

# Hao Wu

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/2996869/hao-wu-publications-by-citations.pdf>

**Version:** 2024-04-23

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

174  
papers

20,177  
citations

62  
h-index

141  
g-index

192  
ext. papers

24,059  
ext. citations

12.6  
avg, IF

6.85  
L-index

#	Paper	IF	Citations
174	R/qtl: QTL mapping in experimental crosses. <i>Bioinformatics</i> , <b>2003</b> , 19, 889-90	7.2	2292
173	DNA methylation-related chromatin remodeling in activity-dependent BDNF gene regulation. <i>Science</i> , <b>2003</b> , 302, 890-3	33.3	1187
172	Brain-Region-Specific Organoids Using Mini-bioreactors for Modeling ZIKV Exposure. <i>Cell</i> , <b>2016</b> , 165, 1238-1254	56.2	1165
171	Increased methylation variation in epigenetic domains across cancer types. <i>Nature Genetics</i> , <b>2011</b> , 43, 768-75	36.3	825
170	Reversing DNA methylation: mechanisms, genomics, and biological functions. <i>Cell</i> , <b>2014</b> , 156, 45-68	56.2	738
169	Editing DNA Methylation in the Mammalian Genome. <i>Cell</i> , <b>2016</b> , 167, 233-247.e17	56.2	690
168	5-hmC-mediated epigenetic dynamics during postnatal neurodevelopment and aging. <i>Nature Neuroscience</i> , <b>2011</b> , 14, 1607-16	25.5	639
167	Dual functions of Tet1 in transcriptional regulation in mouse embryonic stem cells. <i>Nature</i> , <b>2011</b> , 473, 389-93	50.4	496
166	Mechanisms and functions of Tet protein-mediated 5-methylcytosine oxidation. <i>Genes and Development</i> , <b>2011</b> , 25, 2436-52	12.6	487
165	Dnmt3a-dependent nonpromoter DNA methylation facilitates transcription of neurogenic genes. <i>Science</i> , <b>2010</b> , 329, 444-8	33.3	480
164	Large histone H3 lysine 9 dimethylated chromatin blocks distinguish differentiated from embryonic stem cells. <i>Nature Genetics</i> , <b>2009</b> , 41, 246-50	36.3	469
163	Genome-wide profiling of 5-formylcytosine reveals its roles in epigenetic priming. <i>Cell</i> , <b>2013</b> , 153, 678-91	56.2	453
162	Histone modifications around individual BDNF gene promoters in prefrontal cortex are associated with extinction of conditioned fear. <i>Learning and Memory</i> , <b>2007</b> , 14, 268-76	2.8	441
161	Genome-wide analysis of 5-hydroxymethylcytosine distribution reveals its dual function in transcriptional regulation in mouse embryonic stem cells. <i>Genes and Development</i> , <b>2011</b> , 25, 679-84	12.6	431
160	Genome-wide analysis reveals TET- and TDG-dependent 5-methylcytosine oxidation dynamics. <i>Cell</i> , <b>2013</b> , 153, 692-706	56.2	390
159	Comprehensive high-throughput arrays for relative methylation (CHARM). <i>Genome Research</i> , <b>2008</b> , 18, 780-90	9.7	350
158	DNA methylation controls the timing of astroglialogenesis through regulation of JAK-STAT signaling. <i>Development (Cambridge)</i> , <b>2005</b> , 132, 3345-56	6.6	334

157	A positive autoregulatory loop of Jak-STAT signaling controls the onset of astroglialogenesis. <i>Nature Neuroscience</i> , <b>2005</b> , 8, 616-25	25.5	302
156	Genome-scale epigenetic reprogramming during epithelial-to-mesenchymal transition. <i>Nature Structural and Molecular Biology</i> , <b>2011</b> , 18, 867-74	17.6	297
155	CD133+ neural stem cells in the ependyma of mammalian postnatal forebrain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 1026-31	11.5	266
154	Long-Lived Plasma Cells Are Contained within the CD19(-)CD38(hi)CD138(+) Subset in Human Bone Marrow. <i>Immunity</i> , <b>2015</b> , 43, 132-45	32.3	258
153	Epigenomic reprogramming during pancreatic cancer progression links anabolic glucose metabolism to distant metastasis. <i>Nature Genetics</i> , <b>2017</b> , 49, 367-376	36.3	250
152	A Bayesian hierarchical model to detect differentially methylated loci from single nucleotide resolution sequencing data. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, e69	20.1	245
151	Rescue of Fragile X Syndrome Neurons by DNA Methylation Editing of the FMR1 Gene. <i>Cell</i> , <b>2018</b> , 172, 979-992.e6	56.2	239
150	Kdm2b maintains murine embryonic stem cell status by recruiting PRC1 complex to CpG islands of developmental genes. <i>Nature Cell Biology</i> , <b>2013</b> , 15, 373-84	23.4	225
149	U1 small nuclear ribonucleoprotein complex and RNA splicing alterations in Alzheimer's disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 16562-7	11.5	200
148	Differential methylation analysis for BS-seq data under general experimental design. <i>Bioinformatics</i> , <b>2016</b> , 32, 1446-53	7.2	183
147	Coupling of cell migration with neurogenesis by proneural bHLH factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 1319-24	11.5	177
146	Epitranscriptomic mA Regulation of Axon Regeneration in the Adult Mammalian Nervous System. <i>Neuron</i> , <b>2018</b> , 97, 313-325.e6	13.9	171
145	Phosphorylation of MeCP2 at Serine 80 regulates its chromatin association and neurological function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 4882-7	11.5	171
144	Detection of differentially methylated regions from whole-genome bisulfite sequencing data without replicates. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, e141	20.1	144
143	Genome-wide analysis reveals methyl-CpG-binding protein 2-dependent regulation of microRNAs in a mouse model of Rett syndrome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 18161-6	11.5	140
142	Cellular resolution maps of X chromosome inactivation: implications for neural development, function, and disease. <i>Neuron</i> , <b>2014</b> , 81, 103-19	13.9	139
141	A new shrinkage estimator for dispersion improves differential expression detection in RNA-seq data. <i>Biostatistics</i> , <b>2013</b> , 14, 232-43	3.7	139
140	Genome-wide DNA hydroxymethylation changes are associated with neurodevelopmental genes in the developing human cerebellum. <i>Human Molecular Genetics</i> , <b>2012</b> , 21, 5500-10	5.6	135

139	Deletion of astroglial Dicer causes non-cell-autonomous neuronal dysfunction and degeneration. <i>Journal of Neuroscience</i> , <b>2011</b> , 31, 8306-19	6.6	135
138	Fat mass and obesity-associated (FTO) protein regulates adult neurogenesis. <i>Human Molecular Genetics</i> , <b>2017</b> , 26, 2398-2411	5.6	134
137	MAANOVA: A Software Package for the Analysis of Spotted cDNA Microarray Experiments <b>2003</b> , 313-341		131
136	DNA N6-methyladenine is dynamically regulated in the mouse brain following environmental stress. <i>Nature Communications</i> , <b>2017</b> , 8, 1122	17.4	123
135	Redefining CpG islands using hidden Markov models. <i>Biostatistics</i> , <b>2010</b> , 11, 499-514	3.7	122
134	Molecular signatures associated with ZIKV exposure in human cortical neural progenitors. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 8610-8620	20.1	119
133	Tet1 and 5-hydroxymethylation: a genome-wide view in mouse embryonic stem cells. <i>Cell Cycle</i> , <b>2011</b> , 10, 2428-36	4.7	113
132	Integrative genomic and functional analyses reveal neuronal subtype differentiation bias in human embryonic stem cell lines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 13821-6	11.5	112
131	Epigenetic regulation of stem cell differentiation. <i>Pediatric Research</i> , <b>2006</b> , 59, 21R-5R	3.2	111
130	Single-base resolution analysis of active DNA demethylation using methylase-assisted bisulfite sequencing. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 1231-40	44.5	107
129	Sliced Human Cortical Organoids for Modeling Distinct Cortical Layer Formation. <i>Cell Stem Cell</i> , <b>2020</b> , 26, 766-781.e9	18	106
128	Inhibition of ileal bile acid uptake protects against nonalcoholic fatty liver disease in high-fat diet-fed mice. <i>Science Translational Medicine</i> , <b>2016</b> , 8, 357ra122	17.5	106
127	Cell-cycle control of developmentally regulated transcription factors accounts for heterogeneity in human pluripotent cells. <i>Stem Cell Reports</i> , <b>2013</b> , 1, 532-44	8	98
126	Ago2 immunoprecipitation identifies predicted microRNAs in human embryonic stem cells and neural precursors. <i>PLoS ONE</i> , <b>2009</b> , 4, e7192	3.7	94
125	R/qtlbim: QTL with Bayesian Interval Mapping in experimental crosses. <i>Bioinformatics</i> , <b>2007</b> , 23, 641-3	7.2	92
124	Nondestructive, base-resolution sequencing of 5-hydroxymethylcytosine using a DNA deaminase. <i>Nature Biotechnology</i> , <b>2018</b> ,	44.5	91
123	Fragile X mental retardation protein modulates the stability of its m6A-marked messenger RNA targets. <i>Human Molecular Genetics</i> , <b>2018</b> , 27, 3936-3950	5.6	89
122	Complete morphologies of basal forebrain cholinergic neurons in the mouse. <i>ELife</i> , <b>2014</b> , 3, e02444	8.9	87

121	Dissecting Cell-Type Composition and Activity-Dependent Transcriptional State in Mammalian Brains by Massively Parallel Single-Nucleus RNA-Seq. <i>Molecular Cell</i> , <b>2017</b> , 68, 1006-1015.e7	17.6	81
120	Subtelomeric hotspots of aberrant 5-hydroxymethylcytosine-mediated epigenetic modifications during reprogramming to pluripotency. <i>Nature Cell Biology</i> , <b>2013</b> , 15, 700-11	23.4	80
119	Estimating and accounting for tumor purity in the analysis of DNA methylation data from cancer studies. <i>Genome Biology</i> , <b>2017</b> , 18, 17	18.3	78
118	HMMR maintains the stemness and tumorigenicity of glioblastoma stem-like cells. <i>Cancer Research</i> , <b>2014</b> , 74, 3168-79	10.1	73
117	Highly efficient derivation of ventricular cardiomyocytes from induced pluripotent stem cells with a distinct epigenetic signature. <i>Cell Research</i> , <b>2012</b> , 22, 142-54	24.7	70
116	ViRBase: a resource for virus-host ncRNA-associated interactions. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D578-821	28.1	68
115	NanoStringDiff: a novel statistical method for differential expression analysis based on NanoString nCounter data. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, e151	20.1	67
114	Ten-eleven translocation 2 interacts with forkhead box O3 and regulates adult neurogenesis. <i>Nature Communications</i> , <b>2017</b> , 8, 15903	17.4	65
113	Fragile X premutation RNA is sufficient to cause primary ovarian insufficiency in mice. <i>Human Molecular Genetics</i> , <b>2012</b> , 21, 5039-47	5.6	65
112	A genome-wide profiling of brain DNA hydroxymethylation in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , <b>2017</b> , 13, 674-688	1.2	61
111	A phenotypic small-molecule screen identifies an orphan ligand-receptor pair that regulates neural stem cell differentiation. <i>Chemistry and Biology</i> , <b>2007</b> , 14, 1019-30		61
110	The nuclear matrix protein HNRNPU maintains 3D genome architecture globally in mouse hepatocytes. <i>Genome Research</i> , <b>2018</b> , 28, 192-202	9.7	57
109	Modeling Parkinson's disease in monkeys for translational studies, a critical analysis. <i>Experimental Neurology</i> , <b>2014</b> , 256, 133-43	5.7	57
108	Open-ringed structure of the Cdt1-Mcm2-7 complex as a precursor of the MCM double hexamer. <i>Nature Structural and Molecular Biology</i> , <b>2017</b> , 24, 300-308	17.6	56
107	Lin28A Binds Active Promoters and Recruits Tet1 to Regulate Gene Expression. <i>Molecular Cell</i> , <b>2016</b> , 61, 153-60	17.6	55
106	Zika virus directly infects peripheral neurons and induces cell death. <i>Nature Neuroscience</i> , <b>2017</b> , 20, 1209-1212	23.5	49
105	Genome-wide alteration of 5-hydroxymethylcytosine in a mouse model of fragile X-associated tremor/ataxia syndrome. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 1095-107	5.6	49
104	PROPER: comprehensive power evaluation for differential expression using RNA-seq. <i>Bioinformatics</i> , <b>2015</b> , 31, 233-41	7.2	48

103	Charting oxidized methylcytosines at base resolution. <i>Nature Structural and Molecular Biology</i> , <b>2015</b> , 22, 656-61	17.6	47
102	A species-generalized probabilistic model-based definition of CpG islands. <i>Mammalian Genome</i> , <b>2009</b> , 20, 674-80	3.2	47
101	miR-29c-3p regulates DNMT3B and LATS1 methylation to inhibit tumor progression in hepatocellular carcinoma. <i>Cell Death and Disease</i> , <b>2019</b> , 10, 48	9.8	45
100	Morphologic diversity of cutaneous sensory afferents revealed by genetically directed sparse labeling. <i>ELife</i> , <b>2012</b> , 1, e00181	8.9	43
99	Copy number variant analysis of human embryonic stem cells. <i>Stem Cells</i> , <b>2008</b> , 26, 1484-9	5.8	42
98	Active N-Methyladenine Demethylation by DMAD Regulates Gene Expression by Coordinating with Polycomb Protein in Neurons. <i>Molecular Cell</i> , <b>2018</b> , 71, 848-857.e6	17.6	40
97	N6-methyladenosine dynamics in neurodevelopment and aging, and its potential role in Alzheimer's disease. <i>Genome Biology</i> , <b>2021</b> , 22, 17	18.3	38
96	MacroH2A1 associates with nuclear lamina and maintains chromatin architecture in mouse liver cells. <i>Scientific Reports</i> , <b>2015</b> , 5, 17186	4.9	36
95	The ups and downs of BDNF in Rett syndrome. <i>Neuron</i> , <b>2006</b> , 49, 321-3	13.9	36
94	Predicting tumor purity from methylation microarray data. <i>Bioinformatics</i> , <b>2015</b> , 31, 3401-5	7.2	35
93	High glucose microenvironments inhibit the proliferation and migration of bone mesenchymal stem cells by activating GSK3β. <i>Journal of Bone and Mineral Metabolism</i> , <b>2016</b> , 34, 140-50	2.9	34
92	Hypoxia-inducible protein 2 Hig2/Hilpda mediates neutral lipid accumulation in macrophages and contributes to atherosclerosis in apolipoprotein E-deficient mice. <i>FASEB Journal</i> , <b>2017</b> , 31, 4971-4984	0.9	34
91	Base-resolution methylation patterns accurately predict transcription factor bindings in vivo. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 2757-66	20.1	33
90	Euchromatin islands in large heterochromatin domains are enriched for CTCF binding and differentially DNA-methylated regions. <i>BMC Genomics</i> , <b>2012</b> , 13, 566	4.5	33
89	A novel statistical method for quantitative comparison of multiple ChIP-seq datasets. <i>Bioinformatics</i> , <b>2015</b> , 31, 1889-96	7.2	32
88	Network-based survival-associated module biomarker and its crosstalk with cell death genes in ovarian cancer. <i>Scientific Reports</i> , <b>2015</b> , 5, 11566	4.9	31
87	Reversing DNA methylation: new insights from neuronal activity-induced Gadd45b in adult neurogenesis. <i>Science Signaling</i> , <b>2009</b> , 2, pe17	8.8	31
86	Negative Allosteric Modulation of mGluR5 Partially Corrects Pathophysiology in a Mouse Model of Rett Syndrome. <i>Journal of Neuroscience</i> , <b>2016</b> , 36, 11946-11958	6.6	29

85	Massively parallel and time-resolved RNA sequencing in single cells with scNT-seq. <i>Nature Methods</i> , <b>2020</b> , 17, 991-1001	21.6	29
84	Deletion of atbf1/zfhx3 in mouse prostate causes neoplastic lesions, likely by attenuation of membrane and secretory proteins and multiple signaling pathways. <i>Neoplasia</i> , <b>2014</b> , 16, 377-89	6.4	28
83	Integrating Next-Generation Genomic Sequencing and Mass Spectrometry To Estimate Allele-Specific Protein Abundance in Human Brain. <i>Journal of Proteome Research</i> , <b>2017</b> , 16, 3336-3347	5.6	28
82	N-cadherin prevents the premature differentiation of anterior heart field progenitors in the pharyngeal mesodermal microenvironment. <i>Cell Research</i> , <b>2014</b> , 24, 1420-32	24.7	27
81	Overlapping euchromatin/heterochromatin-associated marks are enriched in imprinted gene regions and predict allele-specific modification. <i>Genome Research</i> , <b>2008</b> , 18, 1806-13	9.7	27
80	Ten-Eleven Translocation Proteins Modulate the Response to Environmental Stress in Mice. <i>Cell Reports</i> , <b>2018</b> , 25, 3194-3203.e4	10.6	27
79	Regulation and function of mammalian DNA methylation patterns: a genomic perspective. <i>Briefings in Functional Genomics</i> , <b>2012</b> , 11, 240-50	4.9	24
78	InfiniumPurify: An R package for estimating and accounting for tumor purity in cancer methylation research. <i>Genes and Diseases</i> , <b>2018</b> , 5, 43-45	6.6	23
77	Reply to <b>Reassessing the abundance of H3K9me2 chromatin domains in embryonic stem cells</b> <i>Nature Genetics</i> , <b>2010</b> , 42, 5-6	36.3	22
76	Intensity normalization improves color calling in SOLiD sequencing. <i>Nature Methods</i> , <b>2010</b> , 7, 336-7	21.6	22
75	Base-resolution profiling of active DNA demethylation using MAB-seq and caMAB-seq. <i>Nature Protocols</i> , <b>2016</b> , 11, 1081-100	18.8	22
74	Plasmodium knowlesi gene expression differs in ex vivo compared to in vitro blood-stage cultures. <i>Malaria Journal</i> , <b>2015</b> , 14, 110	3.6	21
73	Single-cell transcriptomic analysis of adult mouse pituitary reveals sexual dimorphism and physiologic demand-induced cellular plasticity. <i>Protein and Cell</i> , <b>2020</b> , 11, 565-583	7.2	21
72	Two-phase differential expression analysis for single cell RNA-seq. <i>Bioinformatics</i> , <b>2018</b> , 34, 3340-3348	7.2	21
71	Neural progenitors populate the cerebrospinal fluid of preterm patients with hydrocephalus. <i>Journal of Pediatrics</i> , <b>2006</b> , 148, 337-340	3.6	21
70	Disease prediction by cell-free DNA methylation. <i>Briefings in Bioinformatics</i> , <b>2019</b> , 20, 585-597	13.4	21
69	Glioblastoma extracellular vesicles induce the tumour-promoting transformation of neural stem cells. <i>Cancer Letters</i> , <b>2019</b> , 466, 1-12	9.9	18
68	Accounting for tumor purity improves cancer subtype classification from DNA methylation data. <i>Bioinformatics</i> , <b>2017</b> , 33, 2651-2657	7.2	17

67	Dissecting differential signals in high-throughput data from complex tissues. <i>Bioinformatics</i> , <b>2019</b> , 35, 3898-3905	7.2	17
66	Endothelin-1 supports clonal derivation and expansion of cardiovascular progenitors derived from human embryonic stem cells. <i>Nature Communications</i> , <b>2016</b> , 7, 10774	17.4	17
65	Local false discovery rate estimation using feature reliability in LC/MS metabolomics data. <i>Scientific Reports</i> , <b>2015</b> , 5, 17221	4.9	17
64	TOAST: improving reference-free cell composition estimation by cross-cell type differential analysis. <i>Genome Biology</i> , <b>2019</b> , 20, 190	18.3	16
63	5-Hydroxymethylcytosine alterations in the human postmortem brains of autism spectrum disorder. <i>Human Molecular Genetics</i> , <b>2018</b> , 27, 2955-2964	5.6	16
62	Effects of slow and regular breathing exercise on cardiopulmonary coupling and blood pressure. <i>Medical and Biological Engineering and Computing</i> , <b>2017</b> , 55, 327-341	3.1	15
61	High-fat diet induced insulin resistance in pregnant rats through pancreatic pax6 signaling pathway. <i>International Journal of Clinical and Experimental Pathology</i> , <b>2015</b> , 8, 5196-202	1.4	15
60	A smartphone based respiratory biofeedback system <b>2010</b> ,		14
59	Near-infrared fluorescence imaging-guided focused ultrasound-mediated therapy against Rheumatoid Arthritis by MTX-ICG-loaded iRGD-modified echogenic liposomes. <i>Theranostics</i> , <b>2020</b> , 10, 10092-10105	12.1	14
58	SynBioLGDB: a resource for experimentally validated logic gates in synthetic biology. <i>Scientific Reports</i> , <b>2015</b> , 5, 8090	4.9	12
57	JAMIE: joint analysis of multiple CHIP-chip experiments. <i>Bioinformatics</i> , <b>2010</b> , 26, 1864-70	7.2	12
56	The long noncoding RNA lncCIRBIL disrupts the nuclear translocation of Bclaf1 alleviating cardiac ischemia-reperfusion injury. <i>Nature Communications</i> , <b>2021</b> , 12, 522	17.4	12
55	Early embryos reprogram DNA methylation in two steps. <i>Cell Stem Cell</i> , <b>2012</b> , 10, 487-9	18	11
54	Flat mount imaging of mouse skin and its application to the analysis of hair follicle patterning and sensory axon morphology. <i>Journal of Visualized Experiments</i> , <b>2014</b> , e51749	1.6	10
53	ROC Curve Analysis in the Presence of Imperfect Reference Standards. <i>Statistics in Biosciences</i> , <b>2017</b> , 9, 91-104	1.5	10
52	A human forebrain organoid model of fragile X syndrome exhibits altered neurogenesis and highlights new treatment strategies. <i>Nature Neuroscience</i> , <b>2021</b> , 24, 1377-1391	25.5	10
51	PolyaPeak: detecting transcription factor binding sites from CHIP-seq using peak shape information. <i>PLoS ONE</i> , <b>2014</b> , 9, e89694	3.7	9
50	A Prototype of Wearable Respiration Biofeedback Platform and Its Preliminary Evaluation on Cardiovascular Variability <b>2009</b> ,		9



49	Crystal structure of human coactosin-like protein at 1.9 Å resolution. <i>Protein Science</i> , <b>2004</b> , 13, 2845-51	6.3	9
48	Tumor purity and differential methylation in cancer epigenomics. <i>Briefings in Functional Genomics</i> , <b>2016</b> , 15, 408-419	4.9	9
47	Photobiomodulation with 630-nm LED radiation inhibits the proliferation of human synoviocyte MH7A cells possibly via TRPV4/PI3K/AKT/mTOR signaling pathway. <i>Lasers in Medical Science</i> , <b>2020</b> , 35, 1927-1936	3.1	8
46	Experimental Design and Power Calculation for RNA-seq Experiments. <i>Methods in Molecular Biology</i> , <b>2016</b> , 1418, 379-90	1.4	8
45	Deciphering Rett syndrome with mouse genetics, epigenomics, and human neurons. <i>International Review of Neurobiology</i> , <b>2009</b> , 89, 147-60	4.4	8
44	A comprehensive review of computational prediction of genome-wide features. <i>Briefings in Bioinformatics</i> , <b>2018</b> ,	13.4	8
43	Statistical challenges in analyzing methylation and long-range chromosomal interaction data. <i>Statistics in Biosciences</i> , <b>2016</b> , 8, 284-309	1.5	7
42	Predictive modeling of single-cell DNA methylome data enhances integration with transcriptome data. <i>Genome Research</i> , <b>2021</b> , 31, 101-109	9.7	7
41	Pneumonia scoring systems for severe COVID-19: which one is better. <i>Virology Journal</i> , <b>2021</b> , 18, 33	6.1	7
40	PLMET: A Novel Pseudolikelihood-Based EM Test for Homogeneity in Generalized Exponential Tilt Mixture Models. <i>Journal of the American Statistical Association</i> , <b>2017</b> , 112, 1393-1404	2.8	6
39	Differential gene network analysis from single cell RNA-seq. <i>Journal of Genetics and Genomics</i> , <b>2017</b> , 44, 331-334	4	6
38	Simulation, power evaluation and sample size recommendation for single-cell RNA-seq. <i>Bioinformatics</i> , <b>2020</b> , 36, 4860-4868	7.2	6
37	Palliative Radiofrequency Ablation Accelerates the Residual Tumor Progression Through Increasing Tumor-Infiltrating MDSCs and Reducing T-Cell-Mediated Anti-Tumor Immune Responses in Animal Model. <i>Frontiers in Oncology</i> , <b>2020</b> , 10, 1308	5.3	6
36	Accounting for cell type hierarchy in evaluating single cell RNA-seq clustering. <i>Genome Biology</i> , <b>2020</b> , 21, 123	18.3	5
35	Dual effects of N-methyladenosine on cancer progression and immunotherapy. <i>Molecular Therapy - Nucleic Acids</i> , <b>2021</b> , 24, 25-39	10.7	5
34	A robust approach for ECG-based analysis of cardiopulmonary coupling. <i>Medical Engineering and Physics</i> , <b>2016</b> , 38, 671-678	2.4	5
33	Accurate feature selection improves single-cell RNA-seq cell clustering. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	5
32	Evaluation of some aspects in supervised cell type identification for single-cell RNA-seq: classifier, feature selection, and reference construction. <i>Genome Biology</i> , <b>2021</b> , 22, 264	18.3	5

31	Robust partial reference-free cell composition estimation from tissue expression. <i>Bioinformatics</i> , <b>2020</b> , 36, 3431-3438	7.2	4
30	Tet2-mediated epigenetic drive for astrocyte differentiation from embryonic neural stem cells. <i>Cell Death Discovery</i> , <b>2020</b> , 6, 30	6.9	4
29	A High Throughput Whole Blood Assay for Analysis of Multiple Antigen-Specific T Cell Responses in Human Infection. <i>Journal of Immunology</i> , <b>2018</b> , 200, 3008-3019	5.3	4
28	A comprehensive comparison of supervised and unsupervised methods for cell type identification in single-cell RNA-seq.. <i>Briefings in Bioinformatics</i> , <b>2022</b> ,	13.4	4
27	Ethnicity-specific and overlapping alterations of brain hydroxymethylome in Alzheimer's disease. <i>Human Molecular Genetics</i> , <b>2020</b> , 29, 149-158	5.6	4
26	LIN28 coordinately promotes nucleolar/ribosomal functions and represses the 2C-like transcriptional program in pluripotent stem cells. <i>Protein and Cell</i> , <b>2021</b> , 1	7.2	4
25	Novel immunoassay for diagnosis of ongoing <i>Clostridioides difficile</i> infections using serum and medium enriched for newly synthesized antibodies (MENSA). <i>Journal of Immunological Methods</i> , <b>2021</b> , 492, 112932	2.5	4
24	The molecular mechanism study of insulin on proliferation and differentiation of osteoblasts under high glucose conditions. <i>Cell Biochemistry and Function</i> , <b>2019</b> , 37, 385-394	4.2	3
23	The molecular mechanism study of insulin in promoting wound healing under high-glucose conditions. <i>Journal of Cellular Biochemistry</i> , <b>2019</b> , 120, 16244-16253	4.7	3
22	Building the Quality Control System for Medical Equipments in Hospital <b>2010</b> ,		3
21	Age-related DNA hydroxymethylation is enriched for gene expression and immune system processes in human peripheral blood. <i>Epigenetics</i> , <b>2020</b> , 15, 294-306	5.7	3
20	Bisulfite-Free Sequencing of 5-Hydroxymethylcytosine with APOBEC-Coupled Epigenetic Sequencing (ACE-Seq). <i>Methods in Molecular Biology</i> , <b>2021</b> , 2198, 349-367	1.4	3
19	Measuring the spatial correlations of protein binding sites. <i>Bioinformatics</i> , <b>2016</b> , 32, 1766-72	7.2	2
18	Massively parallel, time-resolved single-cell RNA sequencing with scNT-Seq		2
17	Dissecting differential signals in high-throughput data from complex tissues		2
16	Pan-cancer analysis of differential DNA methylation patterns. <i>BMC Medical Genomics</i> , <b>2020</b> , 13, 154	3.7	2
15	Detecting m6A methylation regions from Methylated RNA Immunoprecipitation Sequencing. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	2
14	Differential methylation analysis for bisulfite sequencing using DSS. <i>Quantitative Biology</i> , <b>2019</b> , 7, 327-334		2

13	Downregulation of SOCS gene expression can inhibit the formation of acute and persistent BDV infections. <i>Scandinavian Journal of Immunology</i> , <b>2021</b> , 93, e12974	3.4	2
12	Exploring the cooccurrence patterns of multiple sets of genomic intervals. <i>BioMed Research International</i> , <b>2013</b> , 2013, 617545	3	1
11	Neuronal Yin Yang1 in the prefrontal cortex regulates transcriptional and behavioral responses to chronic stress in mice.. <i>Nature Communications</i> , <b>2022</b> , 13, 55	17.4	1
10	JAMIE: A software tool for jointly analyzing multiple CHIP-chip experiments. <i>Methods in Molecular Biology</i> , <b>2012</b> , 802, 363-75	1.4	1
9	Penalized Latent Dirichlet Allocation Model in Single-Cell RNA Sequencing. <i>Statistics in Biosciences</i> , <b>2021</b> , 13, 1	1.5	1
8	Downregulation of TOP2 modulates neurodegeneration caused by GGGGCC expanded repeats. <i>Human Molecular Genetics</i> , <b>2021</b> , 30, 893-901	5.6	1
7	Non-linear Normalization for Non-UMI Single Cell RNA-Seq. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 612670	4.5	1
6	Detection of Newly Secreted Antibodies Predicts Non-recurrence in Primary Infection.. <i>Journal of Clinical Microbiology</i> , <b>2022</b> , jcm0220121	9.7	0
5	Complete deconvolution of DNA methylation signals from complex tissues: a geometric approach. <i>Bioinformatics</i> , <b>2021</b> , 37, 1052-1059	7.2	0
4	Computer Simulation, Bioinformatics, and Statistical Analysis of Cancer Data and Processes. <i>Cancer Informatics</i> , <b>2015</b> , 14, 247-51	2.4	
3	Statistics for next generation sequencing - meeting report. <i>Frontiers in Genetics</i> , <b>2012</b> , 3, 128	4.5	
2	Influence of painless delivery on the maternal and neonatal outcomes under the guidance of new concept of labor.. <i>American Journal of Translational Research (discontinued)</i> , <b>2021</b> , 13, 12973-12979	3	
1	Differential Methylation Analysis for Bisulfite Sequencing (BS-Seq) Data.. <i>Methods in Molecular Biology</i> , <b>2022</b> , 2432, 211-226	1.4	