

Single-cell RNA sequencing technologies and bioinform

Experimental and Molecular Medicine

50, 1-14

DOI: [10.1038/s12276-018-0071-8](https://doi.org/10.1038/s12276-018-0071-8)

Citation Report

#	ARTICLE	IF	CITATIONS
2	Omics Driven Understanding of the Intestines of Parasitic Nematodes. <i>Frontiers in Genetics</i> , 2019, 10, 652.	1.1	13
3	Recent advances in our understanding of central and peripheral nervous system progenitors. <i>Current Opinion in Cell Biology</i> , 2019, 61, 24-30.	2.6	6
4	Applications and Future Directions for Population Transcriptomics in Marine Invertebrates. <i>Current Molecular Biology Reports</i> , 2019, 5, 116-127.	0.8	14
5	The myriad possibility of kidney organoids. <i>Current Opinion in Nephrology and Hypertension</i> , 2019, 28, 211-218.	1.0	11
6	Eosinophils and Macrophages within the Th2-Induced Granuloma: Balancing Killing and Healing in a Tight Space. <i>Infection and Immunity</i> , 2019, 87, .	1.0	35
7	Internalization and accumulation of model lignin breakdown products in bacteria and fungi. <i>Biotechnology for Biofuels</i> , 2019, 12, 175.	6.2	10
8	Recent Progress in Single-Cell Sequencing. , 2019, , 21-34.		0
9	Exact and efficient hybrid Monte Carlo algorithm for accelerated Bayesian inference of gene expression models from snapshots of single-cell transcripts. <i>Journal of Chemical Physics</i> , 2019, 151, 024106.	1.2	9
10	Single-cell RNA sequencing of oocytes from ovarian endometriosis patients reveals a differential transcriptomic profile associated with lower quality. <i>Human Reproduction</i> , 2019, 34, 1302-1312.	0.4	61
11	Computational approaches for characterizing the tumor immune microenvironment. <i>Immunology</i> , 2019, 158, 70-84.	2.0	30
12	ACTINN: automated identification of cell types in single cell RNA sequencing. <i>Bioinformatics</i> , 2020, 36, 533-538.	1.8	140
13	Simultaneous Profiling of Gene Expression and Chromatin Accessibility in Single Cells. <i>Advanced Biology</i> , 2019, 3, 1900065.	3.0	37
14	Understanding <i>P. falciparum</i> Asymptomatic Infections: A Proposition for a Transcriptomic Approach. <i>Frontiers in Immunology</i> , 2019, 10, 2398.	2.2	27
15	Current Status and Potential Applications of Underexplored Prokaryotes. <i>Microorganisms</i> , 2019, 7, 468.	1.6	17
16	Single cell analysis to dissect molecular heterogeneity and disease evolution in metastatic melanoma. <i>Cell Death and Disease</i> , 2019, 10, 827.	2.7	35
17	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
18	Histone modifications and their regulatory roles in plant development and environmental memory. <i>Journal of Genetics and Genomics</i> , 2019, 46, 467-476.	1.7	76
19	Unravelling fibrosis using single-cell transcriptomics. <i>Current Opinion in Pharmacology</i> , 2019, 49, 71-75.	1.7	8

#	ARTICLE	IF	CITATIONS
20	Author's Reply. Journal of Thoracic Oncology, 2019, 14, e243-e244.	0.5	0
21	SCMarker: Ab initio marker selection for single cell transcriptome profiling. PLoS Computational Biology, 2019, 15, e1007445.	1.5	30
22	A single-cell Systems Biology approach for disease-specific subpathway extraction. , 2019, , .		0
23	Probabilistic cell-type assignment of single-cell RNA-seq for tumor microenvironment profiling. Nature Methods, 2019, 16, 1007-1015.	9.0	241
24	scBFA: modeling detection patterns to mitigate technical noise in large-scale single-cell genomics data. Genome Biology, 2019, 20, 193.	3.8	18
25	Label-Free Assay of Protein Tyrosine Phosphatase Activity in Single Cells. Analytical Chemistry, 2019, 91, 13206-13212.	3.2	8
26	Chromosome-wide co-fluctuation of stochastic gene expression in mammalian cells. PLoS Genetics, 2019, 15, e1008389.	1.5	20
27	Diesel exhaust particles dysregulate multiple immunological pathways in murine macrophages: Lessons from microarray and scRNA-seq technologies. Archives of Biochemistry and Biophysics, 2019, 678, 108116.	1.4	10
28	RNA-based qPCR as a tool to quantify and to characterize dual-species biofilms. Scientific Reports, 2019, 9, 13639.	1.6	25
29	Machine Learning and Integrative Analysis of Biomedical Big Data. Genes, 2019, 10, 87.	1.0	208
30	A 24 h Age Difference Causes Twice as Much Gene Expression Divergence as 100 Generations of Adaptation to a Novel Environment. Genes, 2019, 10, 89.	1.0	11
31	Arrhythmogenic cardiomyopathy: in search of unifying genetic theory. Cardiovascular Research, 2019, 115, 691-692.	1.8	0
32	OMIC Technologies and Vaccine Development: From the Identification of Vulnerable Individuals to the Formulation of Invulnerable Vaccines. Journal of Immunology Research, 2019, 2019, 1-10.	0.9	31
33	Information and Statistical Analysis Pipeline for High-Throughput RNA Sequencing Data. Methods in Molecular Biology, 2019, 2109, 199-208.	0.4	0
34	Expanding the single-cell genomics toolkit. Nature Genetics, 2019, 51, 931-932.	9.4	3
35	Deciphering the adult brain development complexity by single-cell transcriptome analysis—a review. Materials Today Chemistry, 2019, 13, 88-97.	1.7	1
36	Application of single-cell RNA sequencing methodologies in understanding haematopoiesis and immunology. Essays in Biochemistry, 2019, 63, 217-225.	2.1	16
37	Molecular genetic testing methodologies in hematopoietic diseases: current and future methods. International Journal of Laboratory Hematology, 2019, 41, 102-116.	0.7	10

#	ARTICLE	IF	CITATIONS
38	Single-Cell RNA-Sequencing Identifies Activation of TP53 and STAT1 Pathways in Human T Lymphocyte Subpopulations in Response to Ex Vivo Radiation Exposure. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2316.	1.8	10
39	What has single-cell RNA-seq taught us about mammalian spermatogenesis?. <i>Biology of Reproduction</i> , 2019, 101, 617-634.	1.2	46
40	Dean Flow Assisted Single Cell and Bead Encapsulation for High Performance Single Cell Expression Profiling. <i>ACS Sensors</i> , 2019, 4, 1299-1305.	4.0	34
41	Single identical cell toxicity assay on coordinately ordered patterns. <i>Analytica Chimica Acta</i> , 2019, 1065, 56-63.	2.6	2
42	RNA-sequencing in ophthalmology research: considerations for experimental design and analysis. <i>Therapeutic Advances in Ophthalmology</i> , 2019, 11, 251584141983546.	0.8	6
43	Single-Cell RNA-Seq Technologies and Related Computational Data Analysis. <i>Frontiers in Genetics</i> , 2019, 10, 317.	1.1	611
44	Droplet-based single cell RNAseq tools: a practical guide. <i>Lab on A Chip</i> , 2019, 19, 1706-1727.	3.1	77
45	Single-Cell RNA Sequencing Resolves Molecular Relationships Among Individual Plant Cells. <i>Plant Physiology</i> , 2019, 179, 1444-1456.	2.3	348
46	Dissecting CLL through high-dimensional single-cell technologies. <i>Blood</i> , 2019, 133, 1446-1456.	0.6	5
47	Single cell immune profiling in transplantation research. <i>American Journal of Transplantation</i> , 2019, 19, 1278-1287.	2.6	7
48	Exploring the RNA Gap for Improving Diagnostic Yield in Primary Immunodeficiencies. <i>Frontiers in Genetics</i> , 2019, 10, 1204.	1.1	3
49	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
50	Deep generative autoencoder for low-dimensional embedding extraction from single-cell RNAseq data. , 2019, , .		3
51	Analysis of RNA-Seq Data of 10000 Samples of Single-cell Transcriptome. , 2019, , .		0
52	Systematic comparative analysis of single-nucleotide variant detection methods from single-cell RNA sequencing data. <i>Genome Biology</i> , 2019, 20, 242.	3.8	80
53	Single-Cell RNA Sequencing of Plant-Associated Bacterial Communities. <i>Frontiers in Microbiology</i> , 2019, 10, 2452.	1.5	10
54	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
55	Epigenetics and the dynamics of chromatin during adenovirus infections. <i>FEBS Letters</i> , 2019, 593, 3551-3570.	1.3	25

#	ARTICLE	IF	CITATIONS
56	<i>MRAS</i> Variants Cause Cardiomyocyte Hypertrophy in Patient-Specific Induced Pluripotent Stem Cell-Derived Cardiomyocytes. <i>Circulation Genomic and Precision Medicine</i> , 2019, 12, e002648.	1.6	16
57	Transcriptome Signature Reversion as a Method to Reposition Drugs Against Cancer for Precision Oncology. <i>Cancer Journal (Sudbury, Mass)</i> , 2019, 25, 116-120.	1.0	9
58	High-throughput dense reconstruction of cell lineages. <i>Open Biology</i> , 2019, 9, 190229.	1.5	21
60	How to get smarter about medical intervention. <i>Lancet, The</i> , 2019, 394, 2146-2147.	6.3	0
61	Mass Cytometry Imaging for the Study of Human Diseases—Applications and Data Analysis Strategies. <i>Frontiers in Immunology</i> , 2019, 10, 2657.	2.2	139
62	Visualizing structure and transitions in high-dimensional biological data. <i>Nature Biotechnology</i> , 2019, 37, 1482-1492.	9.4	597
63	Single-Cell RNA Sequencing of the Cardiovascular System: New Looks for Old Diseases. <i>Frontiers in Cardiovascular Medicine</i> , 2019, 6, 173.	1.1	47
64	The end of omics? High dimensional single cell analysis in precision medicine. <i>European Journal of Immunology</i> , 2019, 49, 212-220.	1.6	33
65	New frontiers in precision medicine for sepsis-induced immunoparalysis. <i>Expert Review of Clinical Immunology</i> , 2019, 15, 251-263.	1.3	21
66	Modeling genetic epilepsies in a dish. <i>Developmental Dynamics</i> , 2020, 249, 56-75.	0.8	27
67	100 Years of evolving gene—disease complexities and scientific debutants. <i>Briefings in Bioinformatics</i> , 2020, 21, 885-905.	3.2	36
68	Single-cell RNA-Seq: a next generation sequencing tool for a high-resolution view of the individual cell. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 3730-3735.	2.0	2
69	A systems approach to clinical oncology uses deep phenotyping to deliver personalized care. <i>Nature Reviews Clinical Oncology</i> , 2020, 17, 183-194.	12.5	41
70	Transcriptomic Analysis of Cellular Pathways in Healing Flexor Tendons of Plasminogen Activator Inhibitor 1 (PAI-1/Serpine1) Null Mice. <i>Journal of Orthopaedic Research</i> , 2020, 38, 43-58.	1.2	15
71	A paradigm shift in medicine: A comprehensive review of network-based approaches. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194416.	0.9	60
72	Bringing Microscopy-By-Sequencing into View. <i>Trends in Biotechnology</i> , 2020, 38, 154-162.	4.9	10
73	Alternative Splicing of ALS Genes: Misregulation and Potential Therapies. <i>Cellular and Molecular Neurobiology</i> , 2020, 40, 1-14.	1.7	28
74	QUBIC2: a novel and robust biclustering algorithm for analyses and interpretation of large-scale RNA-Seq data. <i>Bioinformatics</i> , 2020, 36, 1143-1149.	1.8	46

#	ARTICLE	IF	CITATIONS
75	Recent progress and challenges in drug development to fight hand, foot and mouth disease. Expert Opinion on Drug Discovery, 2020, 15, 359-371.	2.5	18
76	Elevating pancreatic cystic lesion stratification: Current and future pancreatic cancer biomarker(s). Biochimica Et Biophysica Acta: Reviews on Cancer, 2020, 1873, 188318.	3.3	28
77	Biological computing. , 2020, , 81-104.		0
78	A Single Cell but Many Different Transcripts: A Journey into the World of Long Non-Coding RNAs. International Journal of Molecular Sciences, 2020, 21, 302.	1.8	45
79	Translating "big data": better understanding of host-pathogen interactions to control bacterial foodborne pathogens in poultry. Animal Health Research Reviews, 2020, 21, 15-35.	1.4	11
80	Systems biology and big data in asthma and allergy: recent discoveries and emerging challenges. European Respiratory Journal, 2020, 55, 1900844.	3.1	22
81	New insights into human beta cell biology using human pluripotent stem cells. Seminars in Cell and Developmental Biology, 2020, 103, 31-40.	2.3	15
82	Preserving single cells in space and time for analytical assays. TrAC - Trends in Analytical Chemistry, 2020, 122, 115723.	5.8	4
83	Understanding osteoarthritis pathogenesis: a multiomics system-based approach. Current Opinion in Rheumatology, 2020, 32, 80-91.	2.0	35
84	Data generation and network reconstruction strategies for single cell transcriptomic profiles of CRISPR-mediated gene perturbations. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194441.	0.9	4
85	Biomaterials as Tools to Decode Immunity. Advanced Materials, 2020, 32, e1903367.	11.1	36
86	Semisupervised Generative Autoencoder for Single-Cell Data. Journal of Computational Biology, 2020, 27, 1190-1203.	0.8	12
87	Identification and characterization of a large source of primary mesenchymal stem cells tightly adhered to bone surfaces of human vertebral body marrow cavities. Cytotherapy, 2020, 22, 617-628.	0.3	9
88	What has single-cell RNA sequencing revealed about microglial neuroimmunology?. Immunity, Inflammation and Disease, 2020, 8, 825-839.	1.3	18
89	Expression of Angiogenic Proteins in Tumor and Stroma Affects Survival in Patients With Gastric Cancer. Journal of Surgical Research, 2020, 255, 172-180.	0.8	3
90	Genomics-based immuno-oncology: bridging the gap between immunology and tumor biology. Human Molecular Genetics, 2020, 29, R214-R225.	1.4	3
91	Single cell sequencing unraveling genetic basis of severe COVID19 in obesity. Obesity Medicine, 2020, 20, 100303.	0.5	12
92	The Whole Body as the System in Systems Immunology. IScience, 2020, 23, 101509.	1.9	24

#	ARTICLE	IF	CITATIONS
93	Assessing Cell Activities rather than Identities to Interpret Intra-Tumor Phenotypic Diversity and Its Dynamics. <i>IScience</i> , 2020, 23, 101061.	1.9	1
94	Lessons from single cell sequencing in CNS cell specification and function. <i>Current Opinion in Genetics and Development</i> , 2020, 65, 138-143.	1.5	11
95	Single-cell network biology for resolving cellular heterogeneity in human diseases. <i>Experimental and Molecular Medicine</i> , 2020, 52, 1798-1808.	3.2	72
96	NRF2 and the Ambiguous Consequences of Its Activation during Initiation and the Subsequent Stages of Tumorigenesis. <i>Cancers</i> , 2020, 12, 3609.	1.7	44
97	Microglia Diversity in Health and Multiple Sclerosis. <i>Frontiers in Immunology</i> , 2020, 11, 588021.	2.2	44
98	Application of single-cell RNA sequencing in embryonic development. <i>Genomics</i> , 2020, 112, 4547-4551.	1.3	8
99	Advances in single cell technologies in immunology. <i>BioTechniques</i> , 2020, 69, 226-236.	0.8	9
100	Self-Reporting Transposons Enable Simultaneous Readout of Gene Expression and Transcription Factor Binding in Single Cells. <i>Cell</i> , 2020, 182, 992-1008.e21.	13.5	54
101	Cancer-associated fibroblasts of colorectal cancer and their markers: updates, challenges and translational outlook. <i>Future Oncology</i> , 2020, 16, 2329-2344.	1.1	13
102	Unraveling the Complexity of the Cancer Microenvironment With Multidimensional Genomic and Cytometric Technologies. <i>Frontiers in Oncology</i> , 2020, 10, 1254.	1.3	45
103	Carbon Nanotubes under Scrutiny: Their Toxicity and Utility in Mesothelioma Research. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 4513.	1.3	9
104	scTyper: a comprehensive pipeline for the cell typing analysis of single-cell RNA-seq data. <i>BMC Bioinformatics</i> , 2020, 21, 342.	1.2	19
105	Single-Cell Heterogeneity of Cutaneous T-Cell Lymphomas Revealed Using RNA-Seq Technologies. <i>Cancers</i> , 2020, 12, 2129.	1.7	9
106	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
107	Comparative transcriptomics implicate mitochondrial and neurodevelopmental impairments in larval zebrafish (<i>Danio rerio</i>) exposed to two selective serotonin reuptake inhibitors (SSRIs). <i>Ecotoxicology and Environmental Safety</i> , 2020, 203, 110934.	2.9	13
108	Genomic Cytometry and New Modalities for Deep Single-Cell Interrogation. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2020, 97, 1007-1016.	1.1	2
109	Biomaterial strategies for creating in vitro astrocyte cultures resembling in vivo astrocyte morphologies and phenotypes. <i>Current Opinion in Biomedical Engineering</i> , 2020, 14, 67-74.	1.8	7
110	The future of microfluidics in immune checkpoint blockade. <i>Cancer Gene Therapy</i> , 2021, 28, 895-910.	2.2	8

#	ARTICLE	IF	CITATIONS
111	A review of computational strategies for denoising and imputation of single-cell transcriptomic data. Briefings in Bioinformatics, 2021, 22, .	3.2	27
112	Single-cell transcriptomics in dermatology. JAAD International, 2020, 1, 182-188.	1.1	4
113	Divergent Resistance Mechanisms to Immunotherapy Explain Responses in Different Skin Cancers. Cancers, 2020, 12, 2946.	1.7	6
114	Cancer SLC43A2 alters T cell methionine metabolism and histone methylation. Nature, 2020, 585, 277-282.	13.7	280
115	Transcriptomic profiling in Cutaneous Leishmaniasis patients. Expert Review of Proteomics, 2020, 17, 533-541.	1.3	4
116	Analyzing One Cell at a TIME: Analysis of Myeloid Cell Contributions in the Tumor Immune Microenvironment. Frontiers in Immunology, 2020, 11, 1842.	2.2	28
117	Genomic, proteomic, and systems biology approaches in biomarker discovery for multiple sclerosis. Cellular Immunology, 2020, 358, 104219.	1.4	12
118	Bioorthogonal chemistry-based RNA labeling technologies: evolution and current state. Chemical Communications, 2020, 56, 12307-12318.	2.2	20
119	Tuning parameters of dimensionality reduction methods for single-cell RNA-seq analysis. Genome Biology, 2020, 21, 212.	3.8	18
120	Single-cell transcriptomics in cancer: computational challenges and opportunities. Experimental and Molecular Medicine, 2020, 52, 1452-1465.	3.2	108
121	Analysis of single-cell transcriptomes links enrichment of olfactory receptors with cancer cell differentiation status and prognosis. Communications Biology, 2020, 3, 506.	2.0	18
122	Single-cell multiomics: technologies and data analysis methods. Experimental and Molecular Medicine, 2020, 52, 1428-1442.	3.2	287
123	Single-cell RNA sequencing in <i>Drosophila</i> : Technologies and applications. Wiley Interdisciplinary Reviews: Developmental Biology, 2021, 10, e396.	5.9	47
124	Tempora: Cell trajectory inference using time-series single-cell RNA sequencing data. PLoS Computational Biology, 2020, 16, e1008205.	1.5	49
125	Ion Channel Profiling in Prostate Cancer: Toward Cell Population-Specific Screening. Reviews of Physiology, Biochemistry and Pharmacology, 2020, , 39-56.	0.9	4
126	Pinpointing Cell Identity in Time and Space. Frontiers in Molecular Biosciences, 2020, 7, 209.	1.6	15
127	PCR past, present and future. BioTechniques, 2020, 69, 317-325.	0.8	156
128	The Malignant Role of Exosomes as Nanocarriers of Rare RNA Species. International Journal of Molecular Sciences, 2020, 21, 5866.	1.8	16

#	ARTICLE	IF	CITATIONS
129	Detecting Interactive Gene Groups for Single-Cell RNA-Seq Data Based on Co-Expression Network Analysis and Subgraph Learning. <i>Cells</i> , 2020, 9, 1938.	1.8	11
130	Goals and approaches for each processing step for single-cell RNA sequencing data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	31
131	DrivAER: Identification of driving transcriptional programs in single-cell RNA sequencing data. <i>GigaScience</i> , 2020, 9, .	3.3	10
132	Identification of diverse cell populations in skeletal muscles and biomarkers for intramuscular fat of chicken by single-cell RNA sequencing. <i>BMC Genomics</i> , 2020, 21, 752.	1.2	24
133	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
134	Functional module detection through integration of single-cell RNA sequencing data with protein-protein interaction networks. <i>BMC Genomics</i> , 2020, 21, 756.	1.2	13
135	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
136	Gene regulatory network reconstruction using single-cell RNA sequencing of barcoded genotypes in diverse environments. <i>ELife</i> , 2020, 9, .	2.8	116
137	Single-cell sequencing of miRNAs: A modified technology. <i>Cell Biology International</i> , 2020, 44, 1773-1780.	1.4	8
138	BIOMEX: an interactive workflow for (single cell) omics data interpretation and visualization. <i>Nucleic Acids Research</i> , 2020, 48, W385-W394.	6.5	43
139	Single-Cell RNA Sequencing and Its Combination with Protein and DNA Analyses. <i>Cells</i> , 2020, 9, 1130.	1.8	42
140	Vector Copy Distribution at a Single-Cell Level Enhances Analytical Characterization of Gene-Modified Cell Therapies. <i>Molecular Therapy - Methods and Clinical Development</i> , 2020, 17, 944-956.	1.8	15
141	The promise of single-cell genomics in plants. <i>Current Opinion in Plant Biology</i> , 2020, 54, 114-121.	3.5	26
142	MAPS-seq: magnetic bead-assisted parallel single-cell gene expression profiling. <i>Experimental and Molecular Medicine</i> , 2020, 52, 804-814.	3.2	5
143	Single cell transcriptomics reveals opioid usage evokes widespread suppression of antiviral gene program. <i>Nature Communications</i> , 2020, 11, 2611.	5.8	39
144	Data-based RNA-seq simulations by binomial thinning. <i>BMC Bioinformatics</i> , 2020, 21, 206.	1.2	20
145	scTPA: a web tool for single-cell transcriptome analysis of pathway activation signatures. <i>Bioinformatics</i> , 2020, 36, 4217-4219.	1.8	21
146	Application of information theoretical approaches to assess diversity and similarity in single-cell transcriptomics. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1830-1837.	1.9	11

#	ARTICLE	IF	CITATIONS
147	Adipogenesis, Osteogenesis, and Chondrogenesis of Human Mesenchymal Stem/Stromal Cells: A Comparative Transcriptome Approach. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 561.	1.8	73
148	Towards systems tissue engineering: Elucidating the dynamics, spatial coordination, and individual cells driving emergent behaviors. <i>Biomaterials</i> , 2020, 255, 120189.	5.7	8
149	Physiology-forward identification of bile acid-sensitive vomeronasal receptors. <i>Science Advances</i> , 2020, 6, eaaz6868.	4.7	11
150	Single-cell ATAC sequencing analysis: From data preprocessing to hypothesis generation. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1429-1439.	1.9	91
151	Machine learning approaches to drug response prediction: challenges and recent progress. <i>Npj Precision Oncology</i> , 2020, 4, 19.	2.3	170
152	Comparative performance of the BGI and Illumina sequencing technology for single-cell RNA-sequencing. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa034.	1.5	37
153	Single-Cell Classification Using Mass Spectrometry through Interpretable Machine Learning. <i>Analytical Chemistry</i> , 2020, 92, 9338-9347.	3.2	51
154	Analysis of cell-associated DENV RNA by oligo(dT) primed 5â€™ capture scRNAseq. <i>Scientific Reports</i> , 2020, 10, 9047.	1.6	7
155	Mosquito-Borne Viral Diseases: Control and Prevention in the Genomics Era. , 2020, , .		1
156	A flexible network-based imputing-and-fusing approach towards the identification of cell types from single-cell RNA-seq data. <i>BMC Bioinformatics</i> , 2020, 21, 240.	1.2	2
157	Single-cell genomics and spatial transcriptomics: Discovery of novel cell states and cellular interactions in liver physiology and disease biology. <i>Journal of Hepatology</i> , 2020, 73, 1219-1230.	1.8	156
158	Projected t-SNE for batch correction. <i>Bioinformatics</i> , 2020, 36, 3522-3527.	1.8	10
159	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
160	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
161	Single-Cell Approaches to Profile the Response to Immune Checkpoint Inhibitors. <i>Frontiers in Immunology</i> , 2020, 11, 490.	2.2	38
162	Modulation of tumor microenvironment for immunotherapy: focus on nanomaterial-based strategies. <i>Theranostics</i> , 2020, 10, 3099-3117.	4.6	70
163	Integrative Methods and Practical Challenges for Single-Cell Multi-omics. <i>Trends in Biotechnology</i> , 2020, 38, 1007-1022.	4.9	149
164	Single-cell RNA sequencing in cardiovascular development, disease and medicine. <i>Nature Reviews Cardiology</i> , 2020, 17, 457-473.	6.1	174

#	ARTICLE	IF	CITATIONS
165	National Cancer Institute Think-Tank Meeting Report on Proteomic Cartography and Biomarkers at the Single-Cell Level: Interrogation of Premalignant Lesions. <i>Journal of Proteome Research</i> , 2020, 19, 1900-1912.	1.8	8
166	Induced pluripotent stem cells as models of human neurodevelopmental disorders. , 2020, , 99-127.		0
167	Temporal Dynamics and Heterogeneity of Cell Populations during Skeletal Muscle Regeneration. <i>IScience</i> , 2020, 23, 100993.	1.9	151
168	Pharmacogenomics for immunotherapy and immune-related cardiotoxicity. <i>Human Molecular Genetics</i> , 2020, 29, R186-R196.	1.4	7
169	Understanding the Molecular Mechanisms of Asthma through Transcriptomics. <i>Allergy, Asthma and Immunology Research</i> , 2020, 12, 399.	1.1	17
170	Vascular Homeostasis and Inflammation in Health and Disease—Lessons from Single Cell Technologies. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4688.	1.8	17
171	IL-7 receptor alpha defines heterogeneity and signature of human effector memory CD8+ T cells in high dimensional analysis. <i>Cellular Immunology</i> , 2020, 355, 104155.	1.4	7
172	Single-cell RNA sequencing in breast cancer: Understanding tumor heterogeneity and paving roads to individualized therapy. <i>Cancer Communications</i> , 2020, 40, 329-344.	3.7	110
173	Barrel cortex VIP/ChAT interneurons suppress sensory responses in vivo. <i>PLoS Biology</i> , 2020, 18, e3000613.	2.6	19
174	Comparative Transcriptome Analyses during the Vegetative Cell Cycle in the Mono-Cellular Organism <i>Pseudokronopsis erythrina</i> (Alveolata, Ciliophora). <i>Microorganisms</i> , 2020, 8, 108.	1.6	13
175	Single-Cell RNA Sequencing in Human Retinal Degeneration Reveals Distinct Glial Cell Populations. <i>Cells</i> , 2020, 9, 438.	1.8	35
176	Survival-Associated Metabolic Genes in Human Papillomavirus-Positive Head and Neck Cancers. <i>Cancers</i> , 2020, 12, 253.	1.7	40
177	Beyond mass spectrometry, the next step in proteomics. <i>Science Advances</i> , 2020, 6, eaax8978.	4.7	208
178	The Transcriptome of Hepatic Fibrosis Revealed by Single-cell RNA Sequencing. <i>Hepatology</i> , 2020, 71, 1865-1867.	3.6	8
179	Taking Insect Immunity to the Single-Cell Level. <i>Trends in Immunology</i> , 2020, 41, 190-199.	2.9	10
180	Roles of Brassinosteroids in Plant Reproduction. <i>International Journal of Molecular Sciences</i> , 2020, 21, 872.	1.8	59
181	Ecotype differences in aggression, neural activity and behaviorally relevant gene expression in cichlid fish. <i>Genes, Brain and Behavior</i> , 2020, 19, e12657.	1.1	24
182	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

#	ARTICLE	IF	CITATIONS
183	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
184	Tunable Bidirectional Electroosmotic Flow for Diffusion-Based Separations. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 12894-12899.	7.2	4
185	A restriction enzyme reduced representation sequencing approach for low-cost, high-throughput metagenome profiling. <i>PLoS ONE</i> , 2020, 15, e0219882.	1.1	23
186	A comparison of methods accounting for batch effects in differential expression analysis of UMI count based single cell RNA sequencing. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 861-873.	1.9	28
187	Metabolic changes in human brain evolution. <i>Evolutionary Anthropology</i> , 2020, 29, 201-211.	1.7	8
188	The Genetics of Epilepsy. <i>Annual Review of Genomics and Human Genetics</i> , 2020, 21, 205-230.	2.5	116
189	Harnessing genomics to fast-track genetic improvement in aquaculture. <i>Nature Reviews Genetics</i> , 2020, 21, 389-409.	7.7	286
190	Computational Oncology in the Multi-Omics Era: State of the Art. <i>Frontiers in Oncology</i> , 2020, 10, 423.	1.3	59
191	Tunable Bidirectional Electroosmotic Flow for Diffusion-Based Separations. <i>Angewandte Chemie</i> , 2020, 132, 12994-12999.	1.6	3
192	Post-genomic progress in helminth parasitology. <i>Parasitology</i> , 2020, 147, 835-840.	0.7	24
193	Multiplexed Cre-dependent selection yields systemic AAVs for targeting distinct brain cell types. <i>Nature Methods</i> , 2020, 17, 541-550.	9.0	121
194	Revealing cell fate decisions during reprogramming by scRNA-seq. <i>E3S Web of Conferences</i> , 2020, 145, 01033.	0.2	0
195	Environmental Carcinogenesis at the Single-Cell Level. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1880-1886.	1.1	1
196	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
197	Comparison of high-throughput single-cell RNA sequencing data processing pipelines. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	16
198	Rethinking embryology in vitro: A synergy between engineering, data science and theory. <i>Developmental Biology</i> , 2021, 474, 48-61.	0.9	15
199	Taming human brain organoids one cell at a time. <i>Seminars in Cell and Developmental Biology</i> , 2021, 111, 23-31.	2.3	14
200	Ensemble learning models that predict surface protein abundance from single-cell multimodal omics data. <i>Methods</i> , 2021, 189, 65-73.	1.9	13

#	ARTICLE	IF	CITATIONS
201	Stem cellâ€intrinsic mechanisms regulating adult hair follicle homeostasis. <i>Experimental Dermatology</i> , 2021, 30, 430-447.	1.4	30
202	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
203	LnCeCell: a comprehensive database of predicted lncRNA-associated ceRNA networks at single-cell resolution. <i>Nucleic Acids Research</i> , 2021, 49, D125-D133.	6.5	42
204	Origin and fine-tuning of effector CD8 T cell subpopulations in chronic infection. <i>Current Opinion in Virology</i> , 2021, 46, 27-35.	2.6	4
205	Benchmarking Computational Doublet-Detection Methods for Single-Cell RNA Sequencing Data. <i>Cell Systems</i> , 2021, 12, 176-194.e6.	2.9	99
206	Recent advances in singleâ€cell multimodal analysis to study immune cells. <i>Immunology and Cell Biology</i> , 2021, 99, 157-167.	1.0	4
207	Tribo-informatics: Concept, architecture, and case study. <i>Friction</i> , 2021, 9, 642-655.	3.4	38
208	Single nucleus transcriptomics data integration recapitulates the major cell types in human liver. <i>Hepatology Research</i> , 2021, 51, 233-238.	1.8	7
209	<i>TEngExA</i> : an R package based tool for tissue enrichment and gene expression analysis. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	4
210	Nanoelectrochemical quantification of single-cell metabolism. <i>Analytical and Bioanalytical Chemistry</i> , 2021, 413, 17-24.	1.9	22
211	Systematic determination of the mitochondrial proportion in human and mice tissues for single-cell RNA-sequencing data quality control. <i>Bioinformatics</i> , 2021, 37, 963-967.	1.8	80
212	A single-cell map for the transcriptomic signatures of peripheral blood mononuclear cells in end-stage renal disease. <i>Nephrology Dialysis Transplantation</i> , 2021, 36, 599-608.	0.4	13
213	SCDC: bulk gene expression deconvolution by multiple single-cell RNA sequencing references. <i>Briefings in Bioinformatics</i> , 2021, 22, 416-427.	3.2	156
215	Time-course single-cell RNA sequencing reveals transcriptional dynamics and heterogeneity of limbal stem cells derived from human pluripotent stem cells. <i>Cell and Bioscience</i> , 2021, 11, 24.	2.1	6
216	The Methods and Tools for Molecular Network Construction. , 2021, , 14-28.		0
217	Bioinformatic Analysis of Differentially Expressed Genes (DEGs) Detected from RNA-Sequence Profiles of Mouse Striatum. , 2021, , 101-122.		0
218	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
219	The Molecular Genetics of Marfan Syndrome. <i>International Journal of Medical Sciences</i> , 2021, 18, 2752-2766.	1.1	23

#	ARTICLE	IF	CITATIONS
220	Cell Subtype Classification via Representation Learning Based on a Denoising Autoencoder for Single-Cell RNA Sequencing. IEEE Access, 2021, 9, 14540-14548.	2.6	4
221	Design and Analysis of RNA Sequencing Data. Learning Materials in Biosciences, 2021, , 143-175.	0.2	0
222	Single-Cell Sequencing and Organoids: A Powerful Combination for Modelling Organ Development and Diseases. Reviews of Physiology, Biochemistry and Pharmacology, 2021, 179, 189-210.	0.9	15
223	scDA: Single cell discriminant analysis for single-cell RNA sequencing data. Computational and Structural Biotechnology Journal, 2021, 19, 3234-3244.	1.9	3
225	Longitudinal Intravital Imaging of Tumor-Infiltrating Lymphocyte Motility in Breast Cancer Models. Journal of Breast Cancer, 2021, 24, 463-473.	0.8	1
226	Dynamic single-cell RNA sequencing identifies immunotherapy persister cells following PD-1 blockade. Journal of Clinical Investigation, 2021, 131, .	3.9	35
227	The Road to Effective Cancer Immunotherapy—A Computational Perspective on Tumor Epitopes in Anti-Cancer Immunotherapy. , 2021, , 593-607.		0
228	Systems immunology of flavivirus infection. , 2021, , 221-234.		2
229	Single-Cell RNA Sequencing Technology and Its Application in Embryonic Development. Medical Diagnosis, 2021, 11, 113-119.	0.0	0
230	Single-Cell RNA Sequencing Technologies. , 2021, , 555-584.		0
231	Single-Cell Technologies in Parkinson's Disease. , 2021, , 15-30.		0
232	XenoCell: classification of cellular barcodes in single cell experiments from xenograft samples. BMC Medical Genomics, 2021, 14, 34.	0.7	8
233	Novel application of single-cell next-generation sequencing for determination of intratumoral heterogeneity of canine osteosarcoma cell lines. Journal of Veterinary Diagnostic Investigation, 2021, 33, 261-278.	0.5	15
234	Alternative splicing: Human disease and quantitative analysis from high-throughput sequencing. Computational and Structural Biotechnology Journal, 2021, 19, 183-195.	1.9	57
235	Inference of Gene Regulatory Network from Single-Cell Transcriptomic Data Using pySCENIC. Methods in Molecular Biology, 2021, 2328, 171-182.	0.4	25
236	Single-Cell RNA Sequencing Analysis: A Step-by-Step Overview. Methods in Molecular Biology, 2021, 2284, 343-365.	0.4	65
237	Boron: More Than an Essential Element for Land Plants?. Frontiers in Plant Science, 2020, 11, 610307.	1.7	35
238	FOntCell: Fusion of Ontologies of Cells. Frontiers in Cell and Developmental Biology, 2021, 9, 562908.	1.8	0

#	ARTICLE	IF	CITATIONS
239	New tools for "ZEBRA-FISHING"™. Briefings in Functional Genomics, 2021, , .	1.3	0
240	Flexible comparison of batch correction methods for single-cell RNA-seq using BatchBench. Nucleic Acids Research, 2021, 49, e42-e42.	6.5	41
241	The origin of animals: an ancestral reconstruction of the unicellular-to-multicellular transition. Open Biology, 2021, 11, 200359.	1.5	67
242	Finding needles in a haystack: dissecting tumor heterogeneity with single-cell transcriptomic and chromatin accessibility profiling. Current Opinion in Genetics and Development, 2021, 66, 36-40.	1.5	5
244	Progress and Clinical Application of Single-Cell Transcriptional Sequencing Technology in Cancer Research. Frontiers in Oncology, 2020, 10, 593085.	1.3	18
245	Integrative clustering methods for multi-omics data. Wiley Interdisciplinary Reviews: Computational Statistics, 2022, 14, e1553.	2.1	7
246	RNA Based Approaches to Profile Oncogenic Pathways From Low Quantity Samples to Drive Precision Oncology Strategies. Frontiers in Genetics, 2020, 11, 598118.	1.1	18
247	Enabling single-cell trajectory network enrichment. Nature Computational Science, 2021, 1, 153-163.	3.8	5
248	Spatially mapped single-cell chromatin accessibility. Nature Communications, 2021, 12, 1274.	5.8	53
249	Single-Cell RNA Sequencing of the Adult Mammalian Heart"State-of-the-Art and Future Perspectives. Current Heart Failure Reports, 2021, 18, 64-70.	1.3	10
250	CellWalker integrates single-cell and bulk data to resolve regulatory elements across cell types in complex tissues. Genome Biology, 2021, 22, 61.	3.8	13
251	Unraveling the cartography of the cancer ecosystem. Genome Biology, 2021, 22, 87.	3.8	4
252	Multiplexed Analysis of Retinal Gene Expression and Chromatin Accessibility Using scRNA-Seq and scATAC-Seq. Journal of Visualized Experiments, 2021, , .	0.2	2
253	Estimating and Correcting for Off-Target Cellular Contamination in Brain Cell Type Specific RNA-Seq Data. Frontiers in Molecular Neuroscience, 2021, 14, 637143.	1.4	7
254	Single-cell RNA sequencing in cancer research. Journal of Experimental and Clinical Cancer Research, 2021, 40, 81.	3.5	128
255	Single Cell Transcriptome Data Analysis Defines the Heterogeneity of Peripheral Nerve Cells in Homeostasis and Regeneration. Frontiers in Cellular Neuroscience, 2021, 15, 624826.	1.8	34
256	Next-Generation Sequencing Reveals the Progression of COVID-19. Frontiers in Cellular and Infection Microbiology, 2021, 11, 632490.	1.8	35
258	A survey of dimension reduction and classification methods for RNA-Seq data on malaria vector. Journal of Big Data, 2021, 8, .	6.9	17

#	ARTICLE	IF	CITATIONS
259	Mass molecular testing for COVID19 using NGS-based technology and a highly scalable workflow. <i>Scientific Reports</i> , 2021, 11, 7122.	1.6	12
260	Modeling dynamic correlation in zero-inflated bivariate count data with applications to single-cell RNA sequencing data. <i>Biometrics</i> , 2022, 78, 766-776.	0.8	4
261	Characterization of CRISPR/Cas9 RANKL knockout mesenchymal stem cell clones based on single-cell printing technology and Emulsion Coupling assay as a low-cellularity workflow for single-cell cloning. <i>PLoS ONE</i> , 2021, 16, e0238330.	1.1	5
262	Satellite Glial Cells in Pain Research: A Targeted Viewpoint of Potential and Future Directions. <i>Frontiers in Pain Research</i> , 2021, 2, 646068.	0.9	24
263	New insights for precision treatment of glioblastoma from analysis of single-cell lncRNA expression. <i>Journal of Cancer Research and Clinical Oncology</i> , 2021, 147, 1881-1895.	1.2	3
264	Single-Cell Deconvolution of Head and Neck Squamous Cell Carcinoma. <i>Cancers</i> , 2021, 13, 1230.	1.7	26
265	Genetic basis of mitochondrial diseases. <i>FEBS Letters</i> , 2021, 595, 1132-1158.	1.3	36
266	Application of single-cell transcriptomics to kinetoplastid research. <i>Parasitology</i> , 2021, 148, 1223-1236.	0.7	11
267	Dive into Single, Seek Out Multiple: Probing Cancer Metastases via Single-Cell Sequencing and Imaging Techniques. <i>Cancers</i> , 2021, 13, 1067.	1.7	4
268	High-generation near-isogenic lines combined with multi-omics to study the mechanism of polima cytoplasmic male sterility. <i>BMC Plant Biology</i> , 2021, 21, 130.	1.6	8
269	scGNN is a novel graph neural network framework for single-cell RNA-Seq analyses. <i>Nature Communications</i> , 2021, 12, 1882.	5.8	139
270	Tumour immune microenvironment biomarkers predicting cytotoxic chemotherapy efficacy in colorectal cancer. <i>Journal of Clinical Pathology</i> , 2021, 74, 625-634.	1.0	18
271	Optimization of a Clinically Relevant Chemical-Mechanical Tissue Dissociation Workflow for Single-Cell Analysis. <i>Cellular and Molecular Bioengineering</i> , 2021, 14, 241-258.	1.0	7
272	Detecting cell-type-specific allelic expression imbalance by integrative analysis of bulk and single-cell RNA sequencing data. <i>PLoS Genetics</i> , 2021, 17, e1009080.	1.5	14
273	A hitchhiker's guide to single-cell transcriptomics and data analysis pipelines. <i>Genomics</i> , 2021, 113, 606-619.	1.3	44
274	A Glycolysis-Related Five-Gene Signature Predicts Biochemical Recurrence-Free Survival in Patients With Prostate Adenocarcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 625452.	1.3	14
276	Nucleic acid ligands act as a PAM and agonist depending on the intrinsic ligand binding state of P2RY2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	6
277	Single-Cell Sequencing Methodologies: From Transcriptome to Multi-Dimensional Measurement. <i>Small Methods</i> , 2021, 5, e2100111.	4.6	17

#	ARTICLE	IF	CITATIONS
278	Single-Cell Transcriptomics: Current Methods and Challenges in Data Acquisition and Analysis. <i>Frontiers in Neuroscience</i> , 2021, 15, 591122.	1.4	53
279	Novel Tools and Investigative Approaches for the Study of Oligodendrocyte Precursor Cells (NG2-Glia) in CNS Development and Disease. <i>Frontiers in Cellular Neuroscience</i> , 2021, 15, 673132.	1.8	8
280	Comparison of Short-Read Sequence Aligners Indicates Strengths and Weaknesses for Biologists to Consider. <i>Frontiers in Plant Science</i> , 2021, 12, 657240.	1.7	26
282	Integration of Transformative Platforms for the Discovery of Causative Genes in Cardiovascular Diseases. <i>Cardiovascular Drugs and Therapy</i> , 2021, 35, 637-654.	1.3	2
283	In silico screening using bulk and single-cell RNA-seq data identifies RIMS2 as a prognostic marker in basal-like breast cancer. <i>Medicine (United States)</i> , 2021, 100, e25414.	0.4	8
284	Use of omic technologies in early life gastrointestinal health and disease: from bench to bedside. <i>Expert Review of Proteomics</i> , 2021, 18, 247-259.	1.3	13
285	Best practices on the differential expression analysis of multi-species RNA-seq. <i>Genome Biology</i> , 2021, 22, 121.	3.8	51
286	The Comparison between Bulk RNA-seq and Single-cell RNA-seq. <i>Journal of Physics: Conference Series</i> , 2021, 1893, 012014.	0.3	0
287	A new era for plant science: spatial single-cell transcriptomics. <i>Current Opinion in Plant Biology</i> , 2021, 60, 102041.	3.5	51
288	Modular, efficient and constant-memory single-cell RNA-seq preprocessing. <i>Nature Biotechnology</i> , 2021, 39, 813-818.	9.4	252
289	<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
291	Differential gene expression analysis for multi-subject single-cell RNA-sequencing studies with <i>aggregateBioVar</i>. <i>Bioinformatics</i> , 2021, 37, 3243-3251.	1.8	18
293	Single-cell transcriptomics: a novel precision medicine technique in nephrology. <i>Korean Journal of Internal Medicine</i> , 2021, 36, 479-490.	0.7	5
294	Advances in understanding the molecular pathology of gynecological malignancies: the role and potential of RNA sequencing. <i>International Journal of Gynecological Cancer</i> , 2021, 31, 1159-1164.	1.2	0
295	A top-down measure of gene-to-gene coordination for analyzing cell-to-cell variability. <i>Scientific Reports</i> , 2021, 11, 11075.	1.6	3
296	Maturing heart muscle cells: Mechanisms and transcriptomic insights. <i>Seminars in Cell and Developmental Biology</i> , 2021, 119, 49-60.	2.3	13
297	Differentiation and activation of fibroblastic reticular cells. <i>Immunological Reviews</i> , 2021, 302, 32-46.	2.8	25
298	Isolation of Nuclei from Mammalian Cells and Tissues for Single-Nucleus Molecular Profiling. <i>Current Protocols</i> , 2021, 1, e132.	1.3	21

#	ARTICLE	IF	CITATIONS
299	Tertiary Lymphoid Structures as a Predictive Biomarker of Response to Cancer Immunotherapies. <i>Frontiers in Immunology</i> , 2021, 12, 674565.	2.2	28
300	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
301	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
302	Prediction of tumor purity from gene expression data using machine learning. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	5
303	<i>CyAnno</i>: a semi-automated approach for cell type annotation of mass cytometry datasets. <i>Bioinformatics</i> , 2021, 37, 4164-4171.	1.8	10
304	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
305	Single-cell advances in stromal-leukocyte interactions in cancer. <i>Immunological Reviews</i> , 2021, 302, 286-298.	2.8	10
306	Applications of single-cell and bulk RNA sequencing in onco-immunology. <i>European Journal of Cancer</i> , 2021, 149, 193-210.	1.3	62
307	Tutorial: guidelines for annotating single-cell transcriptomic maps using automated and manual methods. <i>Nature Protocols</i> , 2021, 16, 2749-2764.	5.5	100
308	Transcriptome profiling analysis of the response to walnut polyphenol extract in <i>Helicobacter pylori</i>-infected cells. <i>Journal of Clinical Biochemistry and Nutrition</i> , 2021, 68, 201-214.	0.6	4
309	Tackling Chronic Kidney Transplant Rejection: Challenges and Promises. <i>Frontiers in Immunology</i> , 2021, 12, 661643.	2.2	45
310	Trailblazing precision medicine in Europe: A joint view by Genomic Medicine Sweden and the Centers for Personalized Medicine, ZPM, in Germany. <i>Seminars in Cancer Biology</i> , 2022, 84, 242-254.	4.3	22
311	Robust single-cell discovery of RNA targets of RNA-binding proteins and ribosomes. <i>Nature Methods</i> , 2021, 18, 507-519.	9.0	77
312	Discovering Cellular Mitochondrial Heteroplasmy Heterogeneity with Single Cell RNA and ATAC Sequencing. <i>Biology</i> , 2021, 10, 503.	1.3	6
313	Normalization by distributional resampling of high throughput single-cell RNA-sequencing data. <i>Bioinformatics</i> , 2021, 37, 4123-4128.	1.8	13
314	Single-cell RNA sequencing of human femoral head in vivo. <i>Aging</i> , 2021, 13, 15595-15619.	1.4	13
315	Gene expression variation in <i>Arabidopsis</i> embryos at single-nucleus resolution. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	22
316	Analysis of single-cell RNA sequencing data based on autoencoders. <i>BMC Bioinformatics</i> , 2021, 22, 309.	1.2	15

#	ARTICLE	IF	CITATIONS
317	A convolutional neural network for common coordinate registration of high-resolution histology images. <i>Bioinformatics</i> , 2021, 37, 4216-4226.	1.8	6
318	Retinal Stem Cell "Retirement Plans"™: Growth, Regulation and Species Adaptations in the Retinal Ciliary Marginal Zone. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6528.	1.8	14
319	EcTracker: Tracking and elucidating ectopic expression leveraging large-scale scRNA-seq studies. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	0
320	Integrated analysis of single-cell RNA-seq and bulk RNA-seq reveals distinct cancer-associated fibroblasts in head and neck squamous cell carcinoma. <i>Annals of Translational Medicine</i> , 2021, 9, 1017-1017.	0.7	14
321	Single-cell RNA sequencing in human lung cancer: Applications, challenges, and pathway towards personalized therapy. <i>Journal of the Chinese Medical Association</i> , 2021, 84, 563-576.	0.6	7
322	Single-Cell Transcriptome Analysis as a Promising Tool to Study Pluripotent Stem Cell Reprogramming. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5988.	1.8	3
323	Mammary gland development from a single cell "omics view. <i>Seminars in Cell and Developmental Biology</i> , 2021, 114, 171-185.	2.3	18
324	Single-Cell TCR and Transcriptome Analysis: An Indispensable Tool for Studying T-Cell Biology and Cancer Immunotherapy. <i>Frontiers in Immunology</i> , 2021, 12, 689091.	2.2	16
325	How Machine Learning and Statistical Models Advance Molecular Diagnostics of Rare Disorders Via Analysis of RNA Sequencing Data. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 647277.	1.6	12
326	Progress in mimicking brain microenvironments to understand and treat neurological disorders. <i>APL Bioengineering</i> , 2021, 5, 020902.	3.3	9
327	Integrating single-cell and spatial transcriptomics to elucidate intercellular tissue dynamics. <i>Nature Reviews Genetics</i> , 2021, 22, 627-644.	7.7	423
328	RFCell: A Gene Selection Approach for scRNA-seq Clustering Based on Permutation and Random Forest. <i>Frontiers in Genetics</i> , 2021, 12, 665843.	1.1	3
329	Epithelial Cell Transformation and Senescence as Indicators of Genome Aging: Current Advances and Unanswered Questions. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7544.	1.8	1
330	Proteomics for Low Cell Numbers: How to Optimize the Sample Preparation Workflow for Mass Spectrometry Analysis. <i>Journal of Proteome Research</i> , 2021, 20, 4217-4230.	1.8	16
331	PseudoGA: cell pseudotime reconstruction based on genetic algorithm. <i>Nucleic Acids Research</i> , 2021, 49, 7909-7924.	6.5	5
332	Preparation of single-cell suspensions of mouse glomeruli for high-throughput analysis. <i>Nature Protocols</i> , 2021, 16, 4068-4083.	5.5	10
333	Regulation of CTLA-4 and PD-L1 Expression in Relapsing-Remitting Multiple Sclerosis Patients after Treatment with Fingolimod, IFN β -11a, Glatiramer Acetate, and Dimethyl Fumarate Drugs. <i>Journal of Personalized Medicine</i> , 2021, 11, 721.	1.1	17
334	Immune cell profiling in atherosclerosis: role in research and precision medicine. <i>Nature Reviews Cardiology</i> , 2022, 19, 43-58.	6.1	58

#	ARTICLE	IF	CITATIONS
335	Using machine learning approaches for multi-omics data analysis: A review. <i>Biotechnology Advances</i> , 2021, 49, 107739.	6.0	277
336	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
337	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
338	Exploiting Single-Cell Tools in Gene and Cell Therapy. <i>Frontiers in Immunology</i> , 2021, 12, 702636.	2.2	21
339	Liquid Biopsy, the hype vs. hope in molecular and clinical oncology. <i>Seminars in Oncology</i> , 2021, 48, 259-267.	0.8	9
340	Recent developments in Raman spectral analysis of microbial single cells: Techniques and applications. <i>Critical Reviews in Food Science and Nutrition</i> , 2022, 62, 4294-4308.	5.4	56
341	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
342	Building bridges between fields: bringing together development and homeostasis. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	7
344	An easy-to-operate method for single-cell isolation and retrieval using a microfluidic static droplet array. <i>Mikrochimica Acta</i> , 2021, 188, 242.	2.5	13
345	Single-Cell RNA Sequencing Approaches for Tracing T Cell Development. <i>Journal of Immunology</i> , 2021, 207, 363-370.	0.4	4
346	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
347	Dimensionality reduction by UMAP reinforces sample heterogeneity analysis in bulk transcriptomic data. <i>Cell Reports</i> , 2021, 36, 109442.	2.9	67
348	doubletD: detecting doublets in single-cell DNA sequencing data. <i>Bioinformatics</i> , 2021, 37, i214-i221.	1.8	13
349	Mechanisms of Binding Specificity among bHLH Transcription Factors. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9150.	1.8	45
350	Selecting gene features for unsupervised analysis of single-cell gene expression data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	20
351	Epigenetic promoter alterations in GI tumour immune-editing and resistance to immune checkpoint inhibition. <i>Gut</i> , 2022, 71, 1277-1288.	6.1	23
352	Quantitative analysis of the blood transcriptome of young healthy pigs and its relationship with subsequent disease resilience. <i>BMC Genomics</i> , 2021, 22, 614.	1.2	9
353	Core Gene Signatures of Atopic Dermatitis Using Public RNA-Sequencing Resources: Comparison of Bulk Approach with Single-Cell Approach. <i>Journal of Investigative Dermatology</i> , 2022, 142, 717-721.e5.	0.3	5

#	ARTICLE	IF	CITATIONS
354	A systematic dissection of human primary osteoblasts in vivo at single-cell resolution. <i>Aging</i> , 2021, 13, 20629-20650.	1.4	19
355	A preliminary investigation into the immune cell landscape of schistosoma-associated liver fibrosis in humans. <i>Immunology and Cell Biology</i> , 2021, 99, 803-813.	1.0	4
356	Virus Infection Variability by Single-Cell Profiling. <i>Viruses</i> , 2021, 13, 1568.	1.5	26
357	Isoform Age - Splice Isoform Profiling Using Long-Read Technologies. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 711733.	1.6	31
358	Single cell analyses to understand the immune continuum in atherosclerosis. <i>Atherosclerosis</i> , 2021, 330, 85-94.	0.4	18
359	Current Insights and Advancements in Head and Neck Cancer: Emerging Biomarkers and Therapeutics with Cues from Single Cell and 3D Model Omics Profiling. <i>Frontiers in Oncology</i> , 2021, 11, 676948.	1.3	5
360	Single-cell omics: Overview, analysis, and application in biomedical science. <i>Journal of Cellular Biochemistry</i> , 2021, 122, 1571-1578.	1.2	18
362	Cellular origins and lineage relationships of the intestinal epithelium. <i>American Journal of Physiology - Renal Physiology</i> , 2021, 321, G413-G425.	1.6	11
363	Harnessing model organism genomics to underpin the machine learning-based prediction of essential genes in eukaryotes – Biotechnological implications. <i>Biotechnology Advances</i> , 2022, 54, 107822.	6.0	9
364	Identification of BiP as a CB ₁ Receptor-Interacting Protein That Fine-Tunes Cannabinoid Signaling in the Mouse Brain. <i>Journal of Neuroscience</i> , 2021, 41, 7924-7941.	1.7	14
365	Copy number variation detection using single cell sequencing data. , 2021, , .		0
366	Subretinal fibrosis in neovascular age-related macular degeneration: current concepts, therapeutic avenues, and future perspectives. <i>Cell and Tissue Research</i> , 2022, 387, 361-375.	1.5	39
367	Epigenetics of Schizophrenia. <i>Psychiatry Research</i> , 2021, 305, 114218.	1.7	32
368	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
369	Ensemble Estimation of Generalized Mutual Information With Applications to Genomics. <i>IEEE Transactions on Information Theory</i> , 2021, 67, 5963-5996.	1.5	1
370	Hypothesis-driven science in large-scale studies: the case of GWAS. <i>Biology and Philosophy</i> , 2021, 36, 1.	0.7	1
371	A Single-cell Transcriptome Atlas of Cashmere Goat Hair Follicle Morphogenesis. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 437-451.	3.0	28
372	Identifying Lung Cancer Cell Markers with Machine Learning Methods and Single-Cell RNA-Seq Data. <i>Life</i> , 2021, 11, 940.	1.1	8

#	ARTICLE	IF	CITATIONS
373	Multi-omic approaches to acute kidney injury and repair. <i>Current Opinion in Biomedical Engineering</i> , 2021, 20, 100344.	1.8	6
374	Shifting Gears in Precision Oncology—Challenges and Opportunities of Integrative Data Analysis. <i>Biomolecules</i> , 2021, 11, 1310.	1.8	3
375	Cell-specific gene association network construction from single-cell RNA sequence. <i>Cell Cycle</i> , 2021, 20, 1-16.	1.3	3
376	Inferring gene regulatory networks from single-cell RNA-seq temporal snapshot data requires higher-order moments. <i>Patterns</i> , 2021, 2, 100332.	3.1	2
377	Learning interpretable cellular and gene signature embeddings from single-cell transcriptomic data. <i>Nature Communications</i> , 2021, 12, 5261.	5.8	38
378	Intricacies of single-cell multi-omics data integration. <i>Trends in Genetics</i> , 2022, 38, 128-139.	2.9	25
379	Estimating cellular redundancy in networks of genetic expression. <i>Mathematical Biosciences</i> , 2021, 341, 108713.	0.9	2
380	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
382	Roles of microglia in Alzheimer's disease and impact of new findings on microglial heterogeneity as a target for therapeutic intervention. <i>Biochemical Pharmacology</i> , 2021, 192, 114754.	2.0	24
383	Collective behaviours in organoids. <i>Current Opinion in Cell Biology</i> , 2021, 72, 81-90.	2.6	12
384	Metaheuristics for multiple sequence alignment: A systematic review. <i>Computational Biology and Chemistry</i> , 2021, 94, 107563.	1.1	8
385	Combinatorial therapy in tumor microenvironment: Where do we stand?. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2021, 1876, 188585.	3.3	48
386	Cancer as a tool for preclinical psychoneuroimmunology. <i>Brain, Behavior, & Immunity - Health</i> , 2021, 18, 100351.	1.3	5
387	Machine learning for profile prediction in genomics. <i>Current Opinion in Chemical Biology</i> , 2021, 65, 35-41.	2.8	11
388	Spatial mapping of the tumor immune microenvironment. , 2022, , 293-329.		0
389	GECO: gene expression clustering optimization app for non-linear data visualization of patterns. <i>BMC Bioinformatics</i> , 2021, 22, 29.	1.2	4
390	Autologous cervical tumor lysate pulsed dendritic cell stimulation followed by cisplatin treatment abrogates FOXP3+ cells in vitro. <i>Journal of Gynecologic Oncology</i> , 2021, 32, e59.	1.0	0
391	Analytics methods and tools for integration of biomedical data in medicine. , 2021, , 113-129.		0

#	ARTICLE	IF	CITATIONS
392	Î±-Klotho gene and protein measurements in humans and their role as a clinical biomarker of disease. , 2021, , 265-298.		0
393	Using single-cell cytometry to illustrate integrated multi-perspective evaluation of clustering algorithms using Pareto fronts. <i>Bioinformatics</i> , 2021, 37, 1972-1981.	1.8	2
394	Compression of quantification uncertainty for scRNA-seq counts. <i>Bioinformatics</i> , 2021, 37, 1699-1707.	1.8	4
395	Comparative transcriptomic analysis of rat versus mouse cerebral cortex after traumatic brain injury. <i>Neural Regeneration Research</i> , 2021, 16, 1235.	1.6	6
396	Transcriptional Profiling During Neural Conversion. <i>Methods in Molecular Biology</i> , 2021, 2352, 171-181.	0.4	0
397	Redefining Microglial Identity in Health and Disease at Single-Cell Resolution. <i>Trends in Molecular Medicine</i> , 2021, 27, 47-59.	3.5	18
398	Supervised Adversarial Alignment of Single-Cell RNA-seq Data. <i>Journal of Computational Biology</i> , 2021, 28, 501-513.	0.8	18
399	From Transcriptomics to Treatment in Inherited Optic Neuropathies. <i>Genes</i> , 2021, 12, 147.	1.0	7
400	Single-Cell RNAseq Analysis of lncRNAs. <i>Methods in Molecular Biology</i> , 2021, 2348, 71-90.	0.4	1
401	Targeting epigenetic regulatory machinery to overcome cancer therapy resistance. <i>Seminars in Cancer Biology</i> , 2022, 33, 487-502.	4.3	32
402	Tailoring the resolution of single-cell RNA sequencing for primary cytotoxic T cells. <i>Nature Communications</i> , 2021, 12, 569.	5.8	10
403	Computational strategies for single-cell multi-omics integration. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2588-2596.	1.9	46
404	Single-Cell Transcriptional Profiling of the Intestinal Epithelium. <i>Methods in Molecular Biology</i> , 2020, 2171, 129-153.	0.4	7
405	Guidelines for Setting Up a mRNA Sequencing Experiment and Best Practices for Bioinformatic Data Analysis. <i>Methods in Molecular Biology</i> , 2021, 2264, 137-162.	0.4	1
406	Advances in Diagnostic Procedures and Their Applications in the Era of Cancer Immunotherapy. <i>Advances in Experimental Medicine and Biology</i> , 2020, 1244, 37-50.	0.8	2
407	Supervised Adversarial Alignment of Single-Cell RNA-seq Data. <i>Lecture Notes in Computer Science</i> , 2020, , 72-87.	1.0	6
408	Single-Cell Sequencing in Human Genital Infections. <i>Advances in Experimental Medicine and Biology</i> , 2020, 1255, 203-220.	0.8	2
409	Methods for Single-Cell Isolation and Preparation. <i>Advances in Experimental Medicine and Biology</i> , 2020, 1255, 7-27.	0.8	16

#	ARTICLE	IF	CITATIONS
410	Chemical probes and methods for single-cell detection and quantification of epichaperomes in hematologic malignancies. <i>Methods in Enzymology</i> , 2020, 639, 289-311.	0.4	9
411	Direct cell reprogramming: approaches, mechanisms and progress. <i>Nature Reviews Molecular Cell Biology</i> , 2021, 22, 410-424.	16.1	178
412	Single cell approaches to address adipose tissue stromal cell heterogeneity. <i>Biochemical Journal</i> , 2020, 477, 583-600.	1.7	58
413	Chloride transporters and channels in \hat{I}^2 -cell physiology: revisiting a 40-year-old model. <i>Biochemical Society Transactions</i> , 2019, 47, 1843-1855.	1.6	18
414	Integration of single-cell datasets reveals novel transcriptomic signatures of \hat{I}^2 -cells in human type 2 diabetes. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa097.	1.5	15
415	â€œZooming inâ€ on Glioblastoma: Understanding Tumor Heterogeneity and its Clinical Implications in the Era of Single-Cell Ribonucleic Acid Sequencing. <i>Neurosurgery</i> , 2021, 88, 477-486.	0.6	15
445	Prediction of PBMC Cell Types Using scRNAseq Reference Profiles. , 2020, , .		3
446	Data Denoising and Post-Denoising Corrections in Single Cell RNA Sequencing. <i>Statistical Science</i> , 2020, 35, .	1.6	6
447	A primer for generating and using transcriptome data and gene sets. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	6
448	Single-cell transcriptome landscape of ovarian cells during primordial follicle assembly in mice. <i>PLoS Biology</i> , 2020, 18, e3001025.	2.6	71
449	Heterogeneous expression of CFTR in insulin-secreting \hat{I}^2 -cells of the normal human islet. <i>PLoS ONE</i> , 2020, 15, e0242749.	1.1	15
451	Statistical Methods for RNA Sequencing Data Analysis. , 0, , 85-99.		4
452	A Glioblastoma Genomics Primer for Clinicians. <i>Medical Research Archives</i> , 2020, 8, .	0.1	10
453	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
454	Identification of Pro-Fibrotic Macrophage Populations by Single-Cell Transcriptomic Analysis in West Highland White Terriers Affected With Canine Idiopathic Pulmonary Fibrosis. <i>Frontiers in Immunology</i> , 2020, 11, 611749.	2.2	13
455	The Progress of Multi-Omics Technologies: Determining Function in Lactic Acid Bacteria Using a Systems Level Approach. <i>Frontiers in Microbiology</i> , 2019, 10, 3084.	1.5	54
456	Tracking the important role of JUNB in hepatocellular carcinoma by singleâ€ cell sequencing analysis. <i>Oncology Letters</i> , 2020, 19, 1478-1486.	0.8	14
457	Flura-seq identifies organ-specific metabolic adaptations during early metastatic colonization. <i>ELife</i> , 2019, 8, .	2.8	46

#	ARTICLE	IF	CITATIONS
458	High-dimensional analysis of intestinal immune cells during helminth infection. <i>ELife</i> , 2020, 9, .	2.8	25
459	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
460	Combined transient ablation and single-cell RNA-sequencing reveals the development of medullary thymic epithelial cells. <i>ELife</i> , 2020, 9, .	2.8	53
461	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
462	DISCO: a database of Deeply Integrated human Single-Cell Omics data. <i>Nucleic Acids Research</i> , 2022, 50, D596-D602.	6.5	49
463	Label-Free Identification of Single Mononucleotides by Nanoscale Electrophoresis. <i>Small</i> , 2021, 17, e2102567.	5.2	8
465	Microfluidics applications for high-throughput single cell sequencing. <i>Journal of Nanobiotechnology</i> , 2021, 19, 312.	4.2	44
466	Advanced Genomics-Based Approaches for Defining Allograft Rejection With Single Cell Resolution. <i>Frontiers in Immunology</i> , 2021, 12, 750754.	2.2	5
467	Prostate zones and cancer: lost in transition?. <i>Nature Reviews Urology</i> , 2022, 19, 101-115.	1.9	25
468	Introductory Chapter: Applications of RNA-Seq Diagnostics in Biology and Medicine. , 0, , .		0
469	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
470	Meta-Analysis Reveals Transcription Factor Upregulation in Cells of Injured Mouse Sciatic Nerve. <i>Frontiers in Cellular Neuroscience</i> , 2021, 15, 688243.	1.8	7
471	Machine Learning Detects Anti-DENV Signatures in Antibody Repertoire Sequences. <i>Frontiers in Artificial Intelligence</i> , 2021, 4, 715462.	2.0	4
475	SINGLE CELL ANALYSIS, WHAT IS IN THE FUTURE?. , 2018, , .		1
477	Transcriptomic Approaches for Muscle Biology and Disorders. , 2019, , 79-107.		0
478	Guidelines for Bioinformatics and the Statistical Analysis of Omic Data. , 2019, , 45-75.		0
487	Applications of PCA Based Unsupervised FE to Bioinformatics. <i>Unsupervised and Semi-supervised Learning</i> , 2020, , 119-211.	0.4	1
490	DNA Methylation and Transcriptomic Next-Generation Technologies in Cereal Genomics. <i>Methods in Molecular Biology</i> , 2020, 2072, 65-84.	0.4	0

#	ARTICLE	IF	CITATIONS
495	Tools for the assessment of epigenetic regulation. , 2020, , 33-64.		2
496	Review of Creative Nature (part 2). Scientia Et Fides, 2020, 8, 245.	0.3	1
500	Comparison of Scanpy-based algorithms to remove the batch effect from single-cell RNA-seq data. Cell Regeneration, 2020, 9, 10.	1.1	4
504	The potential application of organoids in breast cancer research and treatment. Human Genetics, 2022, 141, 193-208.	1.8	11
507	Pattern Recognition Applied to the Analysis of Genomic Data and Its Association to Diseases. STEAM-H: Science, Technology, Engineering, Agriculture, Mathematics & Health, 2020, , 35-61.	0.0	1
509	Tumor immune microenvironment lncRNAs. Briefings in Bioinformatics, 2022, 23, .	3.2	77
510	Biomarkers in drug development. , 2022, , 323-342.		3
511	Mass spectrometry for human kinome analysis. , 2022, , 191-216.		1
512	Genomic Tools Used in Molecular Clinical Aging Research. , 2020, , 87-109.		0
514	Toward uncharted territory of cellular heterogeneity: advances and applications of single-cell RNA-seq. , 2021, 5, 1-21.		2
515	Recent Machine Learning Approaches for Single-Cell RNA-seq Data Analysis. Studies in Computational Intelligence, 2020, , 65-79.	0.7	3
519	Olig2-astrocytes express neutral amino acid transporter SLC7A10 (Asc-1) in the adult brain. Molecular Brain, 2021, 14, 163.	1.3	4
520	Single-cell Transcriptional Changes in Neurodegenerative Diseases. Neuroscience, 2021, 479, 192-205.	1.1	11
529	Spatiotemporal strategies to identify aggressive biology in precancerous breast biopsies. WIREs Mechanisms of Disease, 2021, 13, e1506.	1.5	4
530	Emerging roles of long non-coding RNAs in osteonecrosis of the femoral head. American Journal of Translational Research (discontinued), 2020, 12, 5984-5991.	0.0	3
531	CellHeap: A Workflow for Optimizing COVID-19 Single-Cell RNA-Seq Data Processing in the Santos Dumont Supercomputer. Lecture Notes in Computer Science, 2021, , 41-52.	1.0	0
532	Single-cell RNA sequencing to characterize the response of pancreatic cancer to anti-PD-1 immunotherapy. Translational Oncology, 2022, 15, 101262.	1.7	6
533	Updates on Immunotherapy and Immune Landscape in Renal Clear Cell Carcinoma. Cancers, 2021, 13, 5856.	1.7	39

#	ARTICLE	IF	CITATIONS
534	Pathogenic Mechanisms Underlying Idiopathic Pulmonary Fibrosis. Annual Review of Pathology: Mechanisms of Disease, 2022, 17, 515-546.	9.6	174
535	Whole-animal multiplexed single-cell RNA-seq reveals transcriptional shifts across <i>Clytia</i> medusa cell types. Science Advances, 2021, 7, eabh1683.	4.7	47
537	Bringing precision oncology to cellular resolution with single-cell genomics. Clinical and Experimental Metastasis, 2021, , 1.	1.7	1
538	FEM: mining biological meaning from cell level in single-cell RNA sequencing data. PeerJ, 2021, 9, e12570.	0.9	2
539	A Pulmonary Vascular Model From Endothelialized Whole Organ Scaffolds. Frontiers in Bioengineering and Biotechnology, 2021, 9, 760309.	2.0	4
540	Exploring the Mechanism of Action of Canmei Formula Against Colorectal Adenoma Through Multi-Omics Technique. Frontiers in Cell and Developmental Biology, 2021, 9, 778826.	1.8	4
541	A review of the resistome within the digestive tract of livestock. Journal of Animal Science and Biotechnology, 2021, 12, 121.	2.1	17
542	treekoR: identifying cellular-to-phenotype associations by elucidating hierarchical relationships in high-dimensional cytometry data. Genome Biology, 2021, 22, 324.	3.8	3
544	Analysis of the resistance of small peptides from <i>Periplaneta americana</i> to hydrogen peroxide-induced apoptosis in human ovarian granular cells based on RNA-seq. Gene, 2022, 813, 146120.	1.0	5
545	Capturing the third dimension in drug discovery: Spatially-resolved tools for interrogation of complex 3D cell models. Biotechnology Advances, 2022, 55, 107883.	6.0	7
546	SCNMLRR: Single Cell Clustering Based on Low-rank Non-negative Matrix Factorization. , 2020, , .		0
547	Single-cell transcriptomics of lung organoids. Organoid, 0, 1, e9.	0.0	0
548	An Overview on Single-Cell Technology for Hepatocellular Carcinoma Diagnosis. International Journal of Molecular Sciences, 2022, 23, 1402.	1.8	10
549	Towards Tabula Gallus. International Journal of Molecular Sciences, 2022, 23, 613.	1.8	3
550	Challenges and Opportunities for the Translation of Single-Cell RNA Sequencing Technologies to Dermatology. Life, 2022, 12, 67.	1.1	4
551	MGcount: a total RNA-seq quantification tool to address multi-mapping and multi-overlapping alignments ambiguity in non-coding transcripts. BMC Bioinformatics, 2022, 23, 39.	1.2	6
552	SCANNER: a web platform for annotation, visualization and sharing of single cell RNA-seq data. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	3
554	In Vitro Matured Human Pluripotent Stem Cell-Derived Cardiomyocytes Form Grafts With Enhanced Structure and Function in Injured Hearts. Circulation, 2022, 145, 1412-1426.	1.6	42

#	ARTICLE	IF	CITATIONS
556	Network biology and artificial intelligence drive the understanding of the multidrug resistance phenotype in cancer. <i>Drug Resistance Updates</i> , 2022, 60, 100811.	6.5	13
557	Fluorescence based miniaturized microfluidic and nanofluidic systems for biomedical applications. <i>Progress in Molecular Biology and Translational Science</i> , 2022, 186, 217-243.	0.9	1
558	Advanced techniques for gene heterogeneity research: Single-cell sequencing and on-chip gene analysis systems. <i>View</i> , 2022, 3, .	2.7	9
559	Computational Methods for Single-Cell Imaging and Omics Data Integration. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 768106.	1.6	13
560	Single Cell RNA Sequencing in Autoimmune Inflammatory Rheumatic Diseases: Current Applications, Challenges and a Step Toward Precision Medicine. <i>Frontiers in Medicine</i> , 2021, 8, 822804.	1.2	6
561	Discovering cell types using manifold learning and enhanced visualization of single-cell RNA-Seq data. <i>Scientific Reports</i> , 2022, 12, 120.	1.6	12
562	Cytotoxic effects of the biflavonoids isolated from <i>Selaginella trichoclada</i> on MCF-7 cells and its potential mechanism. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2022, 56, 128486.	1.0	11
563	SkewC: Identifying cells with skewed gene body coverage in single-cell RNA sequencing data. <i>IScience</i> , 2022, 25, 103777.	1.9	4
564	Galectin-3 promotes the adipogenic differentiation of PDGFR α ^{hi} cells and ectopic fat formation in regenerating muscle. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	5
565	Subcellular Transcriptomics and Proteomics: A Comparative Methods Review. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100186.	2.5	23
566	HDAC6 involves in regulating the lncRNA-microRNA-mRNA network to promote the proliferation of glioblastoma cells. <i>Journal of Experimental and Clinical Cancer Research</i> , 2022, 41, 47.	3.5	14
567	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
568	Recent advances in T-cell receptor repertoire analysis: Bridging the gap with multimodal single-cell RNA sequencing. <i>Immuninformatics</i> , 2022, 5, 100009.	1.2	27
569	Bibliometric review of ATAC-Seq and its application in gene expression. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	21
570	Transcriptional configurations of myeloproliferative neoplasms. <i>International Review of Cell and Molecular Biology</i> , 2022, 366, 25-39.	1.6	0
571	Discordant Genome Assemblies Drastically Alter the Interpretation of Single-Cell RNA Sequencing Data Which Can Be Mitigated by a Novel Integration Method. <i>Cells</i> , 2022, 11, 608.	1.8	2
572	EMBEDR: Distinguishing signal from noise in single-cell omics data. <i>Patterns</i> , 2022, 3, 100443.	3.1	13
573	Single-cell Iso-Sequencing enables rapid genome annotation for scRNAseq analysis. <i>Genetics</i> , 2022, 220, .	1.2	10

#	ARTICLE	IF	CITATIONS
575	Comparative Analysis of Packages and Algorithms for the Analysis of Spatially Resolved Transcriptomics Data. , 2022, , 165-186.		2
576	Single-Cell in Research. <i>Methods in Molecular Biology</i> , 2022, 2419, 765-778.	0.4	4
577	Enhancing Scanning Electrochemical Microscopy's Potential to Probe Dynamic Co-Culture Systems via Hyperspectral Assisted-Imaging. <i>Analyst, The</i> , 2022, , .	1.7	3
578	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
579	In silico tools and databases for designing cancer immunotherapy. <i>Advances in Protein Chemistry and Structural Biology</i> , 2022, 129, 1-50.	1.0	1
580	Multi-Omics Profiling of the Tumor Microenvironment. <i>Advances in Experimental Medicine and Biology</i> , 2022, 1361, 283-326.	0.8	6
581	Exponential magnetophoretic gradient for the direct isolation of basophils from whole blood in a microfluidic system. <i>Lab on A Chip</i> , 2022, 22, 1690-1701.	3.1	8
582	Managing the Transition to Widespread Metagenomic Monitoring: Policy Considerations for Future Biosurveillance. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
583	PathogenTrack and Yeskit: tools for identifying intracellular pathogens from single-cell RNA-sequencing datasets as illustrated by application to COVID-19. <i>Frontiers of Medicine</i> , 2022, 16, 251-262.	1.5	7
584	Assessing reproducibility of high-throughput experiments in the case of missing data. <i>Statistics in Medicine</i> , 2022, 41, 1884-1899.	0.8	1
585	scGAC: a graph attentional architecture for clustering single-cell RNA-seq data. <i>Bioinformatics</i> , 2022, 38, 2187-2193.	1.8	15
586	Perspectives on Bulk-Tissue RNA Sequencing and Single-Cell RNA Sequencing for Cardiac Transcriptomics. <i>Frontiers in Molecular Medicine</i> , 2022, 2, .	0.6	14
587	A comparative analysis of single cell small RNA sequencing data reveals heterogeneous isomiR expression and regulation. <i>Scientific Reports</i> , 2022, 12, 2834.	1.6	5
588	Deterministic scRNA-seq captures variation in intestinal crypt and organoid composition. <i>Nature Methods</i> , 2022, 19, 323-330.	9.0	33
589	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
590	Sugarcane Transcriptomics in Response to Abiotic and Biotic Stresses: A Review. <i>Sugar Tech</i> , 2022, 24, 1295-1318.	0.9	5
591	Analyzing immune response to engineered hydrogels by hierarchical clustering of inflammatory cell subsets. <i>Science Advances</i> , 2022, 8, eabd8056.	4.7	15
592	Spatially resolved transcriptomics for evaluation of intracranial vessels in a rabbit model: Proof of concept. <i>Interventional Neuroradiology</i> , 2023, 29, 307-314.	0.7	0

#	ARTICLE	IF	CITATIONS
593	Single-cell RNA sequencing of mycosis fungoides reveals a cluster of actively proliferating lymphocytes. <i>Australasian Journal of Dermatology</i> , 2022, , .	0.4	0
594	A novel single-cell RNA-sequencing approach and its applicability connecting genotype to phenotype in ageing disease. <i>Scientific Reports</i> , 2022, 12, 4091.	1.6	12
595	Identification of Significant Modules and Targets of Xian-Lian-Jie-Du Decoction Based on the Analysis of Transcriptomics, Proteomics and Single-Cell Transcriptomics in Colorectal Tumor. <i>Journal of Inflammation Research</i> , 2022, Volume 15, 1483-1499.	1.6	10
596	Single-cell RNA-seq identification of four differentially expressed survival-related genes by a TARGET: Osteosarcoma database analysis. <i>Experimental Biology and Medicine</i> , 2022, 247, 921-930.	1.1	5
597	popsicleR: A R Package for Pre-processing and Quality Control Analysis of Single Cell RNA-seq Data. <i>Journal of Molecular Biology</i> , 2022, 434, 167560.	2.0	7
598	Single-Cell Sequencing Revealed Pivotal Genes Related to Prognosis of Myocardial Infarction Patients. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-15.	0.7	4
599	Spatial transcriptomic profiles of mouse uterine microenvironments at pregnancy day 7.5. <i>Biology of Reproduction</i> , 2022, 107, 529-545.	1.2	10
600	Mouse Oocytes, A Complex Single Cell Transcriptome. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 827937.	1.8	1
601	Recent advances in spatially resolved transcriptomics: challenges and opportunities. <i>BMB Reports</i> , 2022, 55, 113-124.	1.1	12
602	Leukemic stem cell signatures in Acute myeloid leukemia- targeting the Guardians with novel approaches. <i>Stem Cell Reviews and Reports</i> , 2022, 18, 1756-1773.	1.7	7
603	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
604	Next-Generation and Single-Cell Sequencing Approaches to Study Atherosclerosis and Vascular Inflammation Pathophysiology: A Systematic Review. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 849675.	1.1	5
605	Single-cell analysis of circulating tumour cells: enabling technologies and clinical applications. <i>Trends in Biotechnology</i> , 2022, 40, 1041-1060.	4.9	16
606	Temporal transcriptomic analysis using TrendCatcher identifies early and persistent neutrophil activation in severe COVID-19. <i>JCI Insight</i> , 2022, 7, .	2.3	7
607	Exploiting plant transcriptomic databases: Resources, tools, and approaches. <i>Plant Communications</i> , 2022, 3, 100323.	3.6	20
608	scGraph: a graph neural network-based approach to automatically identify cell types. <i>Bioinformatics</i> , 2022, 38, 2996-3003.	1.8	9
609	Construction and validation of a prognostic model for kidney renal clear cell carcinoma based on podocyte-associated genes. <i>Cancer Medicine</i> , 2022, , .	1.3	3
610	Using topic modeling to detect cellular crosstalk in scRNA-seq. <i>PLoS Computational Biology</i> , 2022, 18, e1009975.	1.5	6

#	ARTICLE	IF	CITATIONS
611	Single cell sequencing coupled with bioinformatics reveals PHYH as a potential biomarker in kidney ischemia reperfusion injury. <i>Biochemical and Biophysical Research Communications</i> , 2022, 602, 156-162.	1.0	2
612	Automation enables high-throughput and reproducible single-cell transcriptomics library preparation. <i>SLAS Technology</i> , 2021, , .	1.0	3
614	CCPE: cell cycle pseudotime estimation for single cell RNA-seq data. <i>Nucleic Acids Research</i> , 2022, 50, 704-716.	6.5	11
615	Immunotherapy for Hepatocellular Carcinoma: New Prospects for the Cancer Therapy. <i>Life</i> , 2021, 11, 1355.	1.1	8
616	T-Cell Receptor Repertoire Analysis with Computational Toolsâ€”An Immunologistâ€™s Perspective. <i>Cells</i> , 2021, 10, 3582.	1.8	11
617	Toward Overcoming Treatment Failure in Rheumatoid Arthritis. <i>Frontiers in Immunology</i> , 2021, 12, 755844.	2.2	18
618	Single-Cell Regulatory Network Inference and Clustering Identifies Cell-Type Specific Expression Pattern of Transcription Factors in Mouse Sciatic Nerve. <i>Frontiers in Cellular Neuroscience</i> , 2021, 15, 676515.	1.8	6
619	Analysis of Single-Cell RNA-Sequencing Data: A Step-by-Step Guide. <i>BioMedInformatics</i> , 2022, 2, 43-61.	1.0	3
620	Accurate Prediction of Protein Sequences for Proteogenomics Data Integration. <i>Methods in Molecular Biology</i> , 2022, 2420, 233-260.	0.4	0
621	Cell type identification for single cell RNA data by bulk data reference projection. , 2021, , .		0
622	Single Cell RNA-Seq: Cell Isolation and Data Analysis. <i>Methods in Molecular Biology</i> , 2022, 2403, 81-89.	0.4	1
623	geneBasis: an iterative approach for unsupervised selection of targeted gene panels from scRNA-seq. <i>Genome Biology</i> , 2021, 22, 333.	3.8	15
624	FOXO Transcription Factors Are Required for Normal Somatotrope Function and Growth. <i>Endocrinology</i> , 2022, 163, .	1.4	2
625	Comparative Analysis of Single-Cell RNA Sequencing Platforms and Methods. <i>Journal of Biomolecular Techniques</i> , 2021, 32, 3fc1f5fe.3eccea01.	0.8	5
626	Singleâ€”Cell Sequencing to Unveil the Mystery of Embryonic Development. <i>Advanced Biology</i> , 2022, 6, e2101151.	1.4	2
627	Application and prospects of single cell sequencing in tumors. <i>Biomarker Research</i> , 2021, 9, 88.	2.8	6
628	OUP accepted manuscript. <i>Briefings in Bioinformatics</i> , 2022, , .	3.2	0
629	scIMC: a platform for benchmarking comparison and visualization analysis of scRNA-seq data imputation methods. <i>Nucleic Acids Research</i> , 2022, 50, 4877-4899.	6.5	12

#	ARTICLE	IF	CITATIONS
630	Dynamics of <i>Drosophila</i> endoderm specification. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2112892119.	3.3	4
631	Ulcerative Colitis: Novel Epithelial Insights Provided by Single Cell RNA Sequencing. Frontiers in Medicine, 2022, 9, 868508.	1.2	8
632	Microphysiological stem cell models of the human heart. Materials Today Bio, 2022, 14, 100259.	2.6	4
633	Global Increase in Breast Cancer Incidence: Risk Factors and Preventive Measures. BioMed Research International, 2022, 2022, 1-16.	0.9	156
634	An immune subtype-related prognostic signature of hepatocellular carcinoma based on single-cell sequencing analysis. Aging, 2022, 14, 3276-3292.	1.4	34
635	Leveraging single cell sequencing to unravel intra-tumour heterogeneity and tumour evolution in human cancers. Journal of Pathology, 2022, , .	2.1	6
636	Connecting past and present: single-cell lineage tracing. Protein and Cell, 2022, 13, 790-807.	4.8	30
646	Recent advances in spatially resolved transcriptomics: challenges and opportunities.. BMB Reports, 2022, , .	1.1	0
648	Single-Cell RNA Sequencing in Yeast Using the 10X Genomics Chromium Device. Methods in Molecular Biology, 2022, 2477, 3-20.	0.4	2
649	Quality Control Pipeline for Next Generation Sequencing Data Analysis. Smart Innovation, Systems and Technologies, 2022, , 215-225.	0.5	4
650	Deep Learning applied to computational biology and agricultural sciences. , 2022, , 589-618.		0
651	Integrated analysis of single-cell and bulk RNA sequencing data reveals a pan-cancer stemness signature predicting immunotherapy response. Genome Medicine, 2022, 14, 45.	3.6	73
652	CASSL: A cell-type annotation method for single cell transcriptomics data using semi-supervised learning. Applied Intelligence, 2023, 53, 1287-1305.	3.3	7
653	A State-of-the-Art Roadmap for Biomarker-Driven Drug Development in the Era of Personalized Therapies. Journal of Personalized Medicine, 2022, 12, 669.	1.1	1
654	Global coordination level in single-cell transcriptomic data. Scientific Reports, 2022, 12, 7547.	1.6	3
655	Single-cell analysis reveals the Comma-1D cell line as a unique model for mammary gland development and breast cancer. Journal of Cell Science, 2022, 135, .	1.2	2
656	Assimilating Epigenetics and Transcriptomics for the Identification of Prognostic Novel Biomarkers and Imminent Targets in Colorectal Carcinoma with Therapeutic Potential. Current Molecular Medicine, 2023, 23, 784-798.	0.6	2
657	Spatially informed cell-type deconvolution for spatial transcriptomics. Nature Biotechnology, 2022, 40, 1349-1359.	9.4	121

#	ARTICLE	IF	CITATIONS
658	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
659	High-throughput single-Cell sequencing in cancer research. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 145.	7.1	39
660	Comparative Toxicotranscriptomics of Single Cell RNA-Seq and Conventional RNA-Seq in TCDD-Exposed Testicular Tissue. <i>Frontiers in Toxicology</i> , 2022, 4, .	1.6	7
661	Single-cell sequencing: a promising approach for uncovering the mechanisms of tumor metastasis. <i>Journal of Hematology and Oncology</i> , 2022, 15, 59.	6.9	33
662	Reprogramming neurons for regeneration: The fountain of youth. <i>Progress in Neurobiology</i> , 2022, 214, 102284.	2.8	17
663	Statistical methods for Mendelian randomization in genome-wide association studies: A review. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2338-2351.	1.9	56
664	Artificial intelligence for the prevention and clinical management of hepatocellular carcinoma. <i>Journal of Hepatology</i> , 2022, 76, 1348-1361.	1.8	75
666	Comparison of different machine learning algorithms on Cell Classification with scRNA-seq after Principal Component Analysis. , 2022, , .		1
667	Comprehensive analysis of gene expression profiles to identify differential prognostic factors of primary and metastatic breast cancer. <i>Saudi Journal of Biological Sciences</i> , 2022, 29, 103318.	1.8	3
668	Role of Transcriptional and Epigenetic Regulation in Lymphatic Endothelial Cell Development. <i>Cells</i> , 2022, 11, 1692.	1.8	2
669	SingleCAnalyzer: Interactive Analysis of Single Cell RNA-Seq Data on the Cloud. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	14
670	Extracellular vesicles from lung tissue drive bone marrow neutrophil recruitment in inflammation. <i>Journal of Extracellular Vesicles</i> , 2022, 11, .	5.5	18
671	New insights empowered by single-cell sequencing: From neural crest to enteric nervous system. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2464-2472.	1.9	2
672	Multimomics analysis of male infertility. <i>Biology of Reproduction</i> , 2022, 107, 118-134.	1.2	11
673	Survival-Associated Metabolic Genes and Risk Scoring System in HER2-Positive Breast Cancer. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	4
674	Single-cell views of the Plasmodium life cycle. <i>Trends in Parasitology</i> , 2022, 38, 748-757.	1.5	5
676	Microfluidics Facilitates the Development of Single-Cell RNA Sequencing. <i>Biosensors</i> , 2022, 12, 450.	2.3	8
677	Omics technologies in allergy and asthma research: An <sc>EAACI</sc> position paper. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2022, 77, 2888-2908.	2.7	25

#	ARTICLE	IF	CITATIONS
678	From COVID to fibrosis: lessons from single-cell analyses of the human lung. <i>Human Genomics</i> , 2022, 16, .	1.4	7
680	Analysis of Melanoma Gene Expression Signatures at the Single-Cell Level Uncovers 45-Gene Signature Related to Prognosis. <i>Biomedicines</i> , 2022, 10, 1478.	1.4	3
681	Single-Cell Atlas of the Drosophila Leg Disc Identifies a Long Non-Coding RNA in Late Development. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6796.	1.8	4
682	Paving the Way: Contributions of Big Data to Apicomplexan and Kinetoplastid Research. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	2
683	Benchmarking imputation methods for network inference using a novel method of synthetic scRNA-seq data generation. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	3
684	Single-Cell Sequencing on Marine Life: Application and Future Development. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1
685	Mycobacterium tuberculosis infection drives a type I IFN signature in lung lymphocytes. <i>Cell Reports</i> , 2022, 39, 110983.	2.9	20
686	Growth Performance, Blood Metabolites, Carcass Characteristics and Meat Quality in Finishing Wagyu Crossbred Beef Cattle Receiving Betaineâ€“Biotinâ€“Chromium (BBC) Supplementation. <i>Veterinary Sciences</i> , 2022, 9, 314.	0.6	0
687	Recapitulating influenza virus infection and facilitating antiviral and neuroprotective screening in tractable brain organoids. <i>Theranostics</i> , 2022, 12, 5317-5329.	4.6	2
688	Smooth muscle diversity in the vascular system. , 2022, , 45-55.		1
689	High-throughput imaging of mRNA at the single-cell level in human primary immune cells. <i>Rna</i> , 0, , rna.079239.122.	1.6	1
690	MicroRNAs Promote the Progression of Sepsis-Induced Cardiomyopathy and Neurovascular Dysfunction Through Upregulation of NF-kappaB Signaling Pathway-Associated HDAC7/ACTN4. <i>Frontiers in Neurology</i> , 0, 13, .	1.1	4
691	Statistical learning in preclinical drug proarrhythmic assessment. <i>Journal of Biopharmaceutical Statistics</i> , 0, , 1-24.	0.4	1
692	What We Have Learned so far From Single Cell Sequencing in Acute Kidney Injury. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	3
693	A systematic evaluation of the computational tools for ligand-receptor-based cellâ€“cell interaction inference. <i>Briefings in Functional Genomics</i> , 2022, 21, 339-356.	1.3	7
694	Epigenetic Memories in Hematopoietic Stem and Progenitor Cells. <i>Cells</i> , 2022, 11, 2187.	1.8	3
695	Approaches in Gene Coexpression Analysis in Eukaryotes. <i>Biology</i> , 2022, 11, 1019.	1.3	4
696	Mass spectrometry imaging to explore molecular heterogeneity in cell culture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	24

#	ARTICLE	IF	CITATIONS
697	The Multi-Dimensional Biomarker Landscape in Cancer Immunotherapy. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7839.	1.8	13
698	Single-Cell RNA Sequencing Reveals the Pathogenic Relevance of Intracranial Atherosclerosis in Blood Blister-Like Aneurysms. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	12
699	Drosophila Innate Immunity Involves Multiple Signaling Pathways and Coordinated Communication Between Different Tissues. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	33
700	Histologically resolved multiomics enables precise molecular profiling of human intratumor heterogeneity. <i>PLoS Biology</i> , 2022, 20, e3001699.	2.6	6
701	The role of single-cell genomics in human genetics. <i>Journal of Medical Genetics</i> , 2022, 59, 827-839.	1.5	11
702	Improving the diagnosis of thyroid cancer by machine learning and clinical data. <i>Scientific Reports</i> , 2022, 12, .	1.6	8
703	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
704	Cancer-associated fibroblasts in the single-cell era. <i>Nature Cancer</i> , 2022, 3, 793-807.	5.7	141
705	Single-cell transcriptome of the mouse retinal pigment epithelium in response to a low-dose of doxorubicin. <i>Communications Biology</i> , 2022, 5, .	2.0	6
706	Function of normal oral mucosa revealed by single-cell RNA sequencing. <i>Journal of Cellular Biochemistry</i> , 2022, 123, 1481-1494.	1.2	3
707	Development of Reference Genes for Horticultural Plants. <i>Critical Reviews in Plant Sciences</i> , 2022, 41, 190-208.	2.7	3
708	The Role of NR4A1 in the Pathophysiology of Osteosarcoma: A Comprehensive Bioinformatics Analysis of the Single-Cell RNA Sequencing Dataset. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	2
709	Single-cell RNA sequencing in the context of neuropathic pain: progress, challenges, and prospects. <i>Translational Research</i> , 2023, 251, 96-103.	2.2	5
710	Advances in Single-Cell Toxicogenomics in Environmental Toxicology. <i>Environmental Science & Technology</i> , 2022, 56, 11132-11145.	4.6	7
711	Cell Layers: uncovering clustering structure in unsupervised single-cell transcriptomic analysis. <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	0
712	scGENA: A Single-Cell Gene Coexpression Network Analysis Framework for Clustering Cell Types and Revealing Biological Mechanisms. <i>Bioengineering</i> , 2022, 9, 353.	1.6	5
713	Neuro-immune interactions at single-cell resolution in neurodevelopmental, infectious, and neurodegenerative diseases. <i>Animal Cells and Systems</i> , 2022, 26, 137-147.	0.8	5
714	Identification and Characterization of Genes Related to the Prognosis of Hepatocellular Carcinoma Based on Single-Cell Sequencing. <i>Pathology and Oncology Research</i> , 0, 28, .	0.9	1

#	ARTICLE	IF	CITATIONS
715	Selective Inference for Hierarchical Clustering. <i>Journal of the American Statistical Association</i> , 2024, 119, 332-342.	1.8	17
716	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
717	Gliotransmission of D-serine promotes thirst-directed behaviors in <i>Drosophila</i> . <i>Current Biology</i> , 2022, 32, 3952-3970.e8.	1.8	12
718	Understanding Breast Cancers through Spatial and High-Resolution Visualization Using Imaging Technologies. <i>Cancers</i> , 2022, 14, 4080.	1.7	0
719	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
720	Engineering approaches for cardiac organoid formation and their characterization. <i>Translational Research</i> , 2022, 250, 46-67.	2.2	9
721	Bioinformatics: From NGS Data to Biological Complexity in Variant Detection and Oncological Clinical Practice. <i>Biomedicines</i> , 2022, 10, 2074.	1.4	10
722	Construction of a prognostic model related to copper dependence in breast cancer by single-cell sequencing analysis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
723	SMaSH: a scalable, general marker gene identification framework for single-cell RNA-sequencing. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	13
724	Identification of Human Retinal Organoid Cell Differentiation-Related Genes via Single-Cell Sequencing Data Analysis. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-19.	0.7	0
725	scMTD: a statistical multidimensional imputation method for single-cell RNA-seq data leveraging transcriptome dynamic information. <i>Cell and Bioscience</i> , 2022, 12, .	2.1	3
726	Decoding the Spermatogenesis Program: New Insights from Transcriptomic Analyses. <i>Annual Review of Genetics</i> , 2022, 56, 339-368.	3.2	11
727	Construction and verification of a hypoxia-related nine-gene prognostic model in uveal melanoma based on integrated single-cell and bulk RNA sequencing analyses. <i>Experimental Eye Research</i> , 2022, 223, 109214.	1.2	5
728	The progressive application of single-cell RNA sequencing technology in cardiovascular diseases. <i>Biomedicine and Pharmacotherapy</i> , 2022, 154, 113604.	2.5	5
729	Gaining Insight into SARS-CoV-2 Infection and COVID-19 Severity Using Self-supervised Edge Features and Graph Neural Networks. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2021, 35, 4864-4873.	3.6	6
730	Recent advances in high-throughput single-cell transcriptomics and spatial transcriptomics. <i>Lab on A Chip</i> , 2022, 22, 4774-4791.	3.1	14
731	Transcriptomics. , 2023, , 363-371.		1
732	Interactive Analysis of Single-Cell Data Using Flexible Workflows With SCTK2.0. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0

#	ARTICLE	IF	CITATIONS
733	A Multi-Scale, Multiomic Atlas of Human Normal and Follicular Lymphoma Lymph Nodes. SSRN Electronic Journal, 0, , .	0.4	1
734	Enriching and Characterizing T Cell Repertoires from 3â€² Barcoded Single-Cell Whole Transcriptome Amplification Products. Methods in Molecular Biology, 2022, , 159-182.	0.4	2
735	Computational solutions for spatial transcriptomics. Computational and Structural Biotechnology Journal, 2022, 20, 4870-4884.	1.9	30
736	SPROUT: spectral sparsification helps restore the spatial structure at single-cell resolution. NAR Genomics and Bioinformatics, 2022, 4, .	1.5	2
737	Update on the Molecular Aspects and Methods Underlying the Complex Architecture of FSHD. Cells, 2022, 11, 2687.	1.8	9
739	FTH1- and SAT1-Induced Astrocytic Ferroptosis Is Involved in Alzheimerâ€™s Disease: Evidence from Single-Cell Transcriptomic Analysis. Pharmaceuticals, 2022, 15, 1177.	1.7	15
740	Analysis of Tumor-Infiltrating T-Cell Transcriptomes Reveal a Unique Genetic Signature across Different Types of Cancer. International Journal of Molecular Sciences, 2022, 23, 11065.	1.8	4
741	Cell Taxonomy: a curated repository of cell types with multifaceted characterization. Nucleic Acids Research, 2023, 51, D853-D860.	6.5	12
742	Fibronectin-1 is a dominant mechanism for rheumatoid arthritis via the mediation of synovial fibroblasts activity. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	2
743	Integrated multi-omics reveals the activated retinal microglia with intracellular metabolic reprogramming contributes to inflammation in STZ-induced early diabetic retinopathy. Frontiers in Immunology, 0, 13, .	2.2	11
744	Effects of Procainamide on CTLA-4 and CD28 Expression in Drug-Induced Lupus: A Research Protocol. , 2022, 6, 1-7.		0
746	Transcriptomics and RNA-Based Therapeutics as Potential Approaches to Manage SARS-CoV-2 Infection. International Journal of Molecular Sciences, 2022, 23, 11058.	1.8	2
747	Tmsb10 triggers fetal Leydig differentiation by suppressing the RAS/ERK pathway. Communications Biology, 2022, 5, .	2.0	3
748	Impaired expression of serine/arginine protein kinase 2 (SRPK2) affects melanoma progression. Frontiers in Genetics, 0, 13, .	1.1	2
749	Single-cell sequencing and establishment of an 8-gene prognostic model for pancreatic cancer patients. Frontiers in Oncology, 0, 12, .	1.3	5
750	Integrating Micro and Nano Technologies for Cell Engineering and Analysis: Toward the Next Generation of Cell Therapy Workflows. ACS Nano, 2022, 16, 15653-15680.	7.3	5
751	Transcriptomic plasticity of the hypothalamic osmoregulatory control centre of the Arabian dromedary camel. Communications Biology, 2022, 5, .	2.0	3
752	Pathogenic variants detected by RNA sequencing in Cornelia de Lange syndrome. Genomics, 2022, 114, 110468.	1.3	1

#	ARTICLE	IF	CITATIONS
753	Single-Cell Transcriptome Analysis of Treg. <i>Methods in Molecular Biology</i> , 2023, , 259-278.	0.4	2
754	A single-cell atlas of the cycling murine ovary. <i>ELife</i> , 0, 11, .	2.8	23
755	Finer resolution analysis of transcriptional programming during the active migration of chicken primordial germ cells. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 5911-5924.	1.9	2
756	Transcriptomics and Cocaine Addiction. , 2022, , 2029-2051.		0
757	Genetic susceptibility to autoimmunityâ€”Current status and challenges. <i>Advances in Immunology</i> , 2022, , 25-54.	1.1	2
758	Cellular Heterogeneity and Molecular Reprogramming of the Host Response during Influenza Acute Lung Injury. <i>Journal of Virology</i> , 2022, 96, .	1.5	1
759	Development of an HPV Genotype Detection Platform Based on Aggregation-Induced Emission (AIE) and Flow-Through Hybridization Technologies. <i>Molecules</i> , 2022, 27, 7036.	1.7	2
761	Computational Analysis of Single-Cell RNA-Seq Data. <i>Methods in Molecular Biology</i> , 2023, , 165-172.	0.4	0
762	Dysregulation of B7 family and its association with tumor microenvironment in uveal melanoma. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
764	Imputation Methods for scRNA Sequencing Data. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 10684.	1.3	3
765	Advances in single-cell sequencing technology in the field of hepatocellular carcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
766	Multiplexed Singleâ€Nucleus RNA Sequencing Using Lipidâ€Oligo Barcodes. <i>Current Protocols</i> , 2022, 2, .	1.3	1
767	Discovering biomarkers of hepatocellular carcinoma from single-cell RNA sequencing data by cooperative games on gene regulatory network. <i>Journal of Computational Science</i> , 2022, 65, 101881.	1.5	2
768	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
769	Innovations in integrating machine learning and agent-based modeling of biomedical systems. <i>Frontiers in Systems Biology</i> , 0, 2, .	0.5	6
770	From phenotypical investigation to RNA-sequencing for gene expression analysis: A workflow for single and pooled rare cells. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
771	Tumor Immune Microenvironment and Immunotherapy in Non-Small Cell Lung Cancer: Update and New Challenges. , 2022, 13, 1615.		21
772	Biological Sequence Classification: A Review on Data and General Methods. <i>Research</i> , 2022, 2022, .	2.8	30

#	ARTICLE	IF	CITATIONS
773	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
774	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
775	Advances in Single-Cell Sequencing Technology and Its Application in Poultry Science. <i>Genes</i> , 2022, 13, 2211.	1.0	2
776	Scalable transcriptomics analysis with Dask: applications in data science and machine learning. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	1
777	Upregulated FKBP1A Suppresses Glioblastoma Cell Growth via Apoptosis Pathway. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14935.	1.8	2
778	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
779	Computational approaches and challenges for identification and annotation of non-coding RNAs using RNA-Seq. <i>Functional and Integrative Genomics</i> , 2022, 22, 1105-1112.	1.4	9
780	Single-cell RNA-sequencing data analysis reveals a highly correlated triphasic transcriptional response to SARS-CoV-2 infection. <i>Communications Biology</i> , 2022, 5, .	2.0	1
781	Single-cell and microarray chip analysis revealed the underlying pathogenesis of ulcerative colitis and validated model genes in diagnosis and drug response. <i>Human Cell</i> , 0, , .	1.2	0
782	Getting sweeter: new evidence for glucose transporters in specific cell types of the airway?. <i>American Journal of Physiology - Cell Physiology</i> , 2023, 324, C153-C166.	2.1	1
783	Insights into protein post-translational modification landscapes of individual human cells by trapped ion mobility time-of-flight mass spectrometry. <i>Nature Communications</i> , 2022, 13, .	5.8	23
784	Upcoming progress of transcriptomics studies on plants: An overview. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	19
785	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
786	Large-Scale Single-Nucleus RNA Sequencing Compatible with Complex Archived Samples. <i>Methods in Molecular Biology</i> , 2023, , 333-346.	0.4	0
787	Improving head and neck cancer therapies by immunomodulation of the tumour microenvironment. <i>Nature Reviews Cancer</i> , 2023, 23, 173-188.	12.8	37
788	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
789	Advancements of next generation sequencing in the field of Rheumatoid Arthritis. <i>Egyptian Journal of Basic and Applied Sciences</i> , 2023, 10, 135-156.	0.2	0
790	Insights into osteoarthritis development from single-cell RNA sequencing of subchondral bone. <i>RMD Open</i> , 2022, 8, e002617.	1.8	4

#	ARTICLE	IF	CITATIONS
791	Delineating Plasmodium liver infection across space and time. Trends in Parasitology, 2022, , .	1.5	0
792	Oligodendrocyte lineage cells: Advances in development, disease, and heterogeneity. Journal of Neurochemistry, 2023, 164, 468-480.	2.1	4
793	Single-cell discovery of the scene and potential immunotherapeutic target in hypopharyngeal tumor environment. Cancer Gene Therapy, 0, , .	2.2	1
794	A Framework for Comparison and Assessment of Synthetic RNA-Seq Data. Genes, 2022, 13, 2362.	1.0	3
795	A machine learning approach to elucidating PFOS-induced alterations of repressive epigenetic marks in kidney cancer cells with single-cell imaging. Environmental Advances, 2023, 11, 100344.	2.2	2
796	Artificial intelligence-based multi-omics analysis fuels cancer precision medicine. Seminars in Cancer Biology, 2023, 88, 187-200.	4.3	36
797	Single-cell-led drug repurposing for Alzheimerâ€™s disease. Scientific Reports, 2023, 13, .	1.6	4
798	Making use of noise in biological systems. Progress in Biophysics and Molecular Biology, 2023, 178, 83-90.	1.4	8
799	Single-cell and spatial sequencing application in pathology. Journal of Pathology and Translational Medicine, 2023, 57, 43-51.	0.4	4
800	Recording of cellular physiological histories along optically readable self-assembling protein chains. Nature Biotechnology, 2023, 41, 640-651.	9.4	10
801	Single-Cell Transcriptome Identifies the Renal Cell Type Tropism of Human BK Polyomavirus. International Journal of Molecular Sciences, 2023, 24, 1330.	1.8	1
802	Advances and Challenges in Spatial Transcriptomics for Developmental Biology. Biomolecules, 2023, 13, 156.	1.8	11
803	The multiple roles of enteric glial cells in intestinal homeostasis and regeneration. Seminars in Cell and Developmental Biology, 2023, 150-151, 43-49.	2.3	4
804	Angiogenesis-related gene signatures reveal the prognosis of cervical cancer based on single cell sequencing and co-expression network analysis. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	3
806	Managing the Transition to Widespread Metagenomic Monitoring: Policy Considerations for Future Biosurveillance. Health Security, 2023, 21, 34-45.	0.9	2
807	A Novel and Fast Distributed Computation Method for Fisherâ€™s Exact Test and Its Application in Gene Expression Profiling Studies. , 2022, , .		1
808	SimCH: simulation of single-cell RNA sequencing data by modeling cellular heterogeneity at gene expression level. Briefings in Bioinformatics, 2023, 24, .	3.2	0
809	scARMF: Association Rule Mining-based feature selection Framework for Single-Cell transcriptomics data. , 2022, , .		0

#	ARTICLE	IF	CITATIONS
810	Breast cancer combined prognostic model based on lactate metabolism genes. <i>Medicine (United Kingdom)</i> , 2023, 102, 1000000.	0.4	4
811	Application of Single-Cell RNA Sequencing in Ovarian Development. <i>Biomolecules</i> , 2023, 13, 47.	1.8	7
812	Epigenetic remodeling of the immune landscape in cancer: therapeutic hurdles and opportunities. <i>Journal of Biomedical Science</i> , 2023, 30, .	2.6	7
813	I-CONVEX: Fast and Accurate de Novo Transcriptome Recovery from Long Reads. <i>Communications in Computer and Information Science</i> , 2023, , 339-363.	0.4	0
815	Preparation of Drosophila Ovarioles for Single-Cell RNA Sequencing. <i>Methods in Molecular Biology</i> , 2023, , 323-333.	0.4	0
816	Elucidating Tooth Development and Pulp Biology by Single-Cell Sequencing Technology. , 2023, , 333-352.		0
817	Progress in Discovering Transcriptional Noise in Aging. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3701.	1.8	3
818	Creating an atlas of the bone microenvironment during oral inflammatory-related bone disease using single-cell profiling. <i>ELife</i> , 0, 12, .	2.8	5
820	Cellular heterogeneity and stem cells of vascular endothelial cells in blood vessel formation and homeostasis: Insights from single-cell RNA sequencing. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	1.8	4
821	Identifying TME signatures for cervical cancer prognosis based on GEO and TCGA databases. <i>Heliyon</i> , 2023, 9, e15096.	1.4	2
822	Cell-type classification of cancer single-cell RNA-seq data using the Subsemble ensemble-based machine learning classifier. <i>Frontiers in Bioinformatics</i> , 0, 12, 406.	0.8	0
823	Targeting the metastatic niche: Single-cell lineage tracing in prime time. <i>IScience</i> , 2023, 26, 106174.	1.9	1
824	Spatiotemporal Characterization of Human Early Intervertebral Disc Formation at Single-Cell Resolution. <i>Advanced Science</i> , 2023, 10, .	5.6	6
825	GRACE: Graph autoencoder based single-cell clustering through ensemble similarity learning. <i>PLoS ONE</i> , 2023, 18, e0284527.	1.1	0
826	Single-cell RNA sequencing in skeletal muscle developmental biology. <i>Biomedicine and Pharmacotherapy</i> , 2023, 162, 114631.	2.5	1
827	Interpreting omics data with pathway enrichment analysis. <i>Trends in Genetics</i> , 2023, 39, 308-319.	2.9	10
828	Deep learning in spatial transcriptomics: Learning from the next next-generation sequencing. <i>Biophysics Reviews</i> , 2023, 4, .	1.0	6
829	A combined analysis of bulk and single-cell sequencing data reveals metabolic enzyme, pyruvate dehydrogenase E1 subunit beta (PDHB), as a prediction biomarker for the tumor immune response and immunotherapy. <i>Heliyon</i> , 2023, 9, e13456.	1.4	2

#	ARTICLE	IF	CITATIONS
831	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
832	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
833	Translational veterinary epilepsy: A win-win situation for human and veterinary neurology. <i>Veterinary Journal</i> , 2023, 293, 105956.	0.6	6
835	Cardiomyocyte Pdk4 response is associated with metabolic maladaptation in aging. <i>Aging Cell</i> , 2023, 22, .	3.0	7
836	Current and Emerging Techniques for Diagnosis and MRD Detection in AML: A Comprehensive Narrative Review. <i>Cancers</i> , 2023, 15, 1362.	1.7	1
837	Deep Learning-Based Prediction of Time-Series Single-Cell RNA-Seq Data. <i>Lecture Notes in Networks and Systems</i> , 2023, , 213-226.	0.5	0
839	Sertoli cell-only syndrome: advances, challenges, and perspectives in genetics and mechanisms. <i>Cellular and Molecular Life Sciences</i> , 2023, 80, .	2.4	5
840	Single-cell chemokine receptor profiles delineate the immune contexture of tertiary lymphoid structures in head and neck squamous cell carcinoma. <i>Cancer Letters</i> , 2023, 558, 216105.	3.2	3
841	Advances in Mass Spectrometry-Based Single Cell Analysis. <i>Biology</i> , 2023, 12, 395.	1.3	4
842	Defining Selective Neuronal Resilience and Identifying Targets for Neuroprotection and Axon Regeneration Using Single-Cell RNA Sequencing: Experimental Approaches. <i>Methods in Molecular Biology</i> , 2023, , 1-18.	0.4	1
843	Adipose tissue at single-cell resolution. <i>Cell Metabolism</i> , 2023, 35, 386-413.	7.2	30
844	Single-cell RNA sequencing reveals the role of cell heterogeneity in the sex difference in primary hyperparathyroidism. <i>Frontiers in Endocrinology</i> , 0, 14, .	1.5	2
845	Landscape of Exhausted T Cells in Tuberculosis Revealed by Single-Cell Sequencing. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	4
846	New technologies to study helminth development and host-parasite interactions. <i>International Journal for Parasitology</i> , 2023, 53, 393-403.	1.3	6
847	Omics-based approaches to guide the design of biomaterials. <i>Materials Today</i> , 2023, 64, 98-120.	8.3	5
848	Renal enhanced CT images reveal the tandem mechanism between tumor cells and immunocytes based on bulk/single-cell RNA sequencing. <i>Functional and Integrative Genomics</i> , 2023, 23, .	1.4	1
849	Genetic regulation of nitrogen use efficiency in <i>Gossypium spp</i> . <i>Plant, Cell and Environment</i> , 2023, 46, 1749-1773.	2.8	6
850	The art of Epitranscriptomics. <i>International Physical Medicine & Rehabilitation Journal</i> , 2022, 7, 12-12.	0.1	0

#	ARTICLE	IF	CITATIONS
851	A Strategic Research Framework for Defeating Diabetes in India: A 21st-Century Agenda. <i>Journal of the Indian Institute of Science</i> , 2023, 103, 33-54.	0.9	3
852	Comparative analysis of NovaSeq 6000 and MGISEQ 2000 single-cell RNA sequencing data. <i>Quantitative Biology</i> , 2022, 10, 333-340.	0.3	2
854	Spatial Transcriptomics in Inflammation: Dissecting the Immune Response in 3D in Complex Tissues. , 2023, , 243-279.		0
855	Recent advances in understanding neuronal diversity and neural circuit complexity across different brain regions using single-cell sequencing. <i>Frontiers in Neural Circuits</i> , 0, 17, .	1.4	3
856	Nuclei on the Rise: When Nuclei-Based Methods Meet Next-Generation Sequencing. <i>Cells</i> , 2023, 12, 1051.	1.8	1
857	Phosphorylation of AKT by lysyl oxidase-like 2 activates the PI3K/AKT signaling pathway to promote proliferation, invasion and metastasis in esophageal squamous carcinoma. <i>Clinical and Translational Oncology</i> , 2023, 25, 2487-2498.	1.2	1
858	Comparison of cell subsets in chronic obstructive pulmonary disease and controls based on single-cell transcriptome sequencing. <i>Technology and Health Care</i> , 2023, , 1-16.	0.5	0
859	Standardization and Interpretation of RNA-sequencing for Transplantation. <i>Transplantation</i> , 2023, 107, 2155-2167.	0.5	3
860	Cell annotation using scRNA-seq data: A protein-protein interaction network approach. <i>MethodsX</i> , 2023, 10, 102179.	0.7	0
861	Single-Cell RNA Sequencing for Studying Human Cancers. <i>Annual Review of Biomedical Data Science</i> , 2023, 6, .	2.8	2
862	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
863	Mosaic results after preimplantation genetic testing for aneuploidy may be accompanied by changes in global gene expression. <i>Frontiers in Molecular Biosciences</i> , 0, 10, .	1.6	4
864	Food nutrition and toxicology targeting on specific organs in the era of single-cell sequencing. , 2024, 13, 75-89.		1
865	Emodin-induced Necroptosis in Prostate Cancer Cells via the Mitochondrial Fission HSP90/MLKL/PGAM Pathway. <i>Chemistry and Biodiversity</i> , 0, , .	1.0	1
866	Methods for assessment of the tumour microenvironment and immune interactions in non-small cell lung cancer. A narrative review. <i>Frontiers in Oncology</i> , 0, 13, .	1.3	1
867	Transfer learning in a biomaterial fibrosis model identifies in vivo senescence heterogeneity and contributions to vascularization and matrix production across species and diverse pathologies. <i>GeroScience</i> , 2023, 45, 2559-2587.	2.1	10
876	How Severe is Your COVID-19? Predicting SARS-CoV-2 Infection with Graph Attention Capsule Networks. , 2022, , .		0
879	Single-cell transcriptomics of the ocular anterior segment: a comprehensive review. <i>Eye</i> , 0, , .	1.1	1

#	ARTICLE	IF	CITATIONS
904	Understanding tumour endothelial cell heterogeneity and function from single-cell omics. <i>Nature Reviews Cancer</i> , 2023, 23, 544-564.	12.8	14
906	Meta-analysis of Gene Activity (MAGA) Contributions and Correlation with Gene Expression, Through GAGAM. <i>Lecture Notes in Computer Science</i> , 2023, , 193-207.	1.0	3
908	Applications of single-cell RNA sequencing in drug discovery and development. <i>Nature Reviews Drug Discovery</i> , 2023, 22, 496-520.	21.5	31
913	Single-cell transcriptomics and data analyses for prokaryotes – Past, present and future concepts. <i>Advances in Applied Microbiology</i> , 2023, , 1-39.	1.3	0
933	SSCAE: A Neuromorphic SNN Autoencoder for sc-RNA-seq Dimensionality Reduction. , 2023, , .		0
946	Genomic and Single Cell Transcriptomic Analyses in Autism Spectrum Disorder. , 2023, , .		0
950	Epigenetic control of cell signalling in cancer stem cells. <i>International Review of Cell and Molecular Biology</i> , 2024, , 67-88.	1.6	0
953	Application of Single-Cell Sequencing on Stem Cell Research. , 2023, , 1-26.		0
955	Single B-cell sequencing in monoclonal antibody discovery. , 2024, , 73-95.		0
966	Circulating Tumour Cell Isolation and Molecular Profiling; Potential Therapeutic Intervention. <i>Current Cancer Research</i> , 2023, , 359-385.	0.2	0
975	ESR: Optimizing Gene Feature Selection for scRNA-seq Data. , 2023, , .		0
983	Prognosticating Drug Targets and Responses by Analyzing Metastasis-Related Cancer Pathways. , 2023, , 1-25.		0
985	Root Causal Inference from Single Cell RNA Sequencing with the Negative Binomial. , 2023, , .		2
998	Decoding the role of aberrant RNA alternative splicing in hepatocellular carcinoma: a comprehensive review. <i>Journal of Cancer Research and Clinical Oncology</i> , 2023, 149, 17691-17708.	1.2	0
1007	Research progress and application of single-cell sequencing in head and neck malignant tumors. <i>Cancer Gene Therapy</i> , 2024, 31, 18-27.	2.2	0
1037	The single-cell big data analytics. , 2024, , 115-128.		0
1048	GRAIGH: Gene Regulation accessibility integrating GeneHancer database. , 2023, , .		0
1049	Machine learning applications in cancer genomics. , 2024, , 41-72.		0

#	ARTICLE	IF	CITATIONS
1050	Unravelling the genomics and proteomics aspects of the stemness phenotype in stem cells. , 2024, , 129-147.		0
1051	Diagnosis of infectious diseases: complexity to convenience. Sensors & Diagnostics, 2024, 3, 354-380.	1.9	0
1058	scGAT: A Cell-Type Annotation Framework for Single-Cell Transcriptomics Using Graph Attention Network and Meta Learning. , 2023, , .		0
1059	Genomic Innovations for Improving Crops: The CRISPR Way. , 2023, , 273-286.		0
1064	Open microfluidics: droplet microarrays as next generation multiwell plates for high throughput screening. Lab on A Chip, 2024, 24, 1064-1075.	3.1	0
1083	Trawling the Genome: Drug Target Identification in the Postgenomic Era. , 2024, , 43-88.		0