

# Hao Wu

## List of Publications by Year in descending order

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179  
papers

26,676  
citations

13827

67  
h-index

6818

155  
g-index

192  
all docs

192  
docs citations

192  
times ranked

38079  
citing authors

#	ARTICLE	IF	CITATIONS
1	R/qrtl: QTL mapping in experimental crosses. <i>Bioinformatics</i> , 2003, 19, 889-890.	1.8	3,197
2	Brain-Region-Specific Organoids Using Mini-bioreactors for Modeling ZIKV Exposure. <i>Cell</i> , 2016, 165, 1238-1254.	13.5	1,680
3	DNA Methylation-Related Chromatin Remodeling in Activity-Dependent Bdnf Gene Regulation. <i>Science</i> , 2003, 302, 890-893.	6.0	1,315
4	Increased methylation variation in epigenetic domains across cancer types. <i>Nature Genetics</i> , 2011, 43, 768-775.	9.4	968
5	Editing DNA Methylation in the Mammalian Genome. <i>Cell</i> , 2016, 167, 233-247.e17.	13.5	932
6	Reversing DNA Methylation: Mechanisms, Genomics, and Biological Functions. <i>Cell</i> , 2014, 156, 45-68.	13.5	914
7	5-hmC-mediated epigenetic dynamics during postnatal neurodevelopment and aging. <i>Nature Neuroscience</i> , 2011, 14, 1607-1616.	7.1	746
8	Dual functions of Tet1 in transcriptional regulation in mouse embryonic stem cells. <i>Nature</i> , 2011, 473, 389-393.	13.7	581
9	Mechanisms and functions of Tet protein-mediated 5-methylcytosine oxidation. <i>Genes and Development</i> , 2011, 25, 2436-2452.	2.7	565
10	Dnmt3a-Dependent Nonpromoter DNA Methylation Facilitates Transcription of Neurogenic Genes. <i>Science</i> , 2010, 329, 444-448.	6.0	544
11	Large histone H3 lysine 9 dimethylated chromatin blocks distinguish differentiated from embryonic stem cells. <i>Nature Genetics</i> , 2009, 41, 246-250.	9.4	540
12	Genome-wide Profiling of 5-Formylcytosine Reveals Its Roles in Epigenetic Priming. <i>Cell</i> , 2013, 153, 678-691.	13.5	502
13	Histone modifications around individual BDNF gene promoters in prefrontal cortex are associated with extinction of conditioned fear. <i>Learning and Memory</i> , 2007, 14, 268-276.	0.5	491
14	Genome-wide analysis of 5-hydroxymethylcytosine distribution reveals its dual function in transcriptional regulation in mouse embryonic stem cells. <i>Genes and Development</i> , 2011, 25, 679-684.	2.7	488
15	Genome-wide Analysis Reveals TET- and TDG-Dependent 5-Methylcytosine Oxidation Dynamics. <i>Cell</i> , 2013, 153, 692-706.	13.5	440
16	Long-Lived Plasma Cells Are Contained within the CD19 <sup>hi</sup> CD38 <sup>hi</sup> CD138 <sup>+</sup> Subset in Human Bone Marrow. <i>Immunity</i> , 2015, 43, 132-145.	6.6	415
17	A Bayesian hierarchical model to detect differentially methylated loci from single nucleotide resolution sequencing data. <i>Nucleic Acids Research</i> , 2014, 42, e69-e69.	6.5	405
18	Comprehensive high-throughput arrays for relative methylation (CHARM). <i>Genome Research</i> , 2008, 18, 780-790.	2.4	379

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19	DNA methylation controls the timing of astroglialogenesis through regulation of JAK-STAT signaling. <i>Development (Cambridge)</i> , 2005, 132, 3345-3356.	1.2	371
20	Epigenomic reprogramming during pancreatic cancer progression links anabolic glucose metabolism to distant metastasis. <i>Nature Genetics</i> , 2017, 49, 367-376.	9.4	365
21	Rescue of Fragile X Syndrome Neurons by DNA Methylation Editing of the FMR1 Gene. <i>Cell</i> , 2018, 172, 979-992.e6.	13.5	351
22	A positive autoregulatory loop of Jak-STAT signaling controls the onset of astroglialogenesis. <i>Nature Neuroscience</i> , 2005, 8, 616-625.	7.1	350
23	Genome-scale epigenetic reprogramming during epithelial-to-mesenchymal transition. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 867-874.	3.6	340
24	Differential methylation analysis for BS-seq data under general experimental design. <i>Bioinformatics</i> , 2016, 32, 1446-1453.	1.8	336
25	CD133 <sup>+</sup> 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> , 2008, 105, 1026-1031.	3.3	300
26	Kdm2b maintains murine embryonic stem cell status by recruiting PRC1 complex to CpG islands of developmental genes. <i>Nature Cell Biology</i> , 2013, 15, 373-384.	4.6	292
27	Epitranscriptomic m6A Regulation of Axon Regeneration in the Adult Mammalian Nervous System. <i>Neuron</i> , 2018, 97, 313-325.e6.	3.8	292
28	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> , 2013, 110, 16562-16567.	3.3	268
29	Sliced Human Cortical Organoids for Modeling Distinct Cortical Layer Formation. <i>Cell Stem Cell</i> , 2020, 26, 766-781.e9.	5.2	268
30	Fat mass and obesity-associated (FTO) protein regulates adult neurogenesis. <i>Human Molecular Genetics</i> , 2017, 26, 2398-2411.	1.4	221
31	A new shrinkage estimator for dispersion improves differential expression detection in RNA-seq data. <i>Biostatistics</i> , 2013, 14, 232-243.	0.9	210
32	Detection of differentially methylated regions from whole-genome bisulfite sequencing data without replicates. <i>Nucleic Acids Research</i> , 2015, 43, gkv715.	6.5	203
33	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> , 2009, 106, 4882-4887.	3.3	200
34	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> , 2006, 103, 1319-1324.	3.3	195
35	DNA N6-methyladenine is dynamically regulated in the mouse brain following environmental stress. <i>Nature Communications</i> , 2017, 8, 1122.	5.8	182
36	Cellular Resolution Maps of X Chromosome Inactivation: Implications for Neural Development, Function, and Disease. <i>Neuron</i> , 2014, 81, 103-119.	3.8	179

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37	MAANOVA: A Software Package for the Analysis of Spotted cDNA Microarray Experiments. <i>Statistics in the Health Sciences</i> , 2003, , 313-341.	0.2	165
38	Genome-wide analysis reveals methyl-CpGâ€“binding protein 2â€“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> , 2010, 107, 18161-18166.	3.3	164
39	Inhibition of ileal bile acid uptake protects against nonalcoholic fatty liver disease in high-fat dietâ€“fed mice. <i>Science Translational Medicine</i> , 2016, 8, 357ra122.	5.8	160
40	Genome-wide DNA hydroxymethylation changes are associated with neurodevelopmental genes in the developing human cerebellum. <i>Human Molecular Genetics</i> , 2012, 21, 5500-5510.	1.4	157
41	Molecular signatures associated with ZIKV exposure in human cortical neural progenitors. <i>Nucleic Acids Research</i> , 2016, 44, 8610-8620.	6.5	155
42	Deletion of Astroglial Dicer Causes Non-Cell-Autonomous Neuronal Dysfunction and Degeneration. <i>Journal of Neuroscience</i> , 2011, 31, 8306-8319.	1.7	154
43	Nondestructive, base-resolution sequencing of 5-hydroxymethylcytosine using a DNA deaminase. <i>Nature Biotechnology</i> , 2018, 36, 1083-1090.	9.4	154
44	Epigenetic Regulation of Stem Cell Differentiation. <i>Pediatric Research</i> , 2006, 59, 21R-25R.	1.1	153
45	Redefining CpG islands using hidden Markov models. <i>Biostatistics</i> , 2010, 11, 499-514.	0.9	151
46	Dissecting Cell-Type Composition and Activity-Dependent Transcriptional State in Mammalian Brains by Massively Parallel Single-Nucleus RNA-Seq. <i>Molecular Cell</i> , 2017, 68, 1006-1015.e7.	4.5	143
47	Single-base resolution analysis of active DNA demethylation using methylase-assisted bisulfite sequencing. <i>Nature Biotechnology</i> , 2014, 32, 1231-1240.	9.4	139
48	Complete morphologies of basal forebrain cholinergic neurons in the mouse. <i>ELife</i> , 2014, 3, e02444.	2.8	133
49	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> , 2007, 104, 13821-13826.	3.3	131
50	N6-methyladenosine dynamics in neurodevelopment and aging, and its potential role in Alzheimerâ€™s disease. <i>Genome Biology</i> , 2021, 22, 17.	3.8	131
51	Cell-Cycle Control of Developmentally Regulated Transcription Factors Accounts for Heterogeneity in Human Pluripotent Cells. <i>Stem Cell Reports</i> , 2013, 1, 532-544.	2.3	129
52	Fragile X mental retardation protein modulates the stability of its m6A-marked messenger RNA targets. <i>Human Molecular Genetics</i> , 2018, 27, 3936-3950.	1.4	129
53	Tet1 and 5-hydroxymethylation. <i>Cell Cycle</i> , 2011, 10, 2428-2436.	1.3	121
54	R/qtlbim: QTL with Bayesian Interval Mapping in experimental crosses. <i>Bioinformatics</i> , 2007, 23, 641-643.	1.8	115

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55	Estimating and accounting for tumor purity in the analysis of DNA methylation data from cancer studies. <i>Genome Biology</i> , 2017, 18, 17.	3.8	112
56	Ago2 Immunoprecipitation Identifies Predicted MicroRNAs in Human Embryonic Stem Cells and Neural Precursors. <i>PLoS ONE</i> , 2009, 4, e7192.	1.1	103
57	Massively parallel and time-resolved RNA sequencing in single cells with scNT-seq. <i>Nature Methods</i> , 2020, 17, 991-1001.	9.0	103
58	HMMR Maintains the Stemness and Tumorigenicity of Glioblastoma Stem-like Cells. <i>Cancer Research</i> , 2014, 74, 3168-3179.	0.4	101
59	NanoStringDiff: a novel statistical method for differential expression analysis based on NanoString nCounter data. <i>Nucleic Acids Research</i> , 2016, 44, gkw677.	6.5	100
60	The nuclear matrix protein HNRNPU maintains 3D genome architecture globally in mouse hepatocytes. <i>Genome Research</i> , 2018, 28, 192-202.	2.4	91
61	Subtelomeric hotspots of aberrant 5-hydroxymethylcytosine-mediated epigenetic modifications during reprogramming to pluripotency. <i>Nature Cell Biology</i> , 2013, 15, 700-711.	4.6	87
62	Open-ringed structure of the Cdt1-Mcm2 complex as a precursor of the MCM double hexamer. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 300-308.	3.6	87
63	Zika virus directly infects peripheral neurons and induces cell death. <i>Nature Neuroscience</i> , 2017, 20, 1209-1212.	7.1	85
64	A genome-wide profiling of brain DNA hydroxymethylation in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2017, 13, 674-688.	0.4	83
65	Ten-eleven translocation 2 interacts with forkhead box O3 and regulates adult neurogenesis. <i>Nature Communications</i> , 2017, 8, 15903.	5.8	82
66	ViRBase: a resource for virus-host ncRNA-associated interactions. <i>Nucleic Acids Research</i> , 2015, 43, D578-D582.	6.5	81
67	PROPER: comprehensive power evaluation for differential expression using RNA-seq. <i>Bioinformatics</i> , 2015, 31, 233-241.	1.8	80
68	A human forebrain organoid model of fragile X syndrome exhibits altered neurogenesis and highlights new treatment strategies. <i>Nature Neuroscience</i> , 2021, 24, 1377-1391.	7.1	80
69	Fragile X premutation RNA is sufficient to cause primary ovarian insufficiency in mice. <i>Human Molecular Genetics</i> , 2012, 21, 5039-5047.	1.4	78
70	Highly efficient derivation of ventricular cardiomyocytes from induced pluripotent stem cells with a distinct epigenetic signature. <i>Cell Research</i> , 2012, 22, 142-154.	5.7	77
71	Lin28A Binds Active Promoters and Recruits Tet1 to Regulate Gene Expression. <i>Molecular Cell</i> , 2016, 61, 153-160.	4.5	74
72	miR-29c-3p regulates DNMT3B and LATS1 methylation to inhibit tumor progression in hepatocellular carcinoma. <i>Cell Death and Disease</i> , 2019, 10, 48.	2.7	72

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73	Active N6-Methyladenine Demethylation by DMAD Regulates Gene Expression by Coordinating with Polycomb Protein in Neurons. <i>Molecular Cell</i> , 2018, 71, 848-857.e6.	4.5	71
74	A Phenotypic Small-Molecule Screen Identifies an Orphan Ligand-Receptor Pair that Regulates Neural Stem Cell Differentiation. <i>Chemistry and Biology</i> , 2007, 14, 1019-1030.	6.2	67
75	Modeling Parkinson's disease in monkeys for translational studies, a critical analysis. <i>Experimental Neurology</i> , 2014, 256, 133-143.	2.0	62
76	Charting oxidized methylcytosines at base resolution. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 656-661.	3.6	62
77	Morphologic diversity of cutaneous sensory afferents revealed by genetically directed sparse labeling. <i>ELife</i> , 2012, 1, e00181.	2.8	56
78	Single-cell transcriptomic analysis of adult mouse pituitary reveals sexual dimorphism and physiologic demand-induced cellular plasticity. <i>Protein and Cell</i> , 2020, 11, 565-583.	4.8	55
79	A species-generalized probabilistic model-based definition of CpG islands. <i>Mammalian Genome</i> , 2009, 20, 674-80.	1.0	52
80	Genome-wide alteration of 5-hydroxymethylcytosine in a mouse model of fragile X-associated tremor/ataxia syndrome. <i>Human Molecular Genetics</i> , 2014, 23, 1095-1107.	1.4	52
81	Copy Number Variant Analysis of Human Embryonic Stem Cells. <i>Stem Cells</i> , 2008, 26, 1484-1489.	1.4	50
82	Predicting tumor purity from methylation microarray data. <i>Bioinformatics</i> , 2015, 31, 3401-3405.	1.8	50
83	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> , 2017, 31, 4971-4984.	0.2	50
84	A novel statistical method for quantitative comparison of multiple ChIP-seq datasets. <i>Bioinformatics</i> , 2015, 31, 1889-1896.	1.8	48
85	Integrating Next-Generation Genomic Sequencing and Mass Spectrometry To Estimate Allele-Specific Protein Abundance in Human Brain. <i>Journal of Proteome Research</i> , 2017, 16, 3336-3347.	1.8	48
86	InfiniumPurify: An R package for estimating and accounting for tumor purity in cancer methylation research. <i>Genes and Diseases</i> , 2018, 5, 43-45.	1.5	48
87	Base-resolution methylation patterns accurately predict transcription factor bindings in vivo. <i>Nucleic Acids Research</i> , 2015, 43, 2757-2766.	6.5	46
88	Ten-Eleven Translocation Proteins Modulate the Response to Environmental Stress in Mice. <i>Cell Reports</i> , 2018, 25, 3194-3203.e4.	2.9	46
89	MacroH2A1 associates with nuclear lamina and maintains chromatin architecture in mouse liver cells. <i>Scientific Reports</i> , 2015, 5, 17186.	1.6	44
90	TOAST: improving reference-free cell composition estimation by cross-cell type differential analysis. <i>Genome Biology</i> , 2019, 20, 190.	3.8	42

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91	Negative Allosteric Modulation of mGluR5 Partially Corrects Pathophysiology in a Mouse Model of Rett Syndrome. <i>Journal of Neuroscience</i> , 2016, 36, 11946-11958.	1.7	41
92	High glucose microenvironments inhibit the proliferation and migration of bone mesenchymal stem cells by activating GSK3 $\beta$ . <i>Journal of Bone and Mineral Metabolism</i> , 2016, 34, 140-150.	1.3	41
93	Euchromatin islands in large heterochromatin domains are enriched for CTCF binding and differentially DNA-methylated regions. <i>BMC Genomics</i> , 2012, 13, 566.	1.2	40
94	The Ups and Downs of BDNF in Rett Syndrome. <i>Neuron</i> , 2006, 49, 321-323.	3.8	39
95	Network-based survival-associated module biomarker and its crosstalk with cell death genes in ovarian cancer. <i>Scientific Reports</i> , 2015, 5, 11566.	1.6	36
96	N-cadherin prevents the premature differentiation of anterior heart field progenitors in the pharyngeal mesodermal microenvironment. <i>Cell Research</i> , 2014, 24, 1420-1432.	5.7	35
97	Dissecting differential signals in high-throughput data from complex tissues. <i>Bioinformatics</i> , 2019, 35, 3898-3905.	1.8	35
98	Disease prediction by cell-free DNA methylation. <i>Briefings in Bioinformatics</i> , 2019, 20, 585-597.	3.2	35
99	Reversing DNA Methylation: New Insights from Neuronal Activity-Induced Gadd45b in Adult Neurogenesis. <i>Science Signaling</i> , 2009, 2, pe17.	1.6	34
100	Two-phase differential expression analysis for single cell RNA-seq. <i>Bioinformatics</i> , 2018, 34, 3340-3348.	1.8	34
101	Glioblastoma extracellular vesicles induce the tumour-promoting transformation of neural stem cells. <i>Cancer Letters</i> , 2019, 466, 1-12.	3.2	34
102	Regulation and function of mammalian DNA methylation patterns: a genomic perspective. <i>Briefings in Functional Genomics</i> , 2012, 11, 240-250.	1.3	33
103	Reply to "Reassessing the abundance of H3K9me2 chromatin domains in embryonic stem cells". <i>Nature Genetics</i> , 2010, 42, 5-6.	9.4	32
104	Accounting for tumor purity improves cancer subtype classification from DNA methylation data. <i>Bioinformatics</i> , 2017, 33, 2651-2657.	1.8	32
105	Near-infrared fluorescence imaging-guided focused ultrasound-mediated therapy against Rheumatoid Arthritis by MTX-ICG-loaded iRGD-modified echogenic liposomes. <i>Theranostics</i> , 2020, 10, 10092-10105.	4.6	32
106	The long noncoding RNA lncCIRBIL disrupts the nuclear translocation of Bclaf1 alleviating cardiac ischemia reperfusion injury. <i>Nature Communications</i> , 2021, 12, 522.	5.8	32
107	Intensity normalization improves color calling in SOLiD sequencing. <i>Nature Methods</i> , 2010, 7, 336-337.	9.0	31
108	Deletion of Atbf1/Zfx3 In Mouse Prostate Causes Neoplastic Lesions, Likely by Attenuation of Membrane and Secretory Proteins and Multiple Signaling Pathways. <i>Neoplasia</i> , 2014, 16, 377-389.	2.3	31

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109	Plasmodium knowlesi gene expression differs in ex vivo compared to in vitro blood-stage cultures. <i>Malaria Journal</i> , 2015, 14, 110.	0.8	31
110	Accurate feature selection improves single-cell RNA-seq cell clustering. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	31
111	Base-resolution profiling of active DNA demethylation using MAB-seq and caMAB-seq. <i>Nature Protocols</i> , 2016, 11, 1081-1100.	5.5	30
112	Overlapping euchromatin/heterochromatin-associated marks are enriched in imprinted gene regions and predict allele-specific modification. <i>Genome Research</i> , 2008, 18, 1806-1813.	2.4	29
113	5-Hydroxymethylcytosine alterations in the human postmortem brains of autism spectrum disorder. <i>Human Molecular Genetics</i> , 2018, 27, 2955-2964.	1.4	28
114	LIN28 coordinately promotes nucleolar/ribosomal functions and represses the 2C-like transcriptional program in pluripotent stem cells. <i>Protein and Cell</i> , 2022, 13, 490-512.	4.8	28
115	Effects of slow and regular breathing exercise on cardiopulmonary coupling and blood pressure. <i>Medical and Biological Engineering and Computing</i> , 2017, 55, 327-341.	1.6	26
116	Local false discovery rate estimation using feature reliability in LC/MS metabolomics data. <i>Scientific Reports</i> , 2015, 5, 17221.	1.6	24
117	Neural progenitors populate the cerebrospinal fluid of preterm patients with hydrocephalus. <i>Journal of Pediatrics</i> , 2006, 148, 337-340.e3.	0.9	23
118	A comprehensive comparison of supervised and unsupervised methods for cell type identification in single-cell RNA-seq. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	22
119	Endothelin-1 supports clonal derivation and expansion of cardiovascular progenitors derived from human embryonic stem cells. <i>Nature Communications</i> , 2016, 7, 10774.	5.8	21
120	Differential methylation analysis for bisulfite sequencing using DSS. <i>Quantitative Biology</i> , 2019, 7, 327-334.	0.3	21
121	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
122	Accounting for cell type hierarchy in evaluating single cell RNA-seq clustering. <i>Genome Biology</i> , 2020, 21, 123.	3.8	20
123	Dual effects of N6-methyladenosine on cancer progression and immunotherapy. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 24, 25-39.	2.3	20
124	A smartphone based respiratory biofeedback system. , 2010, , .		18
125	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> , 2014, , e51749.	0.2	17
126	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> , 2020, 10, 1308.	1.3	17



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127	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> , 2020, 35, 1927-1936.	1.0	17
128	High-fat diet induced insulin resistance in pregnant rats through pancreatic pax6 signaling pathway. <i>International Journal of Clinical and Experimental Pathology</i> , 2015, 8, 5196-202.	0.5	17
129	Pneumonia scoring systems for severe COVID-19: which one is better. <i>Virology Journal</i> , 2021, 18, 33.	1.4	15
130	Simulation, power evaluation and sample size recommendation for single-cell RNA-seq. <i>Bioinformatics</i> , 2020, 36, 4860-4868.	1.8	14
131	Neuronal Yin Yang1 in the prefrontal cortex regulates transcriptional and behavioral responses to chronic stress in mice. <i>Nature Communications</i> , 2022, 13, 55.	5.8	14
132	A Prototype of Wearable Respiration Biofeedback Platform and Its Preliminary Evaluation on Cardiovascular Variability. , 2009, , .		13
133	PolyaPeak: Detecting Transcription Factor Binding Sites from ChIP-seq Using Peak Shape Information. <i>PLoS ONE</i> , 2014, 9, e89694.	1.1	13
134	SynBioLGDB: a resource for experimentally validated logic gates in synthetic biology. <i>Scientific Reports</i> , 2015, 5, 8090.	1.6	13
135	Tumor purity and differential methylation in cancer epigenomics. <i>Briefings in Functional Genomics</i> , 2016, 15, elw016.	1.3	13
136	Experimental Design and Power Calculation for RNA-seq Experiments. <i>Methods in Molecular Biology</i> , 2016, 1418, 379-390.	0.4	13
137	ROC Curve Analysis in the Presence of Imperfect Reference Standards. <i>Statistics in Biosciences</i> , 2017, 9, 91-104.	0.6	13
138	JAMIE: joint analysis of multiple ChIP-chip experiments. <i>Bioinformatics</i> , 2010, 26, 1864-1870.	1.8	12
139	A comprehensive review of computational prediction of genome-wide features. <i>Briefings in Bioinformatics</i> , 2020, 21, 120-134.	3.2	12
140	Robust partial reference-free cell composition estimation from tissue expression. <i>Bioinformatics</i> , 2020, 36, 3431-3438.	1.8	12
141	Predictive modeling of single-cell DNA methylome data enhances integration with transcriptome data. <i>Genome Research</i> , 2021, 31, 101-109.	2.4	12
142	Early Embryos Reprogram DNA Methylation in Two Steps. <i>Cell Stem Cell</i> , 2012, 10, 487-489.	5.2	11
143	A High Throughput Whole Blood Assay for Analysis of Multiple Antigen-Specific T Cell Responses in Human <i>Mycobacterium tuberculosis</i> Infection. <i>Journal of Immunology</i> , 2018, 200, 3008-3019.	0.4	11
144	Ethnicity-specific and overlapping alterations of brain hydroxymethylome in Alzheimer's disease. <i>Human Molecular Genetics</i> , 2020, 29, 149-158.	1.4	11

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145	A robust approach for ECG-based analysis of cardiopulmonary coupling. <i>Medical Engineering and Physics</i> , 2016, 38, 671-678.	0.8	10
146	Detecting m6A methylation regions from Methylated RNA Immunoprecipitation Sequencing. <i>Bioinformatics</i> , 2021, 37, 2818-2824.	1.8	10
147	Crystal structure of human coactosin-like protein at 1.9 Å... resolution. <i>Protein Science</i> , 2008, 13, 2845-2851.	3.1	9
148	Deciphering Rett Syndrome with Mouse Genetics, Epigenomics, and Human Neurons. <i>International Review of Neurobiology</i> , 2009, 89, 147-160.	0.9	9
149	Statistical Challenges in Analyzing Methylation and Long-Range Chromosomal Interaction Data. <i>Statistics in Biosciences</i> , 2016, 8, 284-309.	0.6	9
150	The molecular mechanism study of insulin on proliferation and differentiation of osteoblasts under high glucose conditions. <i>Cell Biochemistry and Function</i> , 2019, 37, 385-394.	1.4	9
151	Age-related DNA hydroxymethylation is enriched for gene expression and immune system processes in human peripheral blood. <i>Epigenetics</i> , 2020, 15, 294-306.	1.3	8
152	PLEMT: A Novel Pseudolikelihood-Based EM Test for Homogeneity in Generalized Exponential Tilt Mixture Models. <i>Journal of the American Statistical Association</i> , 2017, 112, 1393-1404.	1.8	7
153	Differential gene network analysis from single cell RNA-seq. <i>Journal of Genetics and Genomics</i> , 2017, 44, 331-334.	1.7	7
154	Pan-cancer analysis of differential DNA methylation patterns. <i>BMC Medical Genomics</i> , 2020, 13, 154.	0.7	7
155	Tet2-mediated epigenetic drive for astrocyte differentiation from embryonic neural stem cells. <i>Cell Death Discovery</i> , 2020, 6, 30.	2.0	7
156	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> , 2021, 492, 112932.	0.6	7
157	Bisulfite-Free Sequencing of 5-Hydroxymethylcytosine with APOBEC-Coupled Epigenetic Sequencing (ACE-Seq). <i>Methods in Molecular Biology</i> , 2021, 2198, 349-367.	0.4	7
158	Altered hydroxymethylome in the substantia nigra of Parkinson's disease. <i>Human Molecular Genetics</i> , 2022, 31, 3494-3503.	1.4	7
159	The molecular mechanism study of insulin in promoting wound healing under high glucose conditions. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 16244-16253.	1.2	6
160	Building the Quality Control System for Medical Equipments in Hospital. , 2010, , .		5
161	Penalized Latent Dirichlet Allocation Model in Single-Cell RNA Sequencing. <i>Statistics in Biosciences</i> , 2021, 13, 543-562.	0.6	5
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