents the aberrant genetic programs and drives the progression of PDAC. BMC Cancer, 2022, 22, .	1.1	0
6245	CD8+ T cells induce interferon-responsive oligodendrocytes and microglia in white matter aging. Nature Neuroscience, 2022, 25, 1446-1457.	7.1	56
6246	Identification of environmental factors that promote intestinal inflammation. Nature, 2022, 611, 801-809.	18.7	47
6248	<i>Tm4sf1</i>-marked Endothelial Subpopulation Is Dysregulated in Pulmonary Arterial Hypertension. American Journal of Respiratory Cell and Molecular Biology, 0, , .	1.4	2
6249	Evaluation of single-cell RNA-seq clustering algorithms on cancer tumor datasets. Computational and Structural Biotechnology Journal, 2022, 20, 6375-6387.	1.9	2
6251	Identify the immune characteristics and immunotherapy value of CD93 in the pan-cancer based on the public data sets. Frontiers in Immunology, 0, 13, .	2.2	6
6252	Multi-omic analyses of changes in the tumor microenvironment of pancreatic adenocarcinoma following neoadjuvant treatment with anti-PD-1 therapy. Cancer Cell, 2022, 40, 1374-1391.e7.	7.7	41
6254	Single cell transcriptomics reveals distinct transcriptional responses to oxycodone and buprenorphine by iPSC-derived brain organoids from patients with opioid use disorder. Molecular Psychiatry, 0, , .	4.1	9

#	ARTICLE	IF	CITATIONS
6255	Identification of MRAP protein family as broad-spectrum GPCR modulators. <i>Clinical and Translational Medicine</i> , 2022, 12, .	1.7	5
6256	Smoking modulates different secretory subpopulations expressing SARS-CoV-2 entry genes in the nasal and bronchial airways. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
6257	Delineating the transcriptional landscape and clonal diversity of virus-specific CD4+ T cells during chronic viral infection. <i>ELife</i> , 0, 11, .	2.8	9
6258	Differences of macrophages in the tumor microenvironment as an underlying key factor in glioma patients. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
6259	Integrative transcriptome analysis reveals <i>TEKT2</i> and <i>PIAS2</i> involvement in diabetic nephropathy. <i>FASEB Journal</i> , 2022, 36, .	0.2	2
6260	Computational Analysis of Single-Cell RNA-Seq Data. <i>Methods in Molecular Biology</i> , 2023, , 165-172.	0.4	0
6261	Genome-wide screening for differentially methylated long noncoding RNAs identifies LIFR-AS1 as an epigenetically regulated lncRNA that inhibits the progression of colorectal cancer. <i>Clinical Epigenetics</i> , 2022, 14, .	1.8	5
6263	Analyses of the autism-associated neuroligin-3 R451C mutation in human neurons reveal a gain-of-function synaptic mechanism. <i>Molecular Psychiatry</i> , 0, , .	4.1	10
6264	De novo analysis of bulk RNA-seq data at spatially resolved single-cell resolution. <i>Nature Communications</i> , 2022, 13, .	5.8	16
6267	Targeting cathepsin B by cycloastragenol enhances antitumor immunity of CD8 T cells via inhibiting MHC-I degradation. , 2022, 10, e004874.		17
6268	Neuronal CaMKK2 promotes immunosuppression and checkpoint blockade resistance in glioblastoma. <i>Nature Communications</i> , 2022, 13, .	5.8	11
6269	Tumor-associated macrophages expressing the transcription factor IRF8 promote T cell exhaustion in cancer. <i>Immunity</i> , 2022, 55, 2044-2058.e5.	6.6	53
6270	Development of Single-Cell Transcriptomics and Its Application in COVID-19. <i>Viruses</i> , 2022, 14, 2271.	1.5	1
6271	Single Cell Transcriptomics to Understand HSC Heterogeneity and Its Evolution upon Aging. <i>Cells</i> , 2022, 11, 3125.	1.8	2
6272	Single-cell mechanistic studies of radiation-mediated bystander effects. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
6274	Intercellular Communication Reveals Therapeutic Potential of Epithelial-Mesenchymal Transition in Triple-Negative Breast Cancer. <i>Biomolecules</i> , 2022, 12, 1478.	1.8	4
6276	Evolution and modulation of antigen-specific T cell responses in melanoma patients. <i>Nature Communications</i> , 2022, 13, .	5.8	10
6277	Time-Varying Gene Expression Network Analysis Reveals Conserved Transition States in Hematopoietic Differentiation between Human and Mouse. <i>Genes</i> , 2022, 13, 1890.	1.0	0

#	ARTICLE	IF	CITATIONS
6278	Anti-CTLA-4 antibodies drive myeloid activation and reprogram the tumor microenvironment through FcγR engagement and type I interferon signaling. <i>Nature Cancer</i> , 2022, 3, 1336-1350.	5.7	26
6279	Enhanced metanephric specification to functional proximal tubule enables toxicity screening and infectious disease modelling in kidney organoids. <i>Nature Communications</i> , 2022, 13, .	5.8	27
6280	Mediators of systemic sclerosis-associated interstitial lung disease (SSc-ILD): systematic review and meta-analyses. <i>Thorax</i> , 2023, 78, 799-807.	2.7	7
6281	Generation of mitochondria-rich kidney organoids from expandable intermediate mesoderm progenitors reprogrammed from human urine cells under defined medium. <i>Cell and Bioscience</i> , 2022, 12, .	2.1	4
6283	TrkA+ Neurons Induce Pathologic Regeneration After Soft Tissue Trauma. <i>Stem Cells Translational Medicine</i> , 2022, 11, 1165-1176.	1.6	2
6284	NetTDP: permutation-based true discovery proportions for differential co-expression network analysis. <i>Briefings in Bioinformatics</i> , 0, , .	3.2	0
6287	Single cell transcriptomic profiling of a neuron-astrocyte assembloid tauopathy model. <i>Nature Communications</i> , 2022, 13, .	5.8	14
6289	Recent reconfiguration of an ancient developmental gene regulatory network in <i>Helicodaris</i> sea urchins. <i>Nature Ecology and Evolution</i> , 2022, 6, 1907-1920.	3.4	12
6290	Single-cell transcriptome profiling reveals the key role of ZNF683 in natural killer cell exhaustion in multiple myeloma. <i>Clinical and Translational Medicine</i> , 2022, 12, .	1.7	11
6292	Single-cell transcriptomic profiling for inferring tumor origin and mechanisms of therapeutic resistance. <i>Npj Precision Oncology</i> , 2022, 6, .	2.3	4
6294	TransCluster: A Cell-Type Identification Method for single-cell RNA-Seq data using deep learning based on transformer. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	6
6295	Colorectal Cancer Metastases in the Liver Establish Immunosuppressive Spatial Networking between Tumor-Associated SPP1+ Macrophages and Fibroblasts. <i>Clinical Cancer Research</i> , 2023, 29, 244-260.	3.2	30
6296	WNT signaling in the tumor microenvironment promotes immunosuppression in murine pancreatic cancer. <i>Journal of Experimental Medicine</i> , 2023, 220, .	4.2	20
6297	Heterogeneity of T cells and macrophages in chlorine-induced acute lung injury in mice using single-cell RNA sequencing. <i>Inhalation Toxicology</i> , 2022, 34, 399-411.	0.8	2
6298	Single-cell RNAseq provides insight into altered immune cell populations in human fracture nonunions. <i>Journal of Orthopaedic Research</i> , 2023, 41, 1060-1069.	1.2	6
6299	Caspase-Mediated Regulation and Cellular Heterogeneity of the cGAS/STING Pathway in Kaposi's Sarcoma-Associated Herpesvirus Infection. <i>MBio</i> , 2022, 13, .	1.8	0
6300	BAF Complex Maintains Glioma Stem Cells in Pediatric H3K27M Glioma. <i>Cancer Discovery</i> , 0, , OF1-OF26.	7.7	8
6301	Single-cell genomic variation induced by mutational processes in cancer. <i>Nature</i> , 2022, 612, 106-115.	13.7	40

#	ARTICLE	IF	CITATIONS
6302	Intermediate cells of in vitro cellular reprogramming and in vivo tissue regeneration require desmoplakin. <i>Science Advances</i> , 2022, 8, .	4.7	5
6304	Venus: An efficient virus infection detection and fusion site discovery method using single-cell and bulk RNA-seq data. <i>PLoS Computational Biology</i> , 2022, 18, e1010636.	1.5	3
6308	Distinct tumor microenvironment landscapes of rectal cancer for prognosis and prediction of immunotherapy response. <i>Cellular Oncology (Dordrecht)</i> , 2022, 45, 1363-1381.	2.1	8
6310	Bronchial Gene Expression Alterations Associated with Radiographic Bronchiectasis. <i>European Respiratory Journal</i> , 0, , 2200120.	3.1	1
6311	Impaired TIGIT expression on B cells drives circulating follicular helper T cell expansion in multiple sclerosis. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	10
6312	Comprehensive analysis of autoimmune-related genes in amyotrophic lateral sclerosis from the perspective of 3P medicine. <i>EPMA Journal</i> , 2022, 13, 699-723.	3.3	1
6313	Decoding the transcriptome of calcified atherosclerotic plaque at single-cell resolution. <i>Communications Biology</i> , 2022, 5, .	2.0	38
6315	ImmCluster: an ensemble resource for immunology cell type clustering and annotations in normal and cancerous tissues. <i>Nucleic Acids Research</i> , 2023, 51, D1325-D1332.	6.5	4
6316	Metabolic control of CD47 expression through LAT2-mediated amino acid uptake promotes tumor immune evasion. <i>Nature Communications</i> , 2022, 13, .	5.8	24
6318	Single-Cell Analysis Reveals a CD4+ T-cell Cluster That Correlates with PD-1 Blockade Efficacy. <i>Cancer Research</i> , 2022, 82, 4641-4653.	0.4	13
6321	Multi-level cellular and functional annotation of single-cell transcriptomes using scPipeline. <i>Communications Biology</i> , 2022, 5, .	2.0	4
6322	The type 1 diabetes gene TYK2 regulates \hat{I}^2 -cell development and its responses to interferon- \hat{I} . <i>Nature Communications</i> , 2022, 13, .	5.8	20
6323	A missense variant in the nuclear localization signal of DKC1 causes Hoyeraal-Hreidarsson syndrome. <i>Npj Genomic Medicine</i> , 2022, 7, .	1.7	3
6324	Online single-cell data integration through projecting heterogeneous datasets into a common cell-embedding space. <i>Nature Communications</i> , 2022, 13, .	5.8	29
6326	CD34+ cell atlas of main organs implicates its impact on fibrosis. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, .	2.4	5
6327	Human prefrontal cortex gene regulatory dynamics from gestation to adulthood at single-cell resolution. <i>Cell</i> , 2022, 185, 4428-4447.e28.	13.5	49
6330	Clonal lineage tracing reveals mechanisms skewing CD8+ T cell fate decisions in chronic infection. <i>Journal of Experimental Medicine</i> , 2023, 220, .	4.2	27
6331	Ischemic Stroke Impacts the Gut Microbiome, Ileal Epithelial and Immune Homeostasis. <i>IScience</i> , 2022, 25, 105437.	1.9	6

#	ARTICLE	IF	CITATIONS
6333	Druggable transcriptomic pathways revealed in Parkinson's patient-derived midbrain neurons. <i>Npj Parkinson's Disease</i> , 2022, 8, .	2.5	9
6335	Single-cell transcriptome analyses reveal microglia types associated with proliferative retinopathy. <i>JCI Insight</i> , 2022, 7, .	2.3	14
6337	Distinct B-Cell Specific Transcriptional Contexts of the BCL2 Oncogene Impact Pre-Malignant Development in Mouse Models. <i>Cancers</i> , 2022, 14, 5337.	1.7	2
6339	Single-cell technologies: From research to application. <i>Innovation(China)</i> , 2022, 3, 100342.	5.2	13
6341	speedingCARS: accelerating the engineering of CAR T cells by signaling domain shuffling and single-cell sequencing. <i>Nature Communications</i> , 2022, 13, .	5.8	20
6342	Single cell sequencing maps skeletal muscle cellular diversity as disease severity increases in dystrophic mouse models. <i>IScience</i> , 2022, 25, 105415.	1.9	12
6343	Cellular plasticity and immune microenvironment of malignant pleural effusion are associated with EGFR-TKI resistance in non-small-cell lung carcinoma. <i>IScience</i> , 2022, 25, 105358.	1.9	1
6344	Identification of a rare Gli1+ progenitor cell population contributing to liver regeneration during chronic injury. <i>Cell Discovery</i> , 2022, 8, .	3.1	3
6345	Integration of single-cell transcriptome and chromatin accessibility of early gonads development among goats, pigs, macaques, and humans. <i>Cell Reports</i> , 2022, 41, 111587.	2.9	5
6346	Blockade of the BLT1-LTB4 axis does not affect mast cell migration towards advanced atherosclerotic lesions in LDLR ^{-/-} mice. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
6347	Single-cell RNA sequencing reveals rebalancing of immunological response in patients with periodontitis after non-surgical periodontal therapy. <i>Journal of Translational Medicine</i> , 2022, 20, .	1.8	4
6348	Molecular and anatomical characterization of parabrachial neurons and their axonal projections. <i>ELife</i> , 0, 11, .	2.8	38
6349	TISCH2: expanded datasets and new tools for single-cell transcriptome analyses of the tumor microenvironment. <i>Nucleic Acids Research</i> , 2023, 51, D1425-D1431.	6.5	79
6350	HUSCH: an integrated single-cell transcriptome atlas for human tissue gene expression visualization and analyses. <i>Nucleic Acids Research</i> , 2023, 51, D1029-D1037.	6.5	11
6352	Uncovering the emergence of HSCs in the human fetal bone marrow by single-cell RNA-seq analysis. <i>Cell Stem Cell</i> , 2022, 29, 1562-1579.e7.	5.2	14
6353	BISC: accurate inference of transcriptional bursting kinetics from single-cell transcriptomic data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	4
6355	Single-cell atlas of murine adrenal glands reveals immune-adrenal crosstalk during systemic <i>Candida albicans</i> infection. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
6356	Estrogen regulates divergent transcriptional and epigenetic cell states in breast cancer. <i>Nucleic Acids Research</i> , 2022, 50, 11492-11508.	6.5	7

#	ARTICLE	IF	CITATIONS
6357	Single-cell RNA sequencing highlights the functional role of human endogenous retroviruses in gallbladder cancer. <i>EBioMedicine</i> , 2022, 85, 104319.	2.7	7
6358	Defects of microtubule cytoskeletal organization in NOA human testes. <i>Reproductive Biology and Endocrinology</i> , 2022, 20, .	1.4	4
6359	Transcriptomic mapping of the metzincin landscape in human trophoblasts. <i>Gene Expression Patterns</i> , 2022, 46, 119283.	0.3	3
6360	Determination of the nanoparticle- and cell-specific toxicological mechanisms in 3D liver spheroids using scRNAseq analysis. <i>Nano Today</i> , 2022, 47, 101652.	6.2	5
6361	Metabolomics and modelling approaches for systems metabolic engineering. <i>Metabolic Engineering Communications</i> , 2022, 15, e00209.	1.9	7
6362	Protocol to isolate live single cells while retaining spatial information by combining cell photolabeling and FACS. <i>STAR Protocols</i> , 2022, 3, 101795.	0.5	0
6363	The transcription factor JUN is a major regulator of quiescent pancreatic stellate cell maintenance. <i>Gene</i> , 2023, 851, 147000.	1.0	1
6364	Single-cell transcriptomics. , 2023, , 67-84.		0
6365	An In Vivo Model of Human Macrophages in Metastatic Melanoma. <i>Journal of Immunology</i> , 2022, 209, 606-620.	0.4	6
6366	AI in Translational Bioinformatics and Precision Medicine. , 2022, , 391-429.		0
6367	Single-nucleus transcriptomic profiling of multiple organs in a rhesus macaque model of SARS-CoV-2 infection. <i>Zoological Research</i> , 2022, 43, 1041-1062.	0.9	8
6368	Single-cell atlas of epithelial and stromal cell heterogeneity by lobe and strain in the mouse prostate. <i>Prostate</i> , 2023, 83, 286-303.	1.2	4
6371	Single-cell transcriptome analysis reveals cellular heterogeneity in mouse intra- and extra articular ligaments. <i>Communications Biology</i> , 2022, 5, .	2.0	4
6372	T cells specific for $\hat{\pm}$ -myosin drive immunotherapy-related myocarditis. <i>Nature</i> , 2022, 611, 818-826.	13.7	100
6374	wnt16 regulates spine and muscle morphogenesis through parallel signals from notochord and dermomyotome. <i>PLoS Genetics</i> , 2022, 18, e1010496.	1.5	6
6376	Pathogenic Interleukin-10 Receptor Alpha Variants in Humans â€” Balancing Natural Selection and Clinical Implications. <i>Journal of Clinical Immunology</i> , 0, , .	2.0	1
6377	Single cell profiling of primary and paired metastatic lymph node tumors in breast cancer patients. <i>Nature Communications</i> , 2022, 13, .	5.8	19
6379	GLI1+ cells are a source of repair-supportive mesenchymal cells (RSMCs) during airway epithelial regeneration. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, .	2.4	7

#	ARTICLE	IF	CITATIONS
6380	Identification of hematopoietic stem cells residing in the meninges of adult mice at steady state. <i>Cell Reports</i> , 2022, 41, 111592.	2.9	10
6381	Protective interaction of human phagocytic APC subsets with <i>Cryptococcus neoformans</i> induces genes associated with metabolism and antigen presentation. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	6
6384	A dietary change to a high-fat diet initiates a rapid adaptation of the intestine. <i>Cell Reports</i> , 2022, 41, 111641.	2.9	26
6385	Single cell sequencing revealed the mechanism of PD-1 resistance affected by the expression profile of peripheral blood immune cells in ESCC. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4
6386	Single-cell RNA-seq uncovers cellular heterogeneity and provides a signature for paediatric sleep apnoea. <i>European Respiratory Journal</i> , 2023, 61, 2201465.	3.1	6
6393	A novel immune signature predicts immunotherapy responsiveness and reveals the landscape of the tumor immune microenvironment in head and neck squamous cell carcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
6395	Tissue nanotransfection causes tumor regression by its effect on nanovesicle cargo that alters microenvironmental macrophage state. <i>Molecular Therapy</i> , 2023, 31, 1402-1417.	3.7	8
6396	Differential effects of periodontal microbiome on the rheumatoid factor induction during rheumatoid arthritis pathogenesis. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
6397	Combined bulk RNA-seq and single-cell RNA-seq identifies a necroptosis-related prognostic signature associated with inhibitory immune microenvironment in glioma. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
6398	Downregulation of zinc finger protein 71 in laryngeal squamous cell carcinoma tissues and its potential molecular mechanism and clinical significance: a study based on immunohistochemistry staining and data mining. <i>World Journal of Surgical Oncology</i> , 2022, 20, .	0.8	2
6402	Disruption of the glucagon receptor increases glucagon expression beyond Î±-cell hyperplasia in zebrafish. <i>Journal of Biological Chemistry</i> , 2022, 298, 102665.	1.6	2
6403	primiReference: a reference for analysis of primary-microRNA expression in single-nucleus sequencing data. <i>Journal of Genetics and Genomics</i> , 2022, , .	1.7	1
6404	Multi-omics integration reveals a six-malignant cell maker gene signature for predicting prognosis in high-risk neuroblastoma. <i>Frontiers in Neuroinformatics</i> , 0, 16, .	1.3	1
6406	Parenchymal border macrophages regulate the flow dynamics of the cerebrospinal fluid. <i>Nature</i> , 2022, 611, 585-593.	13.7	82
6407	scAWMV: an adaptively weighted multi-view learning framework for the integrative analysis of parallel scRNA-seq and scATAC-seq data. <i>Bioinformatics</i> , 2023, 39, .	1.8	1
6408	In mice and humans, brain microvascular contractility matures postnatally. <i>Brain Structure and Function</i> , 2023, 228, 475-492.	1.2	4
6410	Ascertaining cellsâ€™ synaptic connections and RNA expression simultaneously with barcoded rabies virus libraries. <i>Nature Communications</i> , 2022, 13, .	5.8	4
6411	CD8+ T cell metabolic rewiring defined by scRNA-seq identifies a critical role of ASNS expression dynamics in T cell differentiation. <i>Cell Reports</i> , 2022, 41, 111639.	2.9	12

#	ARTICLE	IF	CITATIONS
6412	Single-cell genome-wide association reveals that a nonsynonymous variant in ERAP1 confers increased susceptibility to influenza virus. <i>Cell Genomics</i> , 2022, 2, 100207.	3.0	2
6414	Metastatic recurrence in colorectal cancer arises from residual EMP1+ cells. <i>Nature</i> , 2022, 611, 603-613.	13.7	50
6415	Characterizing microglial gene expression in a model of secondary progressive multiple sclerosis. <i>Glia</i> , 0, , .	2.5	4
6416	A single-nucleus transcriptomics study of alcohol use disorder in the nucleus accumbens. <i>Addiction Biology</i> , 2023, 28, .	1.4	1
6419	Intestinal toxicity to CTLA-4 blockade driven by IL-6 and myeloid infiltration. <i>Journal of Experimental Medicine</i> , 2023, 220, .	4.2	20
6420	Spatially resolved gene regulatory and disease-related vulnerability map of the adult Macaque cortex. <i>Nature Communications</i> , 2022, 13, .	5.8	17
6421	Reevaluation of Piezo1 as a gut RNA sensor. <i>ELife</i> , 0, 11, .	2.8	2
6422	Hyperlipidemia induces proinflammatory responses by activating STING pathway through IRE1 β -XBP1 in retinal endothelial cells. <i>Journal of Nutritional Biochemistry</i> , 2023, 112, 109213.	1.9	9
6423	Environmental pathways affecting gene expression (E.PAGE) as an R package to predict gene-environment associations. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
6424	Early developmental plasticity enables the induction of an intermediate extraembryonic cell state. <i>Science Advances</i> , 2022, 8, .	4.7	4
6426	FLT3ITD drives context-specific changes in cell identity and variable interferon dependence during AML initiation. <i>Blood</i> , 2023, 141, 1442-1456.	0.6	5
6427	Identification of CD73 as a Novel Biomarker Encompassing the Tumor Microenvironment, Prognosis, and Therapeutic Responses in Various Cancers. <i>Cancers</i> , 2022, 14, 5663.	1.7	5
6429	Development of a novel head and neck squamous cell carcinoma prognostic signature by bulk/single-cell sequencing data integration. <i>Oral Diseases</i> , 2024, 30, 128-139.	1.5	1
6432	Single-cell RNA-seq analysis to identify potential biomarkers for diagnosis, and prognosis of non-small cell lung cancer by using comprehensive bioinformatics approaches. <i>Translational Oncology</i> , 2023, 27, 101571.	1.7	9
6434	scBKAP: A Clustering Model for Single-Cell RNA-Seq Data Based on Bisecting K-Means. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 2007-2015.	1.9	3
6435	Pre-processing, Dimension Reduction, and Clustering for Single-Cell RNA-seq Data. <i>Springer Handbooks of Computational Statistics</i> , 2022, , 37-51.	0.2	2
6436	scAnalyzeR: A Comprehensive Software Package With Graphical User Interface for Single-Cell RNA Sequencing Analysis and its Application on Liver Cancer. <i>Technology in Cancer Research and Treatment</i> , 2022, 21, 153303382211427.	0.8	1
6437	Single-cell atlases link macrophages and CD8 ⁺ T-cell subpopulations to disease progression and immunotherapy response in urothelial carcinoma. <i>Theranostics</i> , 2022, 12, 7745-7759.	4.6	8

#	ARTICLE	IF	CITATIONS
6438	Single-cell RNA sequencing highlights the roles of C1QB and NKG7 in the pancreatic islet immune microenvironment in type 1 diabetes mellitus. <i>Pharmacological Research</i> , 2023, 187, 106588.	3.1	1
6439	scWECTA: A weighted ensemble classification framework for cell type assignment based on single cell transcriptome. <i>Computers in Biology and Medicine</i> , 2023, 152, 106409.	3.9	1
6440	Diverse effector and regulatory functions of fibro/adipogenic progenitors during skeletal muscle fibrosis in muscular dystrophy. <i>IScience</i> , 2023, 26, 105775.	1.9	6
6441	Renoprotective anti-CD45RB antibody induces B cell production in systemic lupus erythematosus based on single-cell RNA-seq analysis. <i>Journal of Autoimmunity</i> , 2023, 134, 102949.	3.0	0
6442	Immune index: A gene and cell prognostic signature for immunotherapy response prediction in hepatocellular carcinoma. <i>Pharmacological Research</i> , 2023, 187, 106583.	3.1	2
6443	A retro-inverso modified peptide alleviated ovalbumin-induced asthma model by affecting glycerophospholipid and purine metabolism of immune cells. <i>Pulmonary Pharmacology and Therapeutics</i> , 2023, 78, 102185.	1.1	2
6444	Deep Learning Methods for Single-Cell Omics Data. <i>Springer Handbooks of Computational Statistics</i> , 2022, , 109-132.	0.2	0
6445	Signatures of EMT, immunosuppression, and inflammation in primary and recurrent human cutaneous squamous cell carcinoma at single-cell resolution. <i>Theranostics</i> , 2022, 12, 7532-7549.	4.6	11
6446	Approaches to Marker Gene Identification from Single-Cell RNA-Sequencing Data. <i>Springer Handbooks of Computational Statistics</i> , 2022, , 71-84.	0.2	0
6447	Focused-ultrasound blood-brain barrier opening promotes neuroprotective microglia. , 2022, , .		1
6448	Reprogramming Müller glia to regenerate ganglion-like cells in adult mouse retina with developmental transcription factors. <i>Science Advances</i> , 2022, 8, .	4.7	31
6449	Identification and Validation of UPP1 as a Novel Prognostic Biomarker in Renal Clear Cell Carcinoma. <i>Genes</i> , 2022, 13, 2166.	1.0	0
6450	Where Are They Now: Spatial and Molecular Diversity of Tissue-Resident Macrophages in the Kidney. <i>Seminars in Nephrology</i> , 2022, , 151276.	0.6	3
6451	Image-seq: spatially resolved single-cell sequencing guided by in situ and in vivo imaging. <i>Nature Methods</i> , 2022, 19, 1622-1633.	9.0	15
6454	Single-cell RNA sequencing identifies a paracrine interaction that may drive oncogenic notch signaling in human adenoid cystic carcinoma. <i>Cell Reports</i> , 2022, 41, 111743.	2.9	9
6455	Advances in Single-Cell Sequencing Technology and Its Application in Poultry Science. <i>Genes</i> , 2022, 13, 2211.	1.0	2
6456	Identification of molecular classification and gene signature for predicting prognosis and immunotherapy response in HNSCC using cell differentiation trajectories. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
6457	Long-Term Characteristics of Human-Derived Biliary Organoids under a Single Continuous Culture Condition. <i>Cells</i> , 2022, 11, 3797.	1.8	1

#	ARTICLE	IF	CITATIONS
6459	Dentate gyrus astrocytes exhibit layer-specific molecular, morphological and physiological features. <i>Nature Neuroscience</i> , 2022, 25, 1626-1638.	7.1	16
6460	The E3 ubiquitin ligase WWP2 regulates pro-fibrogenic monocyte infiltration and activity in heart fibrosis. <i>Nature Communications</i> , 2022, 13, .	5.8	9
6461	Evaluation of commercially available glucagon receptor antibodies and glucagon receptor expression. <i>Communications Biology</i> , 2022, 5, .	2.0	7
6462	Interpretable deep learning translation of GWAS and multi-omics findings to identify pathobiology and drug repurposing in Alzheimer's disease. <i>Cell Reports</i> , 2022, 41, 111717.	2.9	20
6463	scRNA-seq for Microcephaly Research [III]: Computational Analysis of scRNA-seq Data. <i>Methods in Molecular Biology</i> , 2023, , 105-121.	0.4	1
6464	Spatial transcriptomics demonstrates the role of CD4 T cells in effector CD8 T cell differentiation during chronic viral infection. <i>Cell Reports</i> , 2022, 41, 111736.	2.9	7
6465	Combined single-cell RNA-seq and bulk RNA-seq to analyze the expression and role of TREM2 in bladder cancer. , 2023, 40, .		3
6466	Cell Differentiation Trajectory Predicts Prognosis and Immunotherapeutic Response in Clear Cell Renal Cell Carcinoma. <i>Genetical Research</i> , 2022, 2022, 1-19.	0.3	1
6467	Isoformic PD-1-mediated immunosuppression underlies resistance to PD-1 blockade in hepatocellular carcinoma patients. <i>Gut</i> , 2023, 72, 1568-1580.	6.1	6
6469	A machine learning framework for scRNA-seq UMI threshold optimization and accurate classification of cell types. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
6470	Single-cell transcriptomic, transcriptomic, and metabolomic characterization of human atherosclerosis. <i>Annals of Translational Medicine</i> , 2022, 10, 1215-1215.	0.7	1
6471	Functional analysis of structural variants in single cells using Strand-seq. <i>Nature Biotechnology</i> , 2023, 41, 832-844.	9.4	14
6473	scAB detects multiresolution cell states with clinical significance by integrating single-cell genomics and bulk sequencing data. <i>Nucleic Acids Research</i> , 2022, 50, 12112-12130.	6.5	5
6475	TXNIP Suppresses the Osteochondrogenic Switch of Vascular Smooth Muscle Cells in Atherosclerosis. <i>Circulation Research</i> , 2023, 132, 52-71.	2.0	11
6477	Marker-free characterization of full-length transcriptomes of single live circulating tumor cells. <i>Genome Research</i> , 0, , gr.276600.122.	2.4	2
6478	Bi-potential hPSC-derived Müllerian duct-like cells for full-thickness and functional endometrium regeneration. <i>Npj Regenerative Medicine</i> , 2022, 7, .	2.5	1
6479	Aberrant metabolic processes promote the immunosuppressive microenvironment in multiple myeloma. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	11
6481	Integrating cell interaction with transcription factors to obtain a robust gene panel for prognostic prediction and therapies in cholangiocarcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0

#	ARTICLE	IF	CITATIONS
6482	Pan-Cancer analysis shows that ACO2 is a potential prognostic and immunotherapeutic biomarker for multiple cancer types including hepatocellular carcinoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	3
6483	Identification of two robust subclasses of sepsis with both prognostic and therapeutic values based on machine learning analysis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
6484	Protein aggregation and calcium dysregulation are hallmarks of familial Parkinson's disease in midbrain dopaminergic neurons. <i>Npj Parkinson's Disease</i> , 2022, 8, .	2.5	14
6485	Inflammation promotes resistance to immune checkpoint inhibitors in high microsatellite instability colorectal cancer. <i>Nature Communications</i> , 2022, 13, .	5.8	33
6486	Spatially aware dimension reduction for spatial transcriptomics. <i>Nature Communications</i> , 2022, 13, .	5.8	42
6487	Immune and non-immune cell subtypes identify novel targets for prognostic and therapeutic strategy: A study based on intratumoral heterogeneity analysis of multicenter scRNA-seq datasets in lung adenocarcinoma. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	0
6489	Myeloid cell reprogramming alleviates immunosuppression and promotes clearance of metastatic lesions. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	1
6490	Epigenetic and transcriptomic reprogramming in monocytes of severe COVID-19 patients reflects alterations in myeloid differentiation and the influence of inflammatory cytokines. <i>Genome Medicine</i> , 2022, 14, .	3.6	10
6491	Lysosomal damage drives mitochondrial proteome remodelling and reprograms macrophage immunometabolism. <i>Nature Communications</i> , 2022, 13, .	5.8	16
6492	Immunoepigenomic analysis identifies attenuated interferon responses in naïve CD4 ⁺ T cells of adolescents with peanut and multi-food allergy. <i>Pediatric Allergy and Immunology</i> , 2022, 33, .	1.1	3
6493	Identification of Hub Genes in the Remodeling of Non-Infarcted Myocardium Following Acute Myocardial Infarction. <i>Journal of Cardiovascular Development and Disease</i> , 2022, 9, 409.	0.8	1
6494	Human fetal cerebellar cell atlas informs medulloblastoma origin and oncogenesis. <i>Nature</i> , 2022, 612, 787-794.	13.7	17
6496	Bone Marrow Macrophages Induce Inflammation by Efferocytosis of Apoptotic Prostate Cancer Cells via HIF-1 α Stabilization. <i>Cells</i> , 2022, 11, 3712.	1.8	3
6497	Adaptive sequence divergence forged new neurodevelopmental enhancers in humans. <i>Cell</i> , 2022, 185, 4587-4603.e23.	13.5	29
6501	The integrated transcriptome bioinformatics analysis identifies key genes and cellular components for proliferative diabetic retinopathy. <i>PLoS ONE</i> , 2022, 17, e0277952.	1.1	0
6504	St18 specifies globus pallidus projection neuron identity in MGE lineage. <i>Nature Communications</i> , 2022, 13, .	5.8	0
6505	Data analysis guidelines for single-cell RNA-seq in biomedical studies and clinical applications. <i>Military Medical Research</i> , 2022, 9, .	1.9	4
6506	Meta-Analysis of Human Cancer Single-Cell RNA-Seq Datasets Using the IMMUcan Database. <i>Cancer Research</i> , 2023, 83, 363-373.	0.4	10

#	ARTICLE	IF	CITATIONS
6507	Single-cell chromatin landscapes of mouse skin development. <i>Scientific Data</i> , 2022, 9, .	2.4	1
6508	Rapid induction and long-term self-renewal of neural crest-derived ectodermal chondrogenic cells from hPSCs. <i>Npj Regenerative Medicine</i> , 2022, 7, .	2.5	3
6509	A single-cell transcriptomic landscape of mouse testicular aging. <i>Journal of Advanced Research</i> , 2023, 53, 219-234.	4.4	10
6510	The Pan-Cancer Multi-Omics Landscape of FOXO Family Relevant to Clinical Outcome and Drug Resistance. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15647.	1.8	24
6512	Genomic characterization and therapeutic utilization of IL-13-responsive sequences in asthma. <i>Cell Genomics</i> , 2023, 3, 100229.	3.0	5
6513	Single-cell profiles reveal tumor cell heterogeneity and immunosuppressive microenvironment in Waldenström macroglobulinemia. <i>Journal of Translational Medicine</i> , 2022, 20, .	1.8	6
6514	Ensuring Quality Cell Input for Single Cell Sequencing Experiments by Viability and Singlet Enrichment Using Cell Sorting. <i>Methods in Molecular Biology</i> , 2023, , 183-189.	0.4	0
6515	Identifying Gene Markers Associated with Cell Subpopulations. <i>Methods in Molecular Biology</i> , 2023, , 251-268.	0.4	0
6516	Diversity of Circulating NKT Cells in Defense against Carbapenem-Resistant <i>Klebsiella Pneumoniae</i> Infection. <i>Journal of Personalized Medicine</i> , 2022, 12, 2025.	1.1	0
6518	Integrated single-cell transcriptome analysis of the tumor ecosystems underlying cervical cancer metastasis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
6519	Ikaros family proteins redundantly regulate temporal patterning in the developing mouse retina. <i>Development (Cambridge)</i> , 2023, 150, .	1.2	9
6520	scRNA-seq profiling of neonatal and adult thymus-derived CD4+ T cells by a T cell origin-time tracing model. <i>Journal of Molecular Cell Biology</i> , 2023, 14, .	1.5	1
6521	Persistent post-“COVID-19 smell loss is associated with immune cell infiltration and altered gene expression in olfactory epithelium. <i>Science Translational Medicine</i> , 2022, 14, .	5.8	57
6523	p53/p21 pathway activation contributes to the ependymal fate decision downstream of GemC1. <i>Cell Reports</i> , 2022, 41, 111810.	2.9	5
6524	High cardiomyocyte diversity in human early prenatal heart development. <i>iScience</i> , 2023, 26, 105857.	1.9	3
6527	Cellular features of localized microenvironments in human meniscal degeneration: a single-cell transcriptomic study. <i>ELife</i> , 0, 11, .	2.8	9
6529	Single-cell transcriptome reveals dominant subgenome expression and transcriptional response to heat stress in Chinese cabbage. <i>Genome Biology</i> , 2022, 23, .	3.8	16
6530	Development of a Cancer-Associated Fibroblast-Related Prognostic Model in Breast Cancer via Bulk and Single-Cell RNA Sequencing. <i>BioMed Research International</i> , 2022, 2022, 1-26.	0.9	3

#	ARTICLE	IF	CITATIONS
6532	Robust Graph Regularized NMF with Dissimilarity and Similarity Constraints for ScRNA-seq Data Clustering. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 6271-6286.	2.5	6
6533	Interferon-dependent SLC14A1+ cancer-associated fibroblasts promote cancer stemness via WNT5A in bladder cancer. <i>Cancer Cell</i> , 2022, 40, 1550-1565.e7.	7.7	39
6534	The dynamic dysregulated network identifies stage-specific markers during lung adenocarcinoma malignant progression and metastasis. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 30, 633-647.	2.3	2
6535	Deep Learning of Dual Plasma Fingerprints for High-Performance Infection Classification. <i>Small</i> , 0, , 2206349.	5.2	1
6536	SUMO1 regulates post-infarct cardiac repair based on cellular heterogeneity. <i>Journal of Pharmaceutical Analysis</i> , 2023, 13, 170-186.	2.4	1
6537	Large-Scale Single-Nucleus RNA Sequencing Compatible with Complex Archived Samples. <i>Methods in Molecular Biology</i> , 2023, , 333-346.	0.4	0
6538	Niche-Dependent Regulation of Lkb1 in the Proliferation of Lung Epithelial Progenitor Cells. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15065.	1.8	2
6539	Single-cell RNA sequencing reveals the Müller subtypes and inner blood-retinal barrier regulatory network in early diabetic retinopathy. <i>Frontiers in Molecular Neuroscience</i> , 0, 15, .	1.4	2
6540	The Infiltration of Neutrophil Granulocytes Due to Loss of PTEN Was Associated with Poor Response to Immunotherapy in Renal Cell Carcinoma. <i>Journal of Inflammation Research</i> , 0, Volume 15, 6553-6567.	1.6	3
6541	Single-cell and spatial multi-omics in the plant sciences: Technical advances, applications, and perspectives. <i>Plant Communications</i> , 2023, 4, 100508.	3.6	14
6543	An immune risk score predicts progression-free survival of melanoma patients in South China receiving anti-PD-1 inhibitor therapy—a retrospective cohort study examining 66 circulating immune cell subsets. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
6544	What Causes Seizures in Neurocysticercosis?. <i>Epilepsy Currents</i> , 2023, 23, 105-112.	0.4	3
6545	Distance covariance entropy reveals primed states and bifurcation dynamics in single-cell RNA-Seq data. <i>IScience</i> , 2022, 25, 105709.	1.9	0
6546	Robust generation of human-chambered cardiac organoids from pluripotent stem cells for improved modelling of cardiovascular diseases. <i>Stem Cell Research and Therapy</i> , 2022, 13, .	2.4	7
6547	CBP and p300 Jointly Maintain Neural Progenitor Viability but Play Unique Roles in the Differentiation of Neural Lineages. <i>Cells</i> , 2022, 11, 4118.	1.8	2
6548	Temporal molecular program of human hematopoietic stem and progenitor cells after birth. <i>Developmental Cell</i> , 2022, 57, 2745-2760.e6.	3.1	6
6549	The single-cell landscape of cystic echinococcosis in different stages provided insights into endothelial and immune cell heterogeneity. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
6551	Single-cell profiling of the microenvironment in decidual tissue from women with missed abortions. <i>Fertility and Sterility</i> , 2022, , .	0.5	1

#	ARTICLE	IF	CITATIONS
6552	Asx1 deletion disrupts MYC and RNA polymerase II function in granulocyte progenitors. <i>Leukemia</i> , 0, , .	3.3	1
6553	Learning single-cell chromatin accessibility profiles using meta-analytic marker genes. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	1
6554	Single-cell RNA sequencing to dissect the immunological network of liver fibrosis in <i>Schistosoma japonicum</i> -infected mice. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
6555	Cross-species cell-type assignment from single-cell RNA-seq data by a heterogeneous graph neural network. <i>Genome Research</i> , 2023, 33, 96-111.	2.4	11
6556	Recruitment of <i>TRIM33</i> to cell-context specific <i>PML</i> nuclear bodies regulates nodal signaling in <i>mESCs</i> . <i>EMBO Journal</i> , 2023, 42, .	3.5	5
6561	Clustering of single-cell multi-omics data with a multimodal deep learning method. <i>Nature Communications</i> , 2022, 13, .	5.8	17
6562	Distinct and redundant roles for zebrafish <i>her</i> genes during mineralization and craniofacial patterning. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	2
6563	Dynamic gene screening enabled identification of a 10-gene panel for early detection and progression assessment of gastric cancer. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 677-687.	1.9	2
6564	Direct Reprogramming Improves Cardiac Function and Reverses Fibrosis in Chronic Myocardial Infarction. <i>Circulation</i> , 2023, 147, 223-238.	1.6	31
6565	Lipid-laden lung mesenchymal cells foster breast cancer metastasis via metabolic reprogramming of tumor cells and natural killer cells. <i>Cell Metabolism</i> , 2022, 34, 1960-1976.e9.	7.2	17
6566	Notch-dependent cooperativity between myeloid lineages promotes Langerhans cell histiocytosis pathology. <i>Science Immunology</i> , 2022, 7, .	5.6	8
6572	A pan-cancer and single-cell sequencing analysis of CD161, a promising onco-immunological biomarker in tumor microenvironment and immunotherapy. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4
6577	Single-Cell and Spatial Transcriptomics Decodes Wharton's Jelly-Derived Mesenchymal Stem Cells Heterogeneity and a Subpopulation with Wound Repair Signatures. <i>Advanced Science</i> , 2023, 10, .	5.6	8
6578	SPATIAL RNA SEQUENCING METHODS SHOWED HIGH RESOLUTION OF SINGLE CELL IN CANCER METASTASIS AND THE FORMATION OF TME. <i>Bioscience Reports</i> , 0, , .	1.1	1
6579	<i>CD226</i> knockout reduces the development of <i>CD8</i> ⁺ T by impairing the <i>TCR</i> sensitivity of double-positive thymocytes. <i>Immunology</i> , 2023, 169, 83-95.	2.0	1
6580	Hyaluronan driven by epithelial <i>aPKC</i> deficiency remodels the microenvironment and creates a vulnerability in mesenchymal colorectal cancer. <i>Cancer Cell</i> , 2023, 41, 252-271.e9.	7.7	9
6583	Evaluation of pulmonary single-cell identity specificity in scRNA-seq analysis. <i>Clinical and Translational Medicine</i> , 2022, 12, .	1.7	5
6586	Distinct niche structures and intrinsic programs of fallopian tube and ovarian surface epithelial cells. <i>IScience</i> , 2023, 26, 105861.	1.9	3

#	ARTICLE	IF	CITATIONS
6587	Single-cell transcriptome reveals core cell populations and androgen-RXFP2 axis involved in deer antler full regeneration. <i>Cell Regeneration</i> , 2022, 11, .	1.1	1
6588	Cell signaling activation and extracellular matrix remodeling underpin glioma tumor microenvironment heterogeneity and organization. <i>Cellular Oncology (Dordrecht)</i> , 2023, 46, 589-602.	2.1	6
6589	Single Nucleus Sequencing of Human Colon Myenteric Plexus-associated Visceral Smooth Muscle Cells, Platelet Derived Growth Factor Receptor Alpha Cells, and Interstitial Cells of Cajal. , 2023, 2, 380-394.		2
6591	Histopathologic and proteogenomic heterogeneity reveals features of clear cell renal cell carcinoma aggressiveness. <i>Cancer Cell</i> , 2023, 41, 139-163.e17.	7.7	43
6592	Single-cell RNA sequencing provides a high-resolution roadmap for understanding the multicellular compartmentation of specialized metabolism. <i>Nature Plants</i> , 2023, 9, 179-190.	4.7	32
6593	Neuroendocrinology of the lung revealed by single-cell RNA sequencing. <i>ELife</i> , 0, 11, .	2.8	11
6594	Functional-Feature-Based Data Reduction Using Sparsely Connected Autoencoders. <i>Methods in Molecular Biology</i> , 2023, , 231-240.	0.4	0
6595	Single-Cell RNAseq Clustering. <i>Methods in Molecular Biology</i> , 2023, , 241-250.	0.4	0
6596	Personalized health risk assessment based on single-cell RNA sequencing analysis of a male with 45, X/48, XYYY karyotype. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
6598	Ovarian cancer mutational processes drive site-specific immune evasion. <i>Nature</i> , 2022, 612, 778-786.	13.7	51
6600	HIV integration in the human brain is linked to microglial activation and 3D genome remodeling. <i>Molecular Cell</i> , 2022, 82, 4647-4663.e8.	4.5	9
6601	Brain metastatic outgrowth and osimertinib resistance are potentiated by RhoA in EGFR-mutant lung cancer. <i>Nature Communications</i> , 2022, 13, .	5.8	6
6602	Infiltration of LPAR5+ macrophages in osteosarcoma tumor microenvironment predicts better outcomes. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
6603	A mineralizing pool of Gli1-expressing progenitors builds the tendon enthesis and demonstrates therapeutic potential. <i>Cell Stem Cell</i> , 2022, 29, 1669-1684.e6.	5.2	13
6604	Simultaneous isolation of proximal and distal lung progenitor cells from individual mice using a 3D printed guide reduces proximal cell contamination of distal lung epithelial cell isolations. <i>Stem Cell Reports</i> , 2022, 17, 2718-2731.	2.3	1
6605	Structural and functional distinctions of co-resident microglia and monocyte-derived macrophages after retinal degeneration. <i>Journal of Neuroinflammation</i> , 2022, 19, .	3.1	5
6606	Mapping transcriptional heterogeneity and metabolic networks in fatty livers at single-cell resolution. <i>IScience</i> , 2023, 26, 105802.	1.9	4
6607	A molecular atlas of the human postmenopausal fallopian tube and ovary from single-cell RNA and ATAC sequencing. <i>Cell Reports</i> , 2022, 41, 111838.	2.9	10

#	ARTICLE	IF	CITATIONS
6608	Langerhans cells are essential components of the angiogenic niche during murine skin repair. <i>Developmental Cell</i> , 2022, 57, 2699-2713.e5.	3.1	14
6609	Single-cell profiling of T cells uncovers a tissue-resident memory-like T-cell subset associated with bidirectional prognosis for B-cell acute lymphoblastic leukemia. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
6611	A single-cell transcriptomic atlas characterizes cell types and their molecular features in yak ovarian cortex. <i>FASEB Journal</i> , 2023, 37, .	0.2	6
6613	Microbial metabolite succinate activates solitary chemosensory cells in the human sinonasal epithelium. <i>International Forum of Allergy and Rhinology</i> , 2023, 13, 1525-1534.	1.5	2
6614	Eliminating Senescent Cells Can Promote Pulmonary Hypertension Development and Progression. <i>Circulation</i> , 2023, 147, 650-666.	1.6	28
6615	Epiregulin is a dendritic cell-derived EGFR ligand that maintains skin and lung fibrosis. <i>Science Immunology</i> , 2022, 7, .	5.6	8
6616	Single-cell multiomics revealed the dynamics of antigen presentation, immune response and T cell activation in the COVID-19 positive and recovered individuals. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
6617	Secuer: Ultrafast, scalable and accurate clustering of single-cell RNA-seq data. <i>PLoS Computational Biology</i> , 2022, 18, e1010753.	1.5	4
6618	Deep generative modeling and clustering of single cell Hi-C data. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	4
6619	Heterogeneity of fibroblasts is a hallmark of age-associated erectile dysfunction. <i>International Journal of Biochemistry and Cell Biology</i> , 2023, 156, 106343.	1.2	1
6620	A Poisson reduced-rank regression model for association mapping in sequencing data. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	2
6621	Integrating single-cell RNA sequencing and prognostic model revealed the carcinogenicity and clinical significance of FAM83D in ovarian cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	2
6622	A transcriptional switch controls sex determination in <i>Plasmodium falciparum</i> . <i>Nature</i> , 2022, 612, 528-533.	13.7	15
6624	Integrated single-cell and bulk RNA sequencing analyses reveal a prognostic signature of cancer-associated fibroblasts in head and neck squamous cell carcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	6
6626	benchdamic: benchmarking of differential abundance methods for microbiome data. <i>Bioinformatics</i> , 2023, 39, .	1.8	1
6627	Macrophages regulate vascular smooth muscle cell function during atherosclerosis progression through IL-1 β /STAT3 signaling. <i>Communications Biology</i> , 2022, 5, .	2.0	11
6629	Reconstituting human somitogenesis in vitro. <i>Nature</i> , 2023, 614, 509-520.	13.7	40
6630	Generating colorblind-friendly scatter plots for single-cell data. <i>ELife</i> , 0, 11, .	2.8	0

#	ARTICLE	IF	CITATIONS
6631	Reconstruction of the gastric cancer microenvironment after neoadjuvant chemotherapy by longitudinal single-cell sequencing. <i>Journal of Translational Medicine</i> , 2022, 20, .	1.8	8
6634	Silence of a dependence receptor CSF1R in colorectal cancer cells activates tumor-associated macrophages. , 2022, 10, e005610.		8
6635	Comparative single-cell transcriptomic analysis reveals differences in signaling pathways in gonadal primordial germ cells between chicken (<i>Gallus gallus</i>) and zebra finch (<i>Taeniopygia</i>). <i>Development</i> , 2022, 149, 10, 2195-2207.	0.0	0
6638	Integrated single-cell transcriptome analysis of CD34-enriched leukemic stem cells revealed intra- and inter-patient transcriptional heterogeneity in pediatric acute myeloid leukemia. <i>Annals of Hematology</i> , 2023, 102, 73-87.	0.8	3
6639	Embryonic origins of adult pluripotent stem cells. <i>Cell</i> , 2022, 185, 4756-4769.e13.	13.5	16
6640	Single-cell analysis reveals the chemotherapy-induced cellular reprogramming and novel therapeutic targets in relapsed/refractory acute myeloid leukemia. <i>Leukemia</i> , 2023, 37, 308-325.	3.3	15
6643	LFSC: A linear fast semi-supervised clustering algorithm that integrates reference-bulk and single-cell transcriptomes. <i>Frontiers in Genetics</i> , 2023, 13, .	1.1	0
6644	Comparison of the Single-Cell Immune Landscape of Testudines from Different Habitats. <i>Cells</i> , 2022, 11, 4023.	1.8	1
6646	Comprehensive visualization of cell-cell interactions in single-cell and spatial transcriptomics with NICHES. <i>Bioinformatics</i> , 2023, 39, .	1.8	23
6647	Novel biomarkers predict prognosis and drug-induced neuroendocrine differentiation in patients with prostate cancer. <i>Frontiers in Endocrinology</i> , 2023, 13, .	1.5	2
6648	Renal interstitial cells promote nephron regeneration by secreting prostaglandin E2. <i>ELife</i> , 2022, 11, .	2.8	8
6649	Harshening stem cell research and precision medicine: The states of human pluripotent cells stem cell repository diversity, and racial and sex differences in transcriptomes. <i>Frontiers in Cell and Developmental Biology</i> , 2023, 13, .	1.8	3
6650	Temporal and spatial stability of the EM/PM molecular subtypes in adult diffuse glioma. <i>Frontiers of Medicine</i> , 2023, 17, 240-262.	1.5	2
6651	Single-cell transcriptome in silico analysis reveals conserved regulatory programs in macrophages/monocytes of abdominal aortic aneurysm from multiple mouse models and human. <i>Frontiers in Cardiovascular Medicine</i> , 2023, 9, .	1.1	1
6652	Intermittent protein restriction improves glucose homeostasis in Zucker diabetic fatty rats and single-cell sequencing reveals distinct changes in β^2 cells. <i>Journal of Nutritional Biochemistry</i> , 2023, 114, 109275.	1.9	1
6653	PD-1 ^{high} CXCR5 ⁺ CD4 ⁺ peripheral helper T cells promote CXCR3 ⁺ plasmablasts in human acute viral infection. <i>Cell Reports</i> , 2023, 42, 111895.	2.9	9
6654	Genetic landscape and immune mechanism of monocytes associated with the progression of acute-on-chronic liver failure. <i>Hepatology International</i> , 2023, 17, 676-688.	1.9	3
6655	The Breast Cancer Single-Cell Atlas: Defining cellular heterogeneity within model cell lines and primary tumors to inform disease subtype, stemness, and treatment options. <i>Cellular Oncology (Dordrecht)</i> , 2023, 46, 603-628.	2.1	5

#	ARTICLE	IF	CITATIONS
6656	Crosstalk between 5-methylcytosine and N6-methyladenosine machinery defines disease progression, therapeutic response and pharmacogenomic landscape in hepatocellular carcinoma. <i>Molecular Cancer</i> , 2023, 22, .	7.9	37
6657	ApoE isoform and microbiota-dependent progression of neurodegeneration in a mouse model of tauopathy. <i>Science</i> , 2023, 379, .	6.0	75
6658	Structure-preserved dimension reduction using joint triplets sampling for multi-batch integration of single-cell transcriptomic data. <i>Briefings in Bioinformatics</i> , 0, , .	3.2	0
6659	Single-cell computational machine learning approaches to immune-mediated inflammatory disease: New tools uncover novel fibroblast and macrophage interactions driving pathogenesis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4
6660	Recent advances in droplet microfluidics for single-cell analysis. <i>TrAC - Trends in Analytical Chemistry</i> , 2023, 159, 116932.	5.8	20
6661	Single-cell profiling reveals distinct subsets of CD14+ monocytes drive blood immune signatures of active tuberculosis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
6665	Repurposing nitric oxide donating drugs in cancer therapy through immune modulation. <i>Journal of Experimental and Clinical Cancer Research</i> , 2023, 42, .	3.5	8
6666	Adult skin fibroblast state change in murine wound healing. <i>Scientific Reports</i> , 2023, 13, .	1.6	7
6667	CXCR5+PD-1++ CD4+ T cells colonize infant intestines early in life and promote B cell maturation. , 2023, 20, 201-213.		1
6668	Specialized functions and sexual dimorphism explain the functional diversity of the myeloid populations during glioma progression. <i>Cell Reports</i> , 2023, 42, 111971.	2.9	4
6669	The Recurrent-Specific Regulation Network of Prognostic Stemness-Related Signatures in Low-Grade Glioma. <i>Disease Markers</i> , 2023, 2023, 1-29.	0.6	0
6672	Insulin-like growth factor 1 reduces coronary atherosclerosis in pigs with familial hypercholesterolemia. <i>JCI Insight</i> , 2023, 8, .	2.3	3
6673	A single-cell atlas reveals the heterogeneity of meningeal immunity in a mouse model of Methyl CpG binding protein 2 deficiency. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
6674	Disordered T cell-B cell interactions in autoantibody-positive inflammatory arthritis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
6675	Longitudinal Immune Profiling Highlights CD4+ T Cell Exhaustion Correlated with Liver Fibrosis in <i>Schistosoma japonicum</i> Infection. <i>Journal of Immunology</i> , 2023, 210, 82-95.	0.4	3
6676	The aryl hydrocarbon receptor cell intrinsically promotes resident memory CD8+ T cell differentiation and function. <i>Cell Reports</i> , 2023, 42, 111963.	2.9	16
6677	Single-cell RNA sequencing reveals changes in glioma-associated macrophage polarization and cellular states of malignant gliomas with high AQP4 expression. <i>Cancer Gene Therapy</i> , 2023, 30, 716-726.	2.2	3
6678	The human placenta shapes the phenotype of decidual macrophages. <i>Cell Reports</i> , 2023, 42, 111977.	2.9	12

#	ARTICLE	IF	CITATIONS
6679	Single-Cell Transcriptome Identifies the Renal Cell Type Tropism of Human BK Polyomavirus. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1330.	1.8	1
6680	CDK8/19 inhibition plays an important role in pancreatic $\hat{1}^2$ -cell induction from human iPSCs. <i>Stem Cell Research and Therapy</i> , 2023, 14, .	2.4	2
6682	Identification of astrocyte regulators by nucleic acid cytometry. <i>Nature</i> , 2023, 614, 326-333.	13.7	20
6683	Comprehensive bulk and single-cell transcriptome profiling give useful insights into the characteristics of osteoarthritis associated synovial macrophages. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
6684	Characterizing the tumor microenvironment at the single-cell level reveals a novel immune evasion mechanism in osteosarcoma. <i>Bone Research</i> , 2023, 11, .	5.4	16
6685	Single-cell technologies uncover intra-tumor heterogeneity in childhood cancers. <i>Seminars in Immunopathology</i> , 2023, 45, 61-69.	2.8	3
6686	Development of a 32-gene signature using machine learning for accurate prediction of inflammatory bowel disease. <i>Cell Regeneration</i> , 2023, 12, .	1.1	1
6688	Phagocytosis of Glioma Cells Enhances the Immunosuppressive Phenotype of Bone Marrow-Derived Macrophages. <i>Cancer Research</i> , 2023, 83, 771-785.	0.4	6
6689	The meningeal transcriptional response to traumatic brain injury and aging. <i>ELife</i> , 0, 12, .	2.8	17
6690	Single-cell transcriptome sequencing reveals <i>Wolbachia</i> -mediated modification in early stages of <i>Drosophila</i> spermatogenesis. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2023, 290, .	1.2	4
6691	Spatially resolved transcriptomics reveals pro-inflammatory fibroblast involved in lymphocyte recruitment through CXCL8 and CXCL10. <i>ELife</i> , 0, 12, .	2.8	12
6693	<i>Chrna5</i> and <i>lynx</i> prototoxins identify acetylcholine super-responder subplate neurons. <i>IScience</i> , 2023, 26, 105992.	1.9	7
6694	Targeting Epsins to Inhibit Fibroblast Growth Factor Signaling While Potentiating Transforming Growth Factor- $\hat{1}^2$ Signaling Constrains Endothelial-to-Mesenchymal Transition in Atherosclerosis. <i>Circulation</i> , 2023, 147, 669-685.	1.6	9
6696	Single-cell transcriptome analysis reveals heterogeneity and convergence of the tumor microenvironment in colorectal cancer. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	6
6697	Microglia drive transient insult-induced brain injury by chemotactic recruitment of CD8+ T lymphocytes. <i>Neuron</i> , 2023, 111, 696-710.e9.	3.8	25
6701	The mutation in splicing factor genes correlates with unfavorable prognosis, genomic instability, anti-tumor immunosuppression and increased immunotherapy response in pan-cancer. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	0
6703	Single-cell RNA-seq integrated with multi-omics reveals SERPINE2 as a target for metastasis in advanced renal cell carcinoma. <i>Cell Death and Disease</i> , 2023, 14, .	2.7	8
6706	Transformer for one stop interpretable cell type annotation. <i>Nature Communications</i> , 2023, 14, .	5.8	26

#	ARTICLE	IF	CITATIONS
6707	Senescent cells perturb intestinal stem cell differentiation through Ptk7 induced noncanonical Wnt and YAP signaling. <i>Nature Communications</i> , 2023, 14, .	5.8	7
6712	Angiogenesis-related gene signatures reveal the prognosis of cervical cancer based on single cell sequencing and co-expression network analysis. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	3
6714	Tissue resident iNKT17 cells facilitate cancer cell extravasation in liver metastasis via interleukin-22. <i>Immunity</i> , 2023, 56, 125-142.e12.	6.6	18
6716	PRC2 disruption in cerebellar progenitors produces cerebellar hypoplasia and aberrant myoid differentiation without blocking medulloblastoma growth. <i>Acta Neuropathologica Communications</i> , 2023, 11, .	2.4	1
6717	Decoding anterior-posterior axis emergence among mouse, monkey, and human embryos. <i>Developmental Cell</i> , 2023, 58, 63-79.e4.	3.1	3
6720	Genetic analysis of potential biomarkers and therapeutic targets in ferroptosis from psoriasis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
6722	T-cell cellular stress and reticulocyte signatures, but not loss of na ⁺ ve T lymphocytes, characterize severe COVID-19 in older adults. <i>GeroScience</i> , 2023, 45, 1713-1728.	2.1	1
6723	Identification of Cell Types and Transcriptome Landscapes of Porcine Epidemic Diarrhea Virus-Infected Porcine Small Intestine Using Single-Cell RNA Sequencing. <i>Journal of Immunology</i> , 2023, 210, 271-282.	0.4	11
6724	Rationally designed donepezil-based hydroxamates modulate Sig-1R and HDAC isoforms to exert anti-glioblastoma effects. <i>European Journal of Medicinal Chemistry</i> , 2023, 248, 115054.	2.6	3
6725	Obesity medication lorcaserin activates brainstem GLP-1 neurons to reduce food intake and augments GLP-1 receptor agonist induced appetite suppression. <i>Molecular Metabolism</i> , 2023, 68, 101665.	3.0	9
6727	Targeting T cell checkpoints 41BB and LAG3 and myeloid cell CXCR1/CXCR2 results in antitumor immunity and durable response in pancreatic cancer. <i>Nature Cancer</i> , 0, , .	5.7	14
6729	Single-cell RNA sequencing revealed the liver heterogeneity between egg-laying duck and ceased-laying duck. <i>BMC Genomics</i> , 2022, 23, .	1.2	0
6730	A deep learning-based unsupervised learning method for spatially resolved transcriptomic data analysis. , 2022, , .		0
6731	An inflammatory state remodels the immune microenvironment and improves risk stratification in acute myeloid leukemia. <i>Nature Cancer</i> , 0, , .	5.7	17
6732	Single-Cell RNA-Sequencing Reveals Epithelial Cell Signature of Multiple Subtypes in Chemically Induced Acute Lung Injury. <i>International Journal of Molecular Sciences</i> , 2023, 24, 277.	1.8	0
6733	Single-nucleus <i>sc</i> RNA and <i>sc</i> ATAC sequencing uncovers the molecular and cellular characteristics in the musk gland of Chinese forest musk deer (<i>Moschus berezovskii</i>). <i>FASEB Journal</i> , 2023, 37, .	0.2	0
6734	Dynamic visualization of high-dimensional data. <i>Nature Computational Science</i> , 2023, 3, 86-100.	3.8	4
6735	Biology-inspired data-driven quality control for scientific discovery in single-cell transcriptomics. <i>Genome Biology</i> , 2022, 23, .	3.8	6

#	ARTICLE	IF	CITATIONS
6736	Transcriptome Analysis Reveals a Two-Gene Signature Links to Motor Progression and Alterations of Immune Cells in Parkinson's Disease. <i>Journal of Parkinson's Disease</i> , 2023, 13, 25-38.	1.5	2
6738	Deletion of PD-1 destabilizes the lineage identity and metabolic fitness of tumor-infiltrating regulatory T cells. <i>Nature Immunology</i> , 2023, 24, 148-161.	7.0	26
6739	HPV status represents dominant trait driving delineation of survival-associated gene co-expression networks in head and neck cancer. <i>Cancer Gene Therapy</i> , 0, , .	2.2	0
6740	Human Placental Endothelial Cell and Trophoblast Heterogeneity and Differentiation Revealed by Single-Cell RNA Sequencing. <i>Cells</i> , 2023, 12, 87.	1.8	7
6741	<i>scShapes</i> : a statistical framework for identifying distribution shapes in single-cell RNA-sequencing data. <i>GigaScience</i> , 2022, 12, .	3.3	1
6742	PLSDA-batch: a multivariate framework to correct for batch effects in microbiome data. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	21
6745	Systematic single-cell dissecting reveals heterogeneous oncofetal reprogramming in the tumor microenvironment of gastric cancer. <i>Human Cell</i> , 2023, 36, 689-701.	1.2	7
6746	YTHDF2 orchestrates tumor-associated macrophage reprogramming and controls antitumor immunity through CD8+ T cells. <i>Nature Immunology</i> , 2023, 24, 255-266.	7.0	31
6748	Single-cell characterization of anti- LAG-3 and anti- PD-1 combination treatment in patients with melanoma. <i>Journal of Clinical Investigation</i> , 2023, 133, .	3.9	20
6751	Comparing the transcriptome of developing native and iPSC-derived mouse retinae by single cell RNA sequencing. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
6752	Denosing adaptive deep clustering with self-attention mechanism on single-cell sequencing data. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	1
6755	Altered host protease determinants for SARS-CoV-2 Omicron. <i>Science Advances</i> , 2023, 9, .	4.7	12
6757	Single-cell spatial explorer: easy exploration of spatial and multimodal transcriptomics. <i>BMC Bioinformatics</i> , 2023, 24, .	1.2	2
6760	Topological identification and interpretation for single-cell gene regulation elucidation across multiple platforms using scMGCA. <i>Nature Communications</i> , 2023, 14, .	5.8	7
6761	The landscape of immune dysregulation in Crohn's disease revealed through single-cell transcriptomic profiling in the ileum and colon. <i>Immunity</i> , 2023, 56, 444-458.e5.	6.6	35
6763	Clustering by antigen-presenting genes reveals immune landscapes and predicts response to checkpoint immunotherapy. <i>Scientific Reports</i> , 2023, 13, .	1.6	2
6764	Inhibition of 2-arachidonoylglycerol degradation enhances glial immunity by single-cell transcriptomic analysis. <i>Journal of Neuroinflammation</i> , 2023, 20, .	3.1	5
6766	Inositol pyrophosphate profiling reveals regulatory roles of IP6K2-dependent enhanced IP7 metabolism in the enteric nervous system. <i>Journal of Biological Chemistry</i> , 2023, 299, 102928.	1.6	4

#	ARTICLE	IF	CITATIONS
6768	Intrathymic dendritic cell-biased precursors promote human T cell lineage specification through IRF8-driven transmembrane TNF. <i>Nature Immunology</i> , 2023, 24, 474-486.	7.0	6
6769	Single-cell T cell receptor sequencing of paired human atherosclerotic plaques and blood reveals autoimmune-like features of expanded effector T cells. , 2023, 2, 112-125.		20
6770	Differential cell composition and split epidermal differentiation in human palm, sole, and hip skin. <i>Cell Reports</i> , 2023, 42, 111994.	2.9	13
6771	Dysregulation and Epigenetic Reprogramming of NRF2 Signaling Axis Promote Acquisition of Cisplatin Resistance and Metastasis in Head and Neck Squamous Cell Carcinoma. <i>Clinical Cancer Research</i> , 2023, 29, 1344-1359.	3.2	5
6772	Treatment with Anti-HER2 Chimeric Antigen Receptor Tumor-Infiltrating Lymphocytes (CAR-TILs) Is Safe and Associated with Antitumor Efficacy in Mice and Companion Dogs. <i>Cancers</i> , 2023, 15, 648.	1.7	6
6773	Combined PD-1, BRAF and MEK inhibition in BRAFV600E colorectal cancer: a phase 2 trial. <i>Nature Medicine</i> , 2023, 29, 458-466.	15.2	28
6775	Proteogenomics of diffuse gliomas reveal molecular subtypes associated with specific therapeutic targets and immune-evasion mechanisms. <i>Nature Communications</i> , 2023, 14, .	5.8	7
6776	Proteomic and single-cell landscape reveals novel pathogenic mechanisms of HBV-infected intrahepatic cholangiocarcinoma. <i>IScience</i> , 2023, 26, 106003.	1.9	1
6778	Single-cell Expression Atlas Reveals Cell Heterogeneity in the Creeping Fat of Crohn's Disease. <i>Inflammatory Bowel Diseases</i> , 2023, 29, 850-865.	0.9	6
6781	Implanted Tissue-Engineered Vascular Graft Cell Isolation with Single-Cell RNA Sequencing Analysis. <i>Tissue Engineering - Part C: Methods</i> , 2023, 29, 72-84.	1.1	1
6783	Multimodal human thymic profiling reveals trajectories and cellular milieu for T agonist selection. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
6784	Single-cell RNA binding protein regulatory network analyses reveal oncogenic HNRNPK-MYC signalling pathway in cancer. <i>Communications Biology</i> , 2023, 6, .	2.0	6
6785	Immune-interacting lymphatic endothelial subtype at capillary terminals drives lymphatic malformation. <i>Journal of Experimental Medicine</i> , 2023, 220, .	4.2	12
6787	Distinct and opposite effects of leukemogenic <i>Idh</i> and <i>Tet2</i> mutations in hematopoietic stem and progenitor cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	7
6788	The evolution of ovary-biased gene expression in Hawaiian <i>Drosophila</i> . <i>PLoS Genetics</i> , 2023, 19, e1010607.	1.5	1
6792	Human endoderm stem cells reverse inflammation-related acute liver failure through cystatin SN-mediated inhibition of interferon signaling. <i>Cell Research</i> , 0, , .	5.7	9
6793	Network analyses of upper and lower airway transcriptomes identify shared mechanisms among children with recurrent wheezing and school-age asthma. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	1
6795	Lineage Tracing by Single-Cell Transcriptomics Decoding Dynamics of Lineage Commitment. <i>Methods in Molecular Biology</i> , 2023, , .	0.4	0

#	ARTICLE	IF	CITATIONS
6798	A clustering method for small scRNA-seq data based on subspace and weighted distance. PeerJ, 0, 11, e14706.	0.9	1
6801	Antithymocyte Globulin Inhibits CD8+ T Cell Effector Functions via the Paracrine Induction of PDL-1 on Monocytes. Cells, 2023, 12, 382.	1.8	2
6804	scRNA-seq data analysis method to improve analysis performance. IET Nanobiotechnology, 2023, 17, 246-256.	1.9	5
6805	Immunotherapy reverses glioma-driven dysfunction of immune system homeostasis. , 2023, 11, e004805.		1
6806	Analysis of Cre lines for targeting embryonic airway smooth muscle. Developmental Biology, 2023, 496, 63-72.	0.9	0
6807	Arginase 1 is a key driver of immune suppression in pancreatic cancer. ELife, 0, 12, .	2.8	17
6808	Integrative single-cell RNA-seq and ATAC-seq analysis of myogenic differentiation in pig. BMC Biology, 2023, 21, .	1.7	9
6809	Oxidative phosphorylation selectively orchestrates tissue macrophage homeostasis. Immunity, 2023, 56, 516-530.e9.	6.6	39
6810	The Evolution of Single-Cell RNA Sequencing Technology and Application: Progress and Perspectives. International Journal of Molecular Sciences, 2023, 24, 2943.	1.8	11
6811	Single-cell transcriptomic profile of satellite glial cells in trigeminal ganglion. Frontiers in Molecular Neuroscience, 0, 16, .	1.4	7
6812	Early-life bisphenol AP exposure impacted neurobehaviors in adulthood through microglial activation in mice. Chemosphere, 2023, 317, 137935.	4.2	4
6813	A cell marker-based clustering strategy (cmCluster) for precise cell type identification of scRNA-seq data. Quantitative Biology, 2023, 11, 163-174.	0.3	1
6814	State of the Art Procedures for the Isolation and Characterization of Mesoangioblasts. Methods in Molecular Biology, 2023, , 99-115.	0.4	0
6816	Quantitative analysis of high-throughput biological data. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2023, 13, .	6.2	2
6818	<i>TIPE2</i> deletion improves the therapeutic potential of adoptively transferred NK cells. , 2023, 11, e006002.		5
6819	A single-cell transcriptional atlas reveals resident progenitor cell niche functions in TMJ disc development and injury. Nature Communications, 2023, 14, .	5.8	3
6820	A theoretical framework of immune cell phenotypic classification and discovery. Frontiers in Immunology, 0, 14, .	2.2	6
6821	Brassinosteroid gene regulatory networks at cellular resolution in the <i>Arabidopsis</i> root. Science, 2023, 379, .	6.0	26

#	ARTICLE	IF	CITATIONS
6823	Dysregulated lung stroma drives emphysema exacerbation by potentiating resident lymphocytes to suppress an epithelial stem cell reservoir. <i>Immunity</i> , 2023, 56, 576-591.e10.	6.6	15
6824	Single-cell RNA sequencing reveals immunosuppressive myeloid cell diversity during malignant progression in a murine model of glioma. <i>Cell Reports</i> , 2023, 42, 112197.	2.9	15
6825	S100A9 Drives the Chronification of Psoriasiform Inflammation by Inducing IL-23/Type 3 Immunity. <i>Journal of Investigative Dermatology</i> , 2023, 143, 1678-1688.e8.	0.3	4
6827	Clinical and biological heterogeneities in triple-negative breast cancer reveals a non-negligible role of HER2-low. <i>Breast Cancer Research</i> , 2023, 25, .	2.2	6
6829	Integrative single-cell sequencing analysis distinguishes survival-associated cells from the breast cancer microenvironment. <i>Cancer Medicine</i> , 2023, 12, 12896-12911.	1.3	2
6830	Ketogenic Diet Alleviates Renal Interstitial Fibrosis in UUO Mice by Regulating Macrophage Proliferation. <i>Journal of Nutritional Biochemistry</i> , 2023, , 109335.	1.9	0
6831	Cux1+ proliferative basal cells promote epidermal hyperplasia in chronic dry skin disease identified by single-cell RNA transcriptomics. <i>Journal of Pharmaceutical Analysis</i> , 2023, 13, 745-759.	2.4	1
6832	Delayed inhibition of collagen deposition by targeting bone morphogenetic protein 1 promotes recovery after spinal cord injury. <i>Matrix Biology</i> , 2023, 118, 69-91.	1.5	3
6833	Tenascin C+ papillary fibroblasts facilitate neuro-immune interaction in a mouse model of psoriasis. <i>Nature Communications</i> , 2023, 14, .	5.8	9
6834	Defining cardiac functional recovery in end-stage heart failure at single-cell resolution. , 0, , .		4
6835	Spatiotemporal single-cell transcriptomic profiling reveals inflammatory cell states in a mouse model of diffuse alveolar damage. <i>Exploration</i> , 2023, 3, .	5.4	0
6836	Single-Cell Sequencing Data Analysis Unveiled HDAC1 as the Therapeutic Target for Chronic Pancreatitis. <i>Molecular Biotechnology</i> , 2024, 66, 68-78.	1.3	0
6837	A single-cell landscape of triptolide-associated testicular toxicity in mice. <i>Journal of Pharmaceutical Analysis</i> , 2023, 13, 880-893.	2.4	3
6838	Aberrant activation of TCL1A promotes stem cell expansion in clonal haematopoiesis. <i>Nature</i> , 2023, 616, 755-763.	13.7	19
6839	Maternal BPAF exposure impaired synaptic development and caused behavior abnormality in offspring. <i>Ecotoxicology and Environmental Safety</i> , 2023, 256, 114859.	2.9	4
6840	Characterization of T-cell receptors and immunoglobulin heavy chains loci and identification of T/B cell clusters in teleost. <i>Fish and Shellfish Immunology</i> , 2023, 136, 108746.	1.6	0
6841	Deciphering the immune heterogeneity dominated by natural killer cells with prognostic and therapeutic implications in hepatocellular carcinoma. <i>Computers in Biology and Medicine</i> , 2023, 158, 106872.	3.9	2
6842	Single cell RNA-seq resolution revealed CCR1+/SELL+/XAF+ CD14 monocytes mediated vascular endothelial cell injuries in Kawasaki disease and COVID-19. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2023, 1869, 166707.	1.8	1

#	ARTICLE	IF	CITATIONS
6843	Promotion of astrocyte-neuron glutamate-glutamine shuttle by SCFA contributes to the alleviation of Alzheimer's disease. <i>Redox Biology</i> , 2023, 62, 102690.	3.9	14
6844	Single-cell RNA-sequencing reveals the transcriptional landscape of ND-42 mediated spermatid elongation via mitochondrial derivative maintenance in <i>Drosophila</i> testes. <i>Redox Biology</i> , 2023, 62, 102671.	3.9	4
6845	The spatial landscape of gene expression isoforms in tissue sections. <i>Nucleic Acids Research</i> , 2023, 51, e47-e47.	6.5	13
6846	ADAD2 interacts with RNF17 in P-bodies to repress the Ping-pong cycle in pachytene piRNA biogenesis. <i>Journal of Cell Biology</i> , 2023, 222, .	2.3	3
6847	Plasticity in airway smooth muscle differentiation during mouse lung development. <i>Developmental Cell</i> , 2023, 58, 338-347.e4.	3.1	4
6848	Single-Cell Spatial Analysis Identifies Regulators of Brain Tumor-Initiating Cells. <i>Cancer Research</i> , 2023, 83, 1725-1741.	0.4	4
6849	Patient-Derived iPSCs Faithfully Represent the Genetic Diversity and Cellular Architecture of Human Acute Myeloid Leukemia. <i>Blood Cancer Discovery</i> , 2023, 4, 318-335.	2.6	4
6850	Single-cell transcriptomic dissection of the toxic impact of di(2-ethylhexyl) phthalate on immature testicular development at the neonatal stage. <i>Food and Chemical Toxicology</i> , 2023, 176, 113780.	1.8	3
6859	Human early-onset dementia caused by DAP12 deficiency reveals a unique signature of dysregulated microglia. <i>Nature Immunology</i> , 2023, 24, 545-557.	7.0	12
6860	Context-dependent gene regulatory network reveals regulation dynamics and cell trajectories using unspliced transcripts. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	1
6861	Thymosin β 4 preserves vascular smooth muscle phenotype in atherosclerosis via regulation of low density lipoprotein related protein 1 (LRP1). <i>International Immunopharmacology</i> , 2023, 115, 109702.	1.7	4
6863	Stemness-related genes revealed by single-cell profiling of naïve and stimulated human CD34 ⁺ cells from CB and mPB. <i>Clinical and Translational Medicine</i> , 2023, 13, .	1.7	1
6865	Generation of a single-cell B cell atlas of antibody repertoires and transcriptomes to identify signatures associated with antigen specificity. <i>iScience</i> , 2023, 26, 106055.	1.9	3
6866	Cognitive impairments in a Down syndrome model with abnormal hippocampal and prefrontal dynamics and cytoarchitecture. <i>iScience</i> , 2023, 26, 106073.	1.9	0
6867	Cell polarity opposes Jak/STAT-mediated Escargot activation that drives intratumor heterogeneity in a <i>Drosophila</i> tumor model. <i>Cell Reports</i> , 2023, 42, 112061.	2.9	4
6868	Overview of single-cell RNA sequencing analysis and its application to spermatogenesis research. <i>Reproductive Medicine and Biology</i> , 2023, 22, .	1.0	3
6869	The blood vasculature instructs lymphatic patterning in a SOX7-dependent manner. <i>EMBO Journal</i> , 2023, 42, .	3.5	5
6870	Deciphering the sequential changes of monocytes/macrophages in the progression of IDD with longitudinal approach using single-cell transcriptome. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	5

#	ARTICLE	IF	CITATIONS
6871	Post-transcriptional regulation in cranial neural crest cells expands developmental potential. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	7
6872	Adenomyosis: single-cell transcriptomic analysis reveals a paracrine mesenchymal-epithelial interaction involving the WNT/SFRP pathway. <i>Fertility and Sterility</i> , 2023, 119, 869-882.	0.5	1
6874	Basal type I interferon signaling has only modest effects on neonatal and juvenile hematopoiesis. <i>Blood Advances</i> , 2023, 7, 2609-2621.	2.5	2
6877	Tissue-specific abundance of interferon-gamma drives regulatory T cells to restrain DC1-mediated priming of cytotoxic T cells against lung cancer. <i>Immunity</i> , 2023, 56, 386-405.e10.	6.6	22
6878	A palmitate-rich metastatic niche enables metastasis growth via p65 acetylation resulting in pro-metastatic NF- κ B signaling. <i>Nature Cancer</i> , 2023, 4, 344-364.	5.7	29
6880	Lactate from glycolysis regulates inflammatory macrophage polarization in breast cancer. <i>Cancer Immunology, Immunotherapy</i> , 2023, 72, 1917-1932.	2.0	5
6881	Aberrant alteration of peripheral B lymphocyte subsets in hepatocellular carcinoma patients. <i>International Journal of Medical Sciences</i> , 2023, 20, 267-277.	1.1	0
6882	Single-cell transcriptomics-based multidisease analysis revealing the molecular dynamics of retinal neurovascular units under inflammatory and hypoxic conditions. <i>Experimental Neurology</i> , 2023, 362, 114345.	2.0	0
6883	The different natural estrogens promote endothelial healing through distinct cell targets. <i>JCI Insight</i> , 2023, 8, .	2.3	4
6884	MUC16 and TP53 family co-regulate tumor-stromal heterogeneity in pancreatic adenocarcinoma. <i>Frontiers in Oncology</i> , 0, 13, .	1.3	4
6885	Review of single-cell RNA-seq data clustering for cell-type identification and characterization. <i>Rna</i> , 2023, 29, 517-530.	1.6	9
6889	LINE-1 retrotransposon expression in cancerous, epithelial and neuronal cells revealed by 5 \times single-cell RNA-Seq. <i>Nucleic Acids Research</i> , 2023, 51, 2033-2045.	6.5	5
6890	Evolutionary route of nasopharyngeal carcinoma metastasis and its clinical significance. <i>Nature Communications</i> , 2023, 14, .	5.8	5
6891	Neonatal Plasma Exosomes Contribute to Endothelial Cell-Mediated Angiogenesis and Cardiac Repair after Acute Myocardial Infarction. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3196.	1.8	4
6892	Denervation during mandibular distraction osteogenesis results in impaired bone formation. <i>Scientific Reports</i> , 2023, 13, .	1.6	2
6895	Remodeling of colon plasma cell repertoire within ulcerative colitis patients. <i>Journal of Experimental Medicine</i> , 2023, 220, .	4.2	3
6896	Identification and Biological Validation of a Chemokine/Chemokine Receptor-Based Risk Model for Predicting Immunotherapeutic Response and Prognosis in Head and Neck Squamous Cell Carcinoma. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3317.	1.8	0
6898	Oncofetal protein glypican-3 is a biomarker and critical regulator of function for neuroendocrine cells in prostate cancer. <i>Journal of Pathology</i> , 2023, 260, 43-55.	2.1	0

#	ARTICLE	IF	CITATIONS
6899	Single-nucleus Atlas of Sevoflurane-induced Hippocampal Cell Type and Sex-specific Effects during Development in Mice. <i>Anesthesiology</i> , 2023, 138, 477-495.	1.3	6
6900	Cartography of Genomic Interactions Enables Deep Analysis of Single-Cell Expression Data. <i>Nature Communications</i> , 2023, 14, .	5.8	8
6901	scMAGS: Marker gene selection from scRNA-seq data for spatial transcriptomics studies. <i>Computers in Biology and Medicine</i> , 2023, 155, 106634.	3.9	0
6902	Human striatal glia differentially contribute to AD- and PD-specific neurodegeneration. <i>Nature Aging</i> , 2023, 3, 346-365.	5.3	8
6903	Assessing Biomaterial-Induced Stem Cell Lineage Fate by Machine Learning-Based Artificial Intelligence. <i>Advanced Materials</i> , 2023, 35, .	11.1	1
6905	Application of high-throughput single-nucleus DNA sequencing in pancreatic cancer. <i>Nature Communications</i> , 2023, 14, .	5.8	6
6907	SARS-CoV-2 leverages airway epithelial protective mechanism for viral infection. <i>IScience</i> , 2023, 26, 106175.	1.9	2
6908	Single-cell RNA landscape of the special fiber initiation process in <i>Bombax ceiba</i> . <i>Plant Communications</i> , 2023, 4, 100554.	3.6	3
6909	Single-cell transcriptomic analysis reveals the developmental trajectory and transcriptional regulatory networks of pigment glands in <i>Gossypium bickii</i> . <i>Molecular Plant</i> , 2023, 16, 694-708.	3.9	12
6910	Preclinical-to-Clinical Anti-Cancer Drug Response Prediction and Biomarker Identification Using TINDL. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 535-550.	3.0	3
6911	Genomic and microenvironmental heterogeneity shaping epithelial-to-mesenchymal trajectories in cancer. <i>Nature Communications</i> , 2023, 14, .	5.8	16
6912	Single-cell RNA sequencing reveals the effects of chemotherapy on human pancreatic adenocarcinoma and its tumor microenvironment. <i>Nature Communications</i> , 2023, 14, .	5.8	29
6913	Single-cell transcriptomics is revolutionizing the improvement of plant biotechnology research: recent advances and future opportunities. <i>Critical Reviews in Biotechnology</i> , 2024, 44, 202-217.	5.1	1
6915	Neurodegeneration cell per cell. <i>Neuron</i> , 2023, 111, 767-786.	3.8	8
6916	Modeling Blast Crisis Using Mutagenized Chronic Myeloid Leukemia-Derived Induced Pluripotent Stem Cells (iPSCs). <i>Cells</i> , 2023, 12, 598.	1.8	6
6917	Soluble adenylyl cyclase coordinates intracellular pH homeostasis and biomineralization in calcifying cells of a marine animal. <i>American Journal of Physiology - Cell Physiology</i> , 2023, 324, C777-C786.	2.1	0
6919	Cell-type-specific responses to the microbiota across all tissues of the larval zebrafish. <i>Cell Reports</i> , 2023, 42, 112095.	2.9	2
6920	Low TCR Binding Strength Results in Increased Progenitor-like CD8+ Tumor-Infiltrating Lymphocytes. <i>Cancer Immunology Research</i> , 2023, 11, 570-582.	1.6	2

#	ARTICLE	IF	CITATIONS
6921	Analysis of <sc>Singleâ€Cell</sc> Transcriptome and Surface Protein Expression in Ankylosing Spondylitis Identifies <sc>OX40</sc>â€Positive and <sc>Glucocorticoidâ€Induced</sc> Tumor Necrosis Factor Receptorâ€Positive Pathogenic Th17 Cells. <i>Arthritis and Rheumatology</i> , 2023, 75, 1176-1186.	2.9	5
6923	Molecular and cellular evolution of the amygdala across species analyzed by single-nucleus transcriptome profiling. <i>Cell Discovery</i> , 2023, 9, .	3.1	14
6927	OX40 agonism enhances PD-L1 checkpoint blockade by shifting the cytotoxic Tâ€cell differentiation spectrum. <i>Cell Reports Medicine</i> , 2023, 4, 100939.	3.3	6
6928	Alpha kinase 3 signaling at the M-band maintains sarcomere integrity and proteostasis in striated muscle. , 2023, 2, 159-173.		5
6929	BOMA, a machine-learning framework for comparative gene expression analysis across brains and organoids. <i>Cell Reports Methods</i> , 2023, 3, 100409.	1.4	4
6931	Fluorescent Light Opening New Horizons. , 2023, , 693-746.		0
6932	Chronic changes in oligodendrocyte <sc>subâ€populations</sc> after middle cerebral artery occlusion in neonatal mice. <i>Glia</i> , 2023, 71, 1429-1450.	2.5	2
6933	Early peripheral blood MCEMP1 and HLA-DRA expression predicts COVID-19 prognosis. <i>EBioMedicine</i> , 2023, 89, 104472.	2.7	10
6934	scENT for Revealing Gene Clusters From Single-Cell RNA-Seq Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, , 1-13.	1.9	0
6935	Repression of the aryl-hydrocarbon receptor prevents oxidative stress and ferroptosis of intestinal intraepithelial lymphocytes. <i>Immunity</i> , 2023, 56, 797-812.e4.	6.6	32
6936	PKR induces TGF-Î² and limits oncolytic immune therapy. , 2023, 11, e006164.		3
6938	Pyrimidine de novo synthesis inhibition selectively blocks effector but not memory T cell development. <i>Nature Immunology</i> , 2023, 24, 501-515.	7.0	6
6940	Precision immunointerception of EGFR-driven tumorigenesis for lung cancer prevention. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	1
6941	Attention-Based Graph Neural Network for Label Propagation in Single-Cell Omics. <i>Genes</i> , 2023, 14, 506.	1.0	1
6942	Long noncoding RNA GATA2-AS1 augments endothelial hypoxia inducible factor 1-Î± induction and regulates hypoxic signaling. <i>Journal of Biological Chemistry</i> , 2023, 299, 103029.	1.6	4
6943	Destin2: Integrative and cross-modality analysis of single-cell chromatin accessibility data. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0
6946	Multilevel proteomic analyses reveal molecular diversity between diffuse-type and intestinal-type gastric cancer. <i>Nature Communications</i> , 2023, 14, .	5.8	3
6949	Sterile liver injury induces a protective tissue-resident cDC1-ILC1 circuit through cDC1-intrinsic cGAS-STING-dependent IL-12 production. <i>Cell Reports</i> , 2023, 42, 112141.	2.9	3

#	ARTICLE	IF	CITATIONS
6950	<tt>recountmethylation</tt>enables flexible analysis of public blood DNA methylation array data. <i>Bioinformatics Advances</i> , 2023, 3, .	0.9	1
6951	Single cell and lineage tracing studies reveal the impact of CD34+ cells on myocardial fibrosis during heart failure. <i>Stem Cell Research and Therapy</i> , 2023, 14, .	2.4	3
6952	Exploring the Mechanism of Microfracture in the Treatment of Porcine Full-Thickness Cartilage Defect. <i>American Journal of Sports Medicine</i> , 2023, 51, 1033-1046.	1.9	4
6953	Single-Cell Analysis Reveals Distinct Immune and Smooth Muscle Cell Populations that Contribute to Chronic Thromboembolic Pulmonary Hypertension. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2023, 207, 1358-1375.	2.5	6
6955	Phenotypic pliancy and the breakdown of epigenetic polycomb mechanisms. <i>PLoS Computational Biology</i> , 2023, 19, e1010889.	1.5	0
6956	Single-cell biological network inference using a heterogeneous graph transformer. <i>Nature Communications</i> , 2023, 14, .	5.8	29
6957	Generation of self-organized autonomic ganglion organoids from fibroblasts. <i>IScience</i> , 2023, 26, 106241.	1.9	1
6958	Molecular mechanisms of coronary artery disease risk at the PDGFD locus. <i>Nature Communications</i> , 2023, 14, .	5.8	9
6959	Cancer-associated fibroblasts are the main contributors to epithelial-to-mesenchymal signatures in the tumor microenvironment. <i>Scientific Reports</i> , 2023, 13, .	1.6	8
6960	Regulon active landscape reveals cell development and functional state changes of human primary osteoblasts in vivo. <i>Human Genomics</i> , 2023, 17, .	1.4	2
6961	Single-Cell RNA-Seq Analysis Reveals Macrophages Are Involved in the Pathogenesis of Human Sporadic Acute Type A Aortic Dissection. <i>Biomolecules</i> , 2023, 13, 399.	1.8	7
6962	Profiling the peripheral immune response to ex vivo TNF stimulation in untreated juvenile idiopathic arthritis using single cell RNA sequencing. <i>Pediatric Rheumatology</i> , 2023, 21, .	0.9	3
6963	Batch alignment of single-cell transcriptomics data using deep metric learning. <i>Nature Communications</i> , 2023, 14, .	5.8	10
6964	The gut microbiota promotes distal tissue regeneration via ROR γ ⁺ regulatory T cell emissaries. <i>Immunity</i> , 2023, 56, 829-846.e8.	6.6	29
6965	Neural connectivity molecules best identify the heterogeneous clock and dopaminergic cell types in the <i>Drosophila</i> adult brain. <i>Science Advances</i> , 2023, 9, .	4.7	10
6967	scTSSR-D: Gene Expression Recovery by Two-side Self-representation and Dropout Information for scRNA-seq Data. <i>Current Bioinformatics</i> , 2023, 18, .	0.7	0
6968	Exploiting moderate hypoxia to benefit patients with brain disease: Molecular mechanisms and translational research in progress. , 2023, 1, 55-65.		6
6973	Canine peripheral blood TCR β ⁺ T cell atlas: Identification of diverse subsets including CD8A ⁺ MAIT-like cells by combined single-cell transcriptome and V(D)J repertoire analysis. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	5

#	ARTICLE	IF	CITATIONS
6976	CD11c+ macrophages are proangiogenic and necessary for experimental choroidal neovascularization. <i>JCI Insight</i> , 2023, 8, .	2.3	8
6978	Spatiotemporal mapping of immune and stem cell dysregulation after volumetric muscle loss. <i>JCI Insight</i> , 2023, 8, .	2.3	7
6979	scSTAR reveals hidden heterogeneity with a real-virtual cell pair structure across conditions in single-cell RNA sequencing data. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	2
6981	Predictive and Prognostic Implications of Circulating CX3CR1+ CD8+ T Cells in Non-“Small Cell Lung Cancer Patients Treated with Chemo-Immunotherapy. <i>Cancer Research Communications</i> , 2023, 3, 510-520.	0.7	2
6982	High-throughput transcriptional profiling of perturbations by Panax ginseng saponins and Panax notoginseng saponins using TCM-seq. <i>Journal of Pharmaceutical Analysis</i> , 2023, , .	2.4	1
6983	Single-cell transcriptome dynamics of the autotaxin-lysophosphatidic acid axis during muscle regeneration reveal proliferative effects in mesenchymal fibro-adipogenic progenitors. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	1.8	1
6985	Pairing of single-cell RNA analysis and T cell antigen receptor profiling indicates breakdown of T cell tolerance checkpoints in atherosclerosis. , 2023, 2, 290-306.		14
6986	Resveratrol attenuates staphylococcal enterotoxin B-activated immune cell metabolism via upregulation of miR-100 and suppression of mTOR signaling pathway. <i>Frontiers in Pharmacology</i> , 0, 14, .	1.6	6
6988	GGC repeat expansion in <i>NOTCH2NLC</i> induces dysfunction in ribosome biogenesis and translation. <i>Brain</i> , 2023, 146, 3373-3391.	3.7	4
6989	Age-associated B cells are heterogeneous and dynamic drivers of autoimmunity in mice. <i>Journal of Experimental Medicine</i> , 2023, 220, .	4.2	19
6990	An artificial intelligence network-guided signature for predicting outcome and immunotherapy response in lung adenocarcinoma patients based on 26 machine learning algorithms. <i>Cell Proliferation</i> , 2023, 56, .	2.4	10
6991	Cross-platform normalization enables machine learning model training on microarray and RNA-seq data simultaneously. <i>Communications Biology</i> , 2023, 6, .	2.0	8
6992	Cell-type profiling of the sympathetic nervous system using spatial transcriptomics and spatial mapping of mRNA. <i>Developmental Dynamics</i> , 2023, 252, 1130-1142.	0.8	1
6993	Skin T _H 17 cell inflammatory responses are hardwired in the thymus by oxysterol sensing via GPR183 and calibrated by dietary cholesterol. <i>Immunity</i> , 2023, 56, 562-575.e6.	6.6	9
6995	Thyroid cells from normal and autoimmune thyroid glands suppress T lymphocytes proliferation upon contact revealing a new regulatory inhibitory type of interaction independent of PD1/PDL1. <i>Journal of Autoimmunity</i> , 2023, 136, 103013.	3.0	1
6996	Phosphorylated signal transducer and activator of transcription proteins 1 in salivary glandular tissue: an important histological marker for diagnosis of primary Sjögren’s syndrome. <i>RMD Open</i> , 2023, 9, e002694.	1.8	1
6997	Complex hierarchical structures in single-cell genomics data unveiled by deep hyperbolic manifold learning. <i>Genome Research</i> , 2023, 33, 232-246.	2.4	3
6999	scPrisma infers, filters and enhances topological signals in single-cell data using spectral template matching. <i>Nature Biotechnology</i> , 2023, 41, 1645-1654.	9.4	3

#	ARTICLE	IF	CITATIONS
7000	T cell egress via lymphatic vessels is tuned by antigen encounter and limits tumor control. <i>Nature Immunology</i> , 2023, 24, 664-675.	7.0	26
7001	Multi-organ single-cell analysis reveals an on/off switch system with potential for personalized treatment of immunological diseases. <i>Cell Reports Medicine</i> , 2023, 4, 100956.	3.3	7
7004	The early neutrophil-committed progenitors aberrantly differentiate into immunoregulatory monocytes during emergency myelopoiesis. <i>Cell Reports</i> , 2023, 42, 112165.	2.9	11
7007	Gene expression variability across cells and species shapes the relationship between renal resident macrophages and infiltrated macrophages. <i>BMC Bioinformatics</i> , 2023, 24, .	1.2	2
7008	Single-cell transcriptomic profiling redefines the origin and specification of early adrenogonadal progenitors. <i>Cell Reports</i> , 2023, 42, 112191.	2.9	4
7009	STEEL enables high-resolution delineation of spatiotemporal transcriptomic data. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	4
7010	Single-cell analysis reveals dynamics of human B cell differentiation and identifies novel B and antibody-secreting cell intermediates. <i>ELife</i> , 0, 12, .	2.8	4
7011	In silico tissue generation and power analysis for spatial omics. <i>Nature Methods</i> , 2023, 20, 424-431.	9.0	13
7012	Insights into pulmonary phosphate homeostasis and osteoclastogenesis emerge from the study of pulmonary alveolar microlithiasis. <i>Nature Communications</i> , 2023, 14, .	5.8	1
7013	Identification of a physiologic vasculogenic fibroblast state to achieve tissue repair. <i>Nature Communications</i> , 2023, 14, .	5.8	6
7014	Fine mapping spatiotemporal mechanisms of genetic variants underlying cardiac traits and disease. <i>Nature Communications</i> , 2023, 14, .	5.8	3
7015	Integration of Single-Cell RNA-Seq Datasets: A Review of Computational Methods. <i>Molecules and Cells</i> , 2023, 46, 106-119.	1.0	8
7016	Ploidy-stratified single cardiomyocyte transcriptomics map Zinc Finger E-Box Binding Homeobox 1 to underly cardiomyocyte proliferation before birth. <i>Basic Research in Cardiology</i> , 2023, 118, .	2.5	3
7017	Hepatocellular carcinoma subtypes based on metabolic pathways reveals potential therapeutic targets. <i>Frontiers in Oncology</i> , 0, 13, .	1.3	3
7018	Characterization of immature ovarian teratomas through single-cell transcriptome. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	2
7020	Nur77 and PPAR γ regulate transcription and polarization in distinct subsets of M2-like reparative macrophages during regenerative inflammation. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	4
7021	Single-cell sequencing reveals the evolution of immune molecules across multiple vertebrate species. <i>Journal of Advanced Research</i> , 2024, 55, 73-87.	4.4	6
7022	Tumor microenvironment remodeling after neoadjuvant immunotherapy in non-small cell lung cancer revealed by single-cell RNA sequencing. <i>Genome Medicine</i> , 2023, 15, .	3.6	23

#	ARTICLE	IF	CITATIONS
7023	Single-cell transcriptome analysis reveals endometrial immune microenvironment in minimal/mild endometriosis. <i>Clinical and Experimental Immunology</i> , 2023, 212, 285-295.	1.1	7
7028	CD36+ cancer-associated fibroblasts provide immunosuppressive microenvironment for hepatocellular carcinoma via secretion of macrophage migration inhibitory factor. <i>Cell Discovery</i> , 2023, 9, .	3.1	42
7031	Ablation of p57+ Quiescent Cancer Stem Cells Suppresses Recurrence after Chemotherapy of Intestinal Tumors. <i>Cancer Research</i> , 2023, 83, 1393-1409.	0.4	3
7033	Cytotoxic CD161 ⁺ CD8 ⁺ TEMRA cells contribute to the pathogenesis of systemic lupus erythematosus. <i>EBioMedicine</i> , 2023, 90, 104507.	2.7	7
7034	Intestinal cell type-specific communication networks underlie homeostasis and response to Western diet. <i>Journal of Experimental Medicine</i> , 2023, 220, .	4.2	5
7035	A novel myeloid cell marker genes related signature can indicate immune infiltration and predict prognosis of hepatocellular carcinoma: Integrated analysis of bulk and single-cell RNA sequencing. <i>Frontiers in Molecular Biosciences</i> , 0, 10, .	1.6	0
7036	Pseudotime dynamics of T _H cells in pancreatic ductal adenocarcinoma inform distinct functional states within the regulatory and cytotoxic T _H cells. <i>IScience</i> , 2023, 26, 106324.	1.9	2
7039	<i>Candida albicans</i> -specific Th17 cell-mediated response contributes to alcohol-associated liver disease. <i>Cell Host and Microbe</i> , 2023, 31, 389-404.e7.	5.1	13
7041	Comprehensive analysis of nicotinamide metabolism-related signature for predicting prognosis and immunotherapy response in breast cancer. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	1
7042	Immature natural killer cells promote progression of triple-negative breast cancer. <i>Science Translational Medicine</i> , 2023, 15, .	5.8	13
7045	Single-cell RNA sequencing reveals cell landscape following antimony exposure during spermatogenesis in <i>Drosophila</i> testes. <i>Cell Death Discovery</i> , 2023, 9, .	2.0	6
7046	N-acetylneuraminic acid links immune exhaustion and accelerated memory deficit in diet-induced obese Alzheimer's disease mouse model. <i>Nature Communications</i> , 2023, 14, .	5.8	7
7047	High-resolution anatomical and spatial transcriptome analyses reveal two types of meristematic cell pools within the secondary vascular tissue of poplar stem. <i>Molecular Plant</i> , 2023, 16, 809-828.	3.9	18
7049	Complex Analysis of Single-Cell RNA Sequencing Data. <i>Biochemistry (Moscow)</i> , 2023, 88, 231-252.	0.7	4
7054	A New Signature That Predicts Progression-Free Survival of Clear Cell Renal Cell Carcinoma with Anti-PD-1 Therapy. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5332.	1.8	1
7056	Single-cell sequencing reveals that endothelial cells, EndMT cells and mural cells contribute to the pathogenesis of cavernous malformations. <i>Experimental and Molecular Medicine</i> , 2023, 55, 628-642.	3.2	8
7057	Digits in a dish: An in vitro system to assess the molecular genetics of hand/foot development at single-cell resolution. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	1.8	1
7059	Single-nuclei RNA sequencing (snRNA-seq) uncovers trophoblast cell types and lineages in the mature bovine placenta. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	7

#	ARTICLE	IF	CITATIONS
7060	The angiotensin receptor Tie2 is atheroprotective in arterial endothelium. , 2023, 2, 307-321.		5
7061	Comprehensive molecular phenotyping of <i>ARID1A</i> -deficient gastric cancer reveals pervasive epigenomic reprogramming and therapeutic opportunities. <i>Gut</i> , 2023, 72, 1651-1663.	6.1	3
7062	Screening of potential immune-related genes expressed during sepsis using gene sequencing technology. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
7064	Myofibroblast <i>Ccn3</i> is regulated by Yap and <i>Wwtr1</i> and contributes to adverse cardiac outcomes. <i>Frontiers in Cardiovascular Medicine</i> , 0, 10, .	1.1	1
7065	Integrated multi-omics approach to distinct molecular characterization and classification of early-onset colorectal cancer. <i>Cell Reports Medicine</i> , 2023, 4, 100974.	3.3	5
7066	Ensemble learning-based gene signature and risk model for predicting prognosis of triple-negative breast cancer. <i>Functional and Integrative Genomics</i> , 2023, 23, .	1.4	3
7070	Smooth muscle contributes to the development and function of a layered intestinal stem cell niche. <i>Developmental Cell</i> , 2023, 58, 550-564.e6.	3.1	4
7072	Inference of Cell-Cell Communication for Detecting Immune Disease-Associated Signaling Pathways using Single-Cell RNA-seq. , 2022, , .		0
7073	Spatial epigenome-transcriptome co-profiling of mammalian tissues. <i>Nature</i> , 2023, 616, 113-122.	13.7	72
7074	Elements of divergence in germline determination in closely related species. <i>iScience</i> , 2023, 26, 106402.	1.9	0
7077	A Primer on Preprocessing, Visualization, Clustering, and Phenotyping of Barcode-Based Spatial Transcriptomics Data. <i>Methods in Molecular Biology</i> , 2023, , 115-140.	0.4	2
7078	Identification of new co-diagnostic genes for sepsis and metabolic syndrome using single-cell data analysis and machine learning algorithms. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	5
7079	A single-cell transcriptome atlas profiles early organogenesis in human embryos. <i>Nature Cell Biology</i> , 2023, 25, 604-615.	4.6	24
7080	Impaired PPAR γ activation by cadmium exacerbates infection-induced lung injury. <i>JCI Insight</i> , 2023, 8, .	2.3	4
7081	Novel mouse models based on intersectional genetics to identify and characterize plasmacytoid dendritic cells. <i>Nature Immunology</i> , 2023, 24, 714-728.	7.0	9
7082	A reference cell tree will serve science better than a reference cell atlas. <i>Cell</i> , 2023, 186, 1103-1114.	13.5	27
7084	Keratinocytes sense and eliminate CRISPR DNA through STING/IFN- β activation and APOBEC3G induction. <i>Journal of Clinical Investigation</i> , 2023, 133, .	3.9	4
7086	New technologies to study helminth development and host-parasite interactions. <i>International Journal for Parasitology</i> , 2023, 53, 393-403.	1.3	6

#	ARTICLE	IF	CITATIONS
7088	Integrated transcriptome study of the tumor microenvironment for treatment response prediction in male predominant hypopharyngeal carcinoma. <i>Nature Communications</i> , 2023, 14, .	5.8	2
7089	Pan-cancer analysis identifies PD-L2 as a tumor promotor in the tumor microenvironment. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	2
7090	A universal framework for single-cell multi-omics data integration with graph convolutional networks. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	7
7092	Combinatorial effects on gene expression at the Lbx1/Fgf8 locus resolve split-hand/foot malformation type 3. <i>Nature Communications</i> , 2023, 14, .	5.8	6
7093	Single-cell dissection of human hematopoietic reconstitution after allogeneic hematopoietic stem cell transplantation. <i>Science Immunology</i> , 2023, 8, .	5.6	8
7094	CCR3 plays a role in murine age-related cognitive changes and T-cell infiltration into the brain. <i>Communications Biology</i> , 2023, 6, .	2.0	5
7095	UGRP1-modulated MARCO+ alveolar macrophages contribute to age-related lung fibrosis. <i>Immunity and Ageing</i> , 2023, 20, .	1.8	2
7096	Pioneer factor ASCL1 cooperates with the mSWI/SNF complex at distal regulatory elements to regulate human neural differentiation. <i>Genes and Development</i> , 2023, 37, 218-242.	2.7	13
7101	Human T _H 17 cell generation is restored in CD3 ϵ severe combined immunodeficiency through adenine base editing. <i>Cell</i> , 2023, 186, 1398-1416.e23.	13.5	21
7104	Current Status and Prospects of the Single-Cell Sequencing Technologies for Revealing the Pathogenesis of Pregnancy-Associated Disorders. <i>Genes</i> , 2023, 14, 756.	1.0	1
7105	Mitochondria-associated gene expression perturbation predicts clinical outcomes and shows potential for targeted therapy in neuroblastoma. <i>Frontiers in Pediatrics</i> , 0, 11, .	0.9	0
7106	Transcriptomic atlas and interaction networks of brain cells in mouse CNS demyelination and remyelination. <i>Cell Reports</i> , 2023, 42, 112293.	2.9	9
7108	IL-6 in the infarcted heart is preferentially formed by fibroblasts and modulated by purinergic signaling. <i>Journal of Clinical Investigation</i> , 2023, 133, .	3.9	5
7109	A transcriptionally distinct subset of influenza-specific effector memory B cells predicts long-lived antibody responses to vaccination in humans. <i>Immunity</i> , 2023, 56, 847-863.e8.	6.6	16
7110	Imputation of single-cell transcriptome data enables the reconstruction of networks predictive of breast cancer metastasis. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 2296-2304.	1.9	0
7111	Multiomics Empowers Predictive Pancreatic Cancer Immunotherapy. <i>Journal of Immunology</i> , 2023, 210, 859-868.	0.4	3
7113	EasyCellType: marker-based cell-type annotation by automatically querying multiple databases. <i>Bioinformatics Advances</i> , 2023, 3, .	0.9	2
7114	Somatic mutations alter the differentiation outcomes of iPSC-derived neurons. <i>Cell Genomics</i> , 2023, 3, 100280.	3.0	2

#	ARTICLE	IF	CITATIONS
7117	The impact of the COVID-19 pandemic on SLE. <i>Modern Rheumatology</i> , 2024, 34, 247-264.	0.9	1
7118	Disease modeling of ADAMTS9-related nephropathy using kidney organoids reveals its roles in tubular cells and podocytes. <i>Frontiers in Medicine</i> , 0, 10, .	1.2	0
7119	Ganglioglioma deep transcriptomics reveals primitive neuroectoderm neural precursor-like population. <i>Acta Neuropathologica Communications</i> , 2023, 11, .	2.4	0
7120	Multi-modal quantification of pathway activity with MAYA. <i>Nature Communications</i> , 2023, 14, .	5.8	4
7121	TBX3 is dynamically expressed in pancreatic organogenesis and fine-tunes regeneration. <i>BMC Biology</i> , 2023, 21, .	1.7	1
7122	Longitudinal single-cell profiling of chemotherapy response in acute myeloid leukemia. <i>Nature Communications</i> , 2023, 14, .	5.8	15
7123	Glycyrrhizic acid inhibits myeloid differentiation of hematopoietic stem cells by binding S100 calcium binding protein A8 to improve cognition in aged mice. <i>Immunity and Ageing</i> , 2023, 20, .	1.8	5
7124	Epigenetic and epitranscriptomic regulation of axon regeneration. <i>Molecular Psychiatry</i> , 2023, 28, 1440-1450.	4.1	3
7125	Domain adaptation for supervised integration of scRNA-seq data. <i>Communications Biology</i> , 2023, 6, .	2.0	3
7126	Bipotent transitional liver progenitor cells contribute to liver regeneration. <i>Nature Genetics</i> , 2023, 55, 651-664.	9.4	22
7127	The Secretome of Irradiated Peripheral Mononuclear Cells Attenuates Hypertrophic Skin Scarring. <i>Pharmaceutics</i> , 2023, 15, 1065.	2.0	0
7128	Single-cell RNA sequencing reveals in vivo osteoimmunology interactions between the immune and skeletal systems. <i>Frontiers in Endocrinology</i> , 0, 14, .	1.5	1
7129	Impaired Reorganization of Centrosome Structure Underlies Human Infantile Dilated Cardiomyopathy. <i>Circulation</i> , 2023, 147, 1291-1303.	1.6	3
7130	An integrated single-cell transcriptomic dataset for non-small cell lung cancer. <i>Scientific Data</i> , 2023, 10, .	2.4	9
7131	Simultaneous profiling of host expression and microbial abundance by spatial metatranscriptome sequencing. <i>Genome Research</i> , 2023, 33, 401-411.	2.4	2
7133	Integrative bulk and single-cell transcriptome profiling analysis reveals <i>IFI272</i> as a novel interferon-stimulated gene in dengue. <i>Journal of Medical Virology</i> , 2023, 95, .	2.5	2
7134	Chromatin access regulates the formation of Müller glia-derived progenitor cells in the retina. <i>Glia</i> , 2023, 71, 1729-1754.	2.5	7
7135	Epigenetic and transcriptomic characterization reveals progression markers and essential pathways in clear cell renal cell carcinoma. <i>Nature Communications</i> , 2023, 14, .	5.8	11

#	ARTICLE	IF	CITATIONS
7136	Stage of Keratinocyte Differentiation is a Key Determinant of Viral Susceptibility in Human Skin. <i>Journal of Investigative Dermatology</i> , 2023, , .	0.3	2
7137	Combined analysis of bulk and single-cell RNA sequencing reveals novel natural killer cell-related prognostic biomarkers for predicting immunotherapeutic response in hepatocellular carcinoma. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	1
7139	PDGF-D-induced immunoproteasome activation and cell-cell interactions. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 2405-2418.	1.9	1
7141	An immunometabolism subtyping system identifies S100A9+ macrophage as an immune therapeutic target in colorectal cancer based on multiomics analysis. <i>Cell Reports Medicine</i> , 2023, 4, 100987.	3.3	5
7143	Formation and function of the meningeal arachnoid barrier around the developing mouse brain. <i>Developmental Cell</i> , 2023, 58, 635-644.e4.	3.1	13
7144	Muscle cell-type diversification is driven by bHLH transcription factor expansion and extensive effector gene duplications. <i>Nature Communications</i> , 2023, 14, .	5.8	7
7145	Droplet-based forward genetic screening of astrocyte-“microglia cross-talk. <i>Science</i> , 2023, 379, 1023-1030.	6.0	35
7146	Tracking of activated cTfh cells following sequential influenza vaccinations reveals transcriptional profile of clonotypes driving a vaccine-induced immune response. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	1
7147	scTransSort: Transformers for Intelligent Annotation of Cell Types by Gene Embeddings. <i>Biomolecules</i> , 2023, 13, 611.	1.8	1
7148	Cellular Distribution of Secreted Phospholipase A2 in Lungs of IPF Patients and Its Inhibition in Bleomycin-Induced Pulmonary Fibrosis in Mice. <i>Cells</i> , 2023, 12, 1044.	1.8	1
7149	Etiology of end-stage liver cirrhosis impacts hepatic natural killer cell heterogeneity. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	3
7150	Single-cell protein-DNA interactomics and multiomics tools for deciphering genome regulation. , 2023, , 20220057.		0
7152	A <i>Mesp1</i> -dependent developmental breakpoint in transcriptional and epigenomic specification of early cardiac precursors. <i>Development (Cambridge)</i> , 0, , .	1.2	1
7153	Integrated single-cell RNA-seq analysis reveals the vital cell types and dynamic development signature of atherosclerosis. <i>Frontiers in Physiology</i> , 0, 14, .	1.3	0
7154	Clustering and machine learning-based integration identify cancer associated fibroblasts genes™ signature in head and neck squamous cell carcinoma. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0
7155	A thalamic-primary auditory cortex circuit mediates resilience to stress. <i>Cell</i> , 2023, 186, 1352-1368.e18.	13.5	10
7156	T cell immunotherapies engage neutrophils to eliminate tumor antigen escape variants. <i>Cell</i> , 2023, 186, 1432-1447.e17.	13.5	49
7157	Delineation of complex gene expression patterns in single cell RNA-seq data with ICARUS v2.0. <i>NAR Genomics and Bioinformatics</i> , 2023, 5, .	1.5	1

#	ARTICLE	IF	CITATIONS
7158	Best practices for single-cell analysis across modalities. <i>Nature Reviews Genetics</i> , 2023, 24, 550-572.	7.7	128
7159	A human skeletal muscle stem/myotube model reveals multiple signaling targets of cancer secretome in skeletal muscle. <i>iScience</i> , 2023, 26, 106541.	1.9	0
7160	Single-cell RNA sequencing reveals that VIM and IFITM3 are vital targets of Dengzhan Shengmai capsule to protect against cerebral ischemic injury. <i>Journal of Ethnopharmacology</i> , 2023, 311, 116439.	2.0	3
7162	Single-cell analysis of peripheral blood from high-altitude pulmonary hypertension patients identifies a distinct monocyte phenotype. <i>Nature Communications</i> , 2023, 14, .	5.8	4
7164	Three-dimensional and single-cell sequencing of liver cancer reveals comprehensive host-virus interactions in HBV infection. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	3
7166	Mapping human adult hippocampal neurogenesis with single-cell transcriptomics: Reconciling controversy or fueling the debate?. <i>Neuron</i> , 2023, 111, 1714-1731.e3.	3.8	15
7167	NDC80 status pinpoints mitotic kinase inhibitors as emerging therapeutic options in clear cell renal cell carcinoma. <i>iScience</i> , 2023, 26, 106531.	1.9	0
7168	Different approaches to Imaging Mass Cytometry data analysis. <i>Bioinformatics Advances</i> , 2023, 3, .	0.9	10
7169	Comparative analysis of dimension reduction methods for cytometry by time-of-flight data. <i>Nature Communications</i> , 2023, 14, .	5.8	7
7170	Hepatocyte-specific knockout of HIF-2 α cannot alleviate carbon tetrachloride-induced liver fibrosis in mice. <i>PeerJ</i> , 0, 11, e15191.	0.9	1
7172	Single-cell RNA-seq of heart reveals intercellular communication drivers of myocardial fibrosis in diabetic cardiomyopathy. <i>ELife</i> , 0, 12, .	2.8	5
7174	scJVAE: A novel method for integrative analysis of multimodal single-cell data. <i>Computers in Biology and Medicine</i> , 2023, 158, 106865.	3.9	0
7175	Structure-preserving visualization for single-cell RNA-Seq profiles using deep manifold transformation with batch-correction. <i>Communications Biology</i> , 2023, 6, .	2.0	0
7176	Effect of age on the risk of immune-related adverse events in patients receiving immune checkpoint inhibitors. <i>Clinical and Experimental Medicine</i> , 2023, 23, 3907-3918.	1.9	5
7177	A Machine Learning Model to Predict Survival and Therapeutic Responses in Multiple Myeloma. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6683.	1.8	2
7179	Effects of 3 β -HAA on HCC by Regulating the Heterogeneous Macrophages—A scRNA-Seq Analysis. <i>Advanced Science</i> , 0, , .	5.6	1
7180	Activation of lineage competence in hemogenic endothelium precedes the formation of hematopoietic stem cell heterogeneity. <i>Cell Research</i> , 2023, 33, 448-463.	5.7	9
7181	Prerequisite endocardial-mesenchymal transition for murine cardiac trabecular angiogenesis. <i>Developmental Cell</i> , 2023, 58, 791-805.e4.	3.1	2

#	ARTICLE	IF	CITATIONS
7182	Diverse rescue potencies of p53 mutations to ATO are predetermined by intrinsic mutational properties. <i>Science Translational Medicine</i> , 2023, 15, .	5.8	13
7183	Nodal coordinates the anterior-posterior patterning of germ layers and induces head formation in zebrafish explants. <i>Cell Reports</i> , 2023, 42, 112351.	2.9	7
7184	Maintaining hypoxia environment of subchondral bone alleviates osteoarthritis progression. <i>Science Advances</i> , 2023, 9, .	4.7	27
7185	A Scd1-mediated metabolic alteration participates in liver responses to low-dose bavachin. <i>Journal of Pharmaceutical Analysis</i> , 2023, 13, 806-816.	2.4	3
7186	Integrative analysis of multi-omics data to identify three immune-related genes in the formation and progression of intracranial aneurysms. <i>Inflammation Research</i> , 2023, 72, 1001-1019.	1.6	2
7187	RBBP4 is an epigenetic barrier for the induced transition of pluripotent stem cells into totipotent 2C-like cells. <i>Nucleic Acids Research</i> , 2023, 51, 5414-5431.	6.5	3
7188	Expansion of macrophage and liver sinusoidal endothelial cell subpopulations during non-alcoholic steatohepatitis progression. <i>IScience</i> , 2023, 26, 106572.	1.9	3
7190	A senescence-based prognostic gene signature for colorectal cancer and identification of the role of SPP1-positive macrophages in tumor senescence. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	9
7191	Graded BMP signaling within intestinal crypt architecture directs self-organization of the Wnt-secreting stem cell niche. <i>Cell Stem Cell</i> , 2023, 30, 433-449.e8.	5.2	15
7192	Autoimmune Valvular Carditis Requires Endothelial Cell TNFR1 Expression. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 0, , .	1.1	0
7193	TREM2+ and interstitial-like macrophages orchestrate airway inflammation in SARS-CoV-2 infection in rhesus macaques. <i>Nature Communications</i> , 2023, 14, .	5.8	10
7194	Multi-omic analyses in immune cell development with lessons learned from T cell development. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	1.8	2
7195	Temporal tracking of microglial and monocyte single-cell transcriptomics in lethal flavivirus infection. <i>Acta Neuropathologica Communications</i> , 2023, 11, .	2.4	7
7196	N,N-Dimethyl-3 β -hydroxycholeamide attenuates neuronal death and retinal inflammation in retinal ischemia/reperfusion injury by inhibiting Ninjurin 1. <i>Journal of Neuroinflammation</i> , 2023, 20, .	3.1	2
7197	Immune landscape and the key role of APOE+ monocytes of lupus nephritis under the single-cell and spatial transcriptional vista. <i>Clinical and Translational Medicine</i> , 2023, 13, .	1.7	1
7198	Metabolic dysregulation impairs lymphocyte function during severe SARS-CoV-2 infection. <i>Communications Biology</i> , 2023, 6, .	2.0	3
7199	exFINDER: identify external communication signals using single-cell transcriptomics data. <i>Nucleic Acids Research</i> , 2023, 51, e58-e58.	6.5	2
7200	Regulation of c-SMAC formation and AKT-mTOR signaling by the TSG101-IFT20 axis in CD4+ T cells. , 0, , .		1

#	ARTICLE	IF	CITATIONS
7201	Standardization and Interpretation of RNA-sequencing for Transplantation. <i>Transplantation</i> , 2023, 107, 2155-2167.	0.5	3
7202	Myocardial Biomechanics and the Consequent Differentially Expressed Genes of the Left Atrial Ligation Chick Embryonic Model of Hypoplastic Left Heart Syndrome. <i>Annals of Biomedical Engineering</i> , 2023, 51, 1063-1078.	1.3	2
7203	Stratification of non-small cell lung adenocarcinoma patients with EGFR actionable mutations based on drug-resistant stem cell genes. <i>Science</i> , 2023, 26, 106584.	1.9	0
7204	IL17RB and IL17REL Expression Are Associated with Improved Prognosis in HPV-Infected Head and Neck Squamous Cell Carcinomas. <i>Pathogens</i> , 2023, 12, 572.	1.2	0
7205	Single-cell transcriptomics reveals immune infiltrate in sepsis. <i>Frontiers in Pharmacology</i> , 0, 14, .	1.6	0
7206	Single-cell analysis reveals novel clonally expanded monocytes associated with IL1 ^{hi} IL1R2 pair in acute inflammatory demyelinating polyneuropathy. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
7207	Multilineage commitment of Sca-1 ⁺ cells in reshaping vein grafts. <i>Theranostics</i> , 2023, 13, 2154-2175.	4.6	3
7208	Single-Cell RNA Sequencing for Studying Human Cancers. <i>Annual Review of Biomedical Data Science</i> , 2023, 6, .	2.8	2
7210	Targeting advanced prostate cancer with STEAP1 chimeric antigen receptor T cell and tumor-localized IL-12 immunotherapy. <i>Nature Communications</i> , 2023, 14, .	5.8	15
7211	Activation of AMPK promotes cardiac differentiation by stimulating the autophagy pathway. <i>Journal of Cell Communication and Signaling</i> , 2023, 17, 939-955.	1.8	2
7212	Distinctive Dynamics and Functions of the CD4 ⁺ CD25 ⁺ FOXP3 ⁺ Regulatory T Cell Population in Patients with Severe and Mild COVID-19. <i>Journal of Immunology</i> , 2023, 210, 1687-1699.	0.4	4
7215	Phenotypic plasticity and reduced tissue retention of exhausted tumor-infiltrating T _H 1 cells following neoadjuvant immunotherapy in head and neck cancer. <i>Cancer Cell</i> , 2023, 41, 887-902.e5.	7.7	13
7216	HILPDA promotes NASH-driven HCC development by restraining intracellular fatty acid flux in hypoxia. <i>Journal of Hepatology</i> , 2023, 79, 378-393.	1.8	8
7217	Research Progress of Single Cell Transcriptome Sequencing Technology in Cutaneous Malignant Melanoma. <i>Hans Journal of Biomedicine</i> , 2023, 13, 199-210.	0.0	0
7218	Stalled oligodendrocyte differentiation in IDH-mutant gliomas. <i>Genome Medicine</i> , 2023, 15, .	3.6	4
7219	Dandelion uses the single-cell adaptive immune receptor repertoire to explore lymphocyte developmental origins. <i>Nature Biotechnology</i> , 2024, 42, 40-51.	9.4	11
7220	Transcriptomic analysis identified SLC40A1 as a key iron metabolism-related gene in airway macrophages in childhood allergic asthma. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	1.8	1
7221	Single-Cell RNA Sequencing Analysis of Gene Regulatory Network Changes in the Development of Lung Adenocarcinoma. <i>Biomolecules</i> , 2023, 13, 671.	1.8	1

#	ARTICLE	IF	CITATIONS
7223	Single-cell RNA sequencing reveals new subtypes of lens superficial tissue in humans. <i>Cell Proliferation</i> , 2023, 56, .	2.4	2
7224	Hedgehog Signaling Regulates Treg to Th17 Conversion Through Metabolic Rewiring in Breast Cancer. <i>Cancer Immunology Research</i> , 2023, 11, 687-702.	1.6	7
7225	Platelet-derived factors dysregulate placental sphingosine-1-phosphate receptor 2 in human trophoblasts. <i>Reproductive BioMedicine Online</i> , 2023, , .	1.1	0
7226	Hepatocyte SREBP signaling mediates clock communication within the liver. <i>Journal of Clinical Investigation</i> , 2023, 133, .	3.9	5
7229	Bulk and single-cell transcriptome profiling reveal extracellular matrix mechanical regulation of lipid metabolism reprogramming through YAP/TEAD4/ACADL axis in hepatocellular carcinoma. <i>International Journal of Biological Sciences</i> , 2023, 19, 2114-2131.	2.6	8
7231	Hypoxia-inducible factor 1A inhibition overcomes castration resistance of prostate tumors. <i>EMBO Molecular Medicine</i> , 0, , .	3.3	4
7234	Lateral mammillary body neurons in mouse brain are disproportionately vulnerable in Alzheimer's disease. <i>Science Translational Medicine</i> , 2023, 15, .	5.8	1
7235	Dissecting order amidst chaos of programmed cell deaths: construction of a diagnostic model for KIRC using transcriptomic information in blood-derived exosomes and single-cell multi-omics data in tumor microenvironment. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	4
7236	Transcriptional re-programming of insulin B-chain epitope-specific T-follicular helper cells into anti-diabetogenic T-regulatory type-1 cells. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	1
7238	PI3K ² controls immune evasion in PTEN-deficient breast tumours. <i>Nature</i> , 2023, 617, 139-146.	13.7	12
7239	Identifying high-impact variants and genes in exomes of Ashkenazi Jewish inflammatory bowel disease patients. <i>Nature Communications</i> , 2023, 14, .	5.8	1
7240	Cell Cycle-Related FAM64A Could be Activated by TGF- β^2 Signaling to Promote Glioma Progression. <i>Cellular and Molecular Neurobiology</i> , 2023, 43, 2975-2987.	1.7	2
7241	Single-cell RNA sequencing reveals transcriptional profiles of monocytes in HBV-infected pregnant women during mid-pregnancy. <i>Journal of Cellular and Molecular Medicine</i> , 0, , .	1.6	0
7242	Large-Scale Integration of Single-Cell RNA-Seq Data Reveals Astrocyte Diversity and Transcriptomic Modules across Six Central Nervous System Disorders. <i>Biomolecules</i> , 2023, 13, 692.	1.8	4
7244	Autophagy-prominent cell clusters among human lens epithelial cells: integrated single-cell RNA-sequencing analysis. <i>BMC Ophthalmology</i> , 2023, 23, .	0.6	3
7245	Single-cell transcriptomic atlas of lung microvascular regeneration after targeted endothelial cell ablation. <i>ELife</i> , 0, 12, .	2.8	8
7246	Ubiquitin Ligases Siah1a/2 Control Alveolar Macrophage Functions to Limit Carcinogen-Induced Lung Adenocarcinoma. <i>Cancer Research</i> , 2023, 83, 2016-2033.	0.4	1
7247	Generative pretraining from large-scale transcriptomes for single-cell deciphering. <i>IScience</i> , 2023, 26, 106536.	1.9	4

#	ARTICLE	IF	CITATIONS
7255	Novel insight into the underlying dysregulation mechanisms of immune cell-to-cell communication by analyzing multitissue single-cell atlas of two COVID-19 patients. <i>Cell Death and Disease</i> , 2023, 14, .	2.7	3
7256	Single-cell analyses reveal cannabidiol rewires tumor microenvironment via inhibiting alternative activation of macrophage and synergizes with anti-PD-1 in colon cancer. <i>Journal of Pharmaceutical Analysis</i> , 2023, 13, 726-744.	2.4	5
7258	Single-cell analysis of immune cells on gingiva-derived mesenchymal stem cells in experimental autoimmune uveitis. <i>IScience</i> , 2023, 26, 106729.	1.9	3
7318	Single-cell transcriptomics of the ocular anterior segment: a comprehensive review. <i>Eye</i> , 0, , .	1.1	1
7331	Deep zero-inflated negative binomial model and its application in scRNA-seq data integration. , 2023, , .		0
7342	Single-cell and spatial transcriptomics: deciphering brain complexity in health and disease. <i>Nature Reviews Neurology</i> , 2023, 19, 346-362.	4.9	33
7394	Single-Cell mRNA Sequencing in Precision Medicine: Promise and Challenges. , 2024, , 59-72.		0
7447	Dimensionality Explorer for Single-Cell Analysis. , 2023, , .		1
7455	Single-Cell RNA Sequencing (scRNA-Seq) Data Analysis of Retinal Homeostasis and Degeneration of Microglia. <i>Methods in Molecular Biology</i> , 2023, , 91-106.	0.4	0
7491	Evaluation of Stem-Cell Embryo Models by Integration with a Human Embryo Single-Cell Transcriptome Atlas. <i>Methods in Molecular Biology</i> , 2023, , 213-250.	0.4	0
7594	Applying SCALEX scRNA-Seq Data Integration for Precise Alzheimer's Disease Biomarker Discovery. <i>IFIP Advances in Information and Communication Technology</i> , 2023, , 294-302.	0.5	0
7599	Multiplexed single-cell 3D spatial gene expression analysis in plant tissue using PHYTOmap. <i>Nature Plants</i> , 2023, 9, 1026-1033.	4.7	16
7693	Single-Cell Transcriptomic Profiling of Müller Glia in the rd10 Retina. <i>Advances in Experimental Medicine and Biology</i> , 2023, , 377-381.	0.8	1
7703	Progress in single-cell multimodal sequencing and multi-omics data integration. <i>Biophysical Reviews</i> , 0, , .	1.5	6
7708	Standardization of Single-Cell RNA-Sequencing Analysis Workflow to Study <i>Drosophila</i> Ovary. <i>Methods in Molecular Biology</i> , 2023, , 151-171.	0.4	0
7921	Dissecting key regulators of transcriptome kinetics through scalable single-cell RNA profiling of pooled CRISPR screens. <i>Nature Biotechnology</i> , 0, , .	9.4	3
7990	ESR: Optimizing Gene Feature Selection for scRNA-seq Data. , 2023, , .		0
8060	Prognosticating Drug Targets and Responses by Analyzing Metastasis-Related Cancer Pathways. , 2023, , 1-25.		0

#	ARTICLE	IF	CITATIONS
8107	Consensus Clustering Strategy for Cell Type Assignments of scRNA-seq Data. , 2023, , .		0
8132	Integrative Analysis of Gene Expression and Alternative Polyadenylation from Single-Cell RNA-seq Data. Lecture Notes in Computer Science, 2023, , 312-324.	1.0	0
8187	Combination of CRISPR-Cas9-RNP and Single-Cell RNAseq to Identify Cell State-Specific FOXJ1 Functions in the Human Airway Epithelium. Methods in Molecular Biology, 2024, , 1-25.	0.4	0
8188	The cellular states and fates of shed intestinal cells. Nature Metabolism, 0, , .	5.1	0
8195	Artificial intelligence and deep learning in molecular testing. , 2024, , 687-730.		0
8216	Computational immunogenomic approaches to predict response to cancer immunotherapies. Nature Reviews Clinical Oncology, 2024, 21, 28-46.	12.5	1
8268	Single Cell RNA-Sequencing and Its Application in Livestock Animals. , 2023, , 226-242.		0
8300	Deciphering the Cluster-Specific Marker Genes via Integration of Single Cell RNA Sequencing Datasets. , 2023, , .		0
8421	HDSCC: A robust clustering approach for Single Cell RNA-seq data using Hyperdimensional Encoding. , 2023, , .		0
8449	Breast cancer remotely imposes a myeloid bias on haematopoietic stem cells by reprogramming the bone marrow niche. Nature Cell Biology, 2023, 25, 1736-1745.	4.6	3
8486	Exploring the advances of single-cell RNA sequencing in thyroid cancer: a narrative review. , 2024, 41, .		0
8564	Single-Nucleus ATAC-seq for Mapping Chromatin Accessibility in Individual Cells of Murine Hearts. Methods in Molecular Biology, 2024, , 245-257.	0.4	0
8602	scBERC: A Batch Effect-Removed Clustering method for single-cell omics. , 2023, , .		0
8605	PLNorm: A Power-Law Distribution-Based Normalization Method for Single-Cell Hi-C Data Analysis. , 2023, , .		0
8606	Using Biological Processes as Prior Knowledge Identifies New Microglial Immune Signatures at Single Cell Level in Alzheimer's Disease. , 2023, , .		0
8607	Co-clustering of single-cell RNA-seq data based on weighted non-negative matrix tri-factorization combined with consensus clustering. , 2023, , .		0
8609	Spectral clustering based on multi-similarity learning method for single-cell RNA-seq data. , 2023, , .		0
8669	scGAT: A Cell-Type Annotation Framework for Single-Cell Transcriptomics Using Graph Attention Network and Meta Learning. , 2023, , .		0

#	ARTICLE	IF	CITATIONS
8755	Data Harmonization to Address the Non-biological Variances in Radiomic Studies. Imaging Informatics for Healthcare Professionals, 2023, , 95-115.	0.4	0
8756	SCpipeline: The Tool and Web Service for Identifying Potential Drug Targets Based on Single-Cell RNA Sequencing Data. IFMBE Proceedings, 2024, , 395-402.	0.2	0