

Hao Wu

List of Publications by Year in Descending Order

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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	Neuronal Yin Yang1 in the prefrontal cortex regulates transcriptional and behavioral responses to chronic stress in mice.. <i>Nature Communications</i> , 2022 , 13, 55	17.4	1
173	A comprehensive comparison of supervised and unsupervised methods for cell type identification in single-cell RNA-seq.. <i>Briefings in Bioinformatics</i> , 2022 ,	13.4	4
172	Detection of Newly Secreted Antibodies Predicts Non-recurrence in Primary Infection.. <i>Journal of Clinical Microbiology</i> , 2022 , jcm0220121	9.7	0
171	Differential Methylation Analysis for Bisulfite Sequencing (BS-Seq) Data.. <i>Methods in Molecular Biology</i> , 2022 , 2432, 211-226	1.4	
170	Downregulation of TOP2 modulates neurodegeneration caused by GGGGCC expanded repeats. <i>Human Molecular Genetics</i> , 2021 , 30, 893-901	5.6	1
169	Detecting m6A methylation regions from Methylated RNA Immunoprecipitation Sequencing. <i>Bioinformatics</i> , 2021 ,	7.2	2
168	Non-linear Normalization for Non-UMI Single Cell RNA-Seq. <i>Frontiers in Genetics</i> , 2021 , 12, 612670	4.5	1
167	Dual effects of N-methyladenosine on cancer progression and immunotherapy. <i>Molecular Therapy - Nucleic Acids</i> , 2021 , 24, 25-39	10.7	5
166	LIN28 coordinately promotes nucleolar/ribosomal functions and represses the 2C-like transcriptional program in pluripotent stem cells. <i>Protein and Cell</i> , 2021 , 1	7.2	4
165	Complete deconvolution of DNA methylation signals from complex tissues: a geometric approach. <i>Bioinformatics</i> , 2021 , 37, 1052-1059	7.2	0
164	Downregulation of SOCS gene expression can inhibit the formation of acute and persistent BDV infections. <i>Scandinavian Journal of Immunology</i> , 2021 , 93, e12974	3.4	2
163	Predictive modeling of single-cell DNA methylome data enhances integration with transcriptome data. <i>Genome Research</i> , 2021 , 31, 101-109	9.7	7
162	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	2.5	4
161	The long noncoding RNA lncCIRBIL disrupts the nuclear translocation of Bclaf1 alleviating cardiac ischemia-reperfusion injury. <i>Nature Communications</i> , 2021 , 12, 522	17.4	12
160	Accurate feature selection improves single-cell RNA-seq cell clustering. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	5
159	Pneumonia scoring systems for severe COVID-19: which one is better. <i>Virology Journal</i> , 2021 , 18, 33	6.1	7
158	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	25.5	10

157	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	18.3	5
156	N6-methyladenosine dynamics in neurodevelopment and aging, and its potential role in Alzheimer's disease. <i>Genome Biology</i> , 2021 , 22, 17	18.3	38
155	Bisulfite-Free Sequencing of 5-Hydroxymethylcytosine with APOBEC-Coupled Epigenetic Sequencing (ACE-Seq). <i>Methods in Molecular Biology</i> , 2021 , 2198, 349-367	1.4	3
154	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> , 2021 , 13, 12973-12979	3	
153	Accounting for cell type hierarchy in evaluating single cell RNA-seq clustering. <i>Genome Biology</i> , 2020 , 21, 123	18.3	5
152	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	7.2	21
151	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	3.1	8
150	Robust partial reference-free cell composition estimation from tissue expression. <i>Bioinformatics</i> , 2020 , 36, 3431-3438	7.2	4
149	Sliced Human Cortical Organoids for Modeling Distinct Cortical Layer Formation. <i>Cell Stem Cell</i> , 2020 , 26, 766-781.e9	18	106
148	Simulation, power evaluation and sample size recommendation for single-cell RNA-seq. <i>Bioinformatics</i> , 2020 , 36, 4860-4868	7.2	6
147	Tet2-mediated epigenetic drive for astrocyte differentiation from embryonic neural stem cells. <i>Cell Death Discovery</i> , 2020 , 6, 30	6.9	4
146	Ethnicity-specific and overlapping alterations of brain hydroxymethylome in Alzheimer's disease. <i>Human Molecular Genetics</i> , 2020 , 29, 149-158	5.6	4
145	Pan-cancer analysis of differential DNA methylation patterns. <i>BMC Medical Genomics</i> , 2020 , 13, 154	3.7	2
144	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	12.1	14
143	Massively parallel and time-resolved RNA sequencing in single cells with scNT-seq. <i>Nature Methods</i> , 2020 , 17, 991-1001	21.6	29
142	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	5.3	6
141	Age-related DNA hydroxymethylation is enriched for gene expression and immune system processes in human peripheral blood. <i>Epigenetics</i> , 2020 , 15, 294-306	5.7	3
140	TOAST: improving reference-free cell composition estimation by cross-cell type differential analysis. <i>Genome Biology</i> , 2019 , 20, 190	18.3	16

139	Glioblastoma extracellular vesicles induce the tumour-promoting transformation of neural stem cells. <i>Cancer Letters</i> , 2019 , 466, 1-12	9.9	18
138	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	4.2	3
137	The molecular mechanism study of insulin in promoting wound healing under high-glucose conditions. <i>Journal of Cellular Biochemistry</i> , 2019 , 120, 16244-16253	4.7	3
136	Dissecting differential signals in high-throughput data from complex tissues. <i>Bioinformatics</i> , 2019 , 35, 3898-3905	7.2	17
135	miR-29c-3p regulates DNMT3B and LATS1 methylation to inhibit tumor progression in hepatocellular carcinoma. <i>Cell Death and Disease</i> , 2019 , 10, 48	9.8	45
134	Differential methylation analysis for bisulfite sequencing using DSS. <i>Quantitative Biology</i> , 2019 , 7, 327-334		2
133	Disease prediction by cell-free DNA methylation. <i>Briefings in Bioinformatics</i> , 2019 , 20, 585-597	13.4	21
132	Two-phase differential expression analysis for single cell RNA-seq. <i>Bioinformatics</i> , 2018 , 34, 3340-3348	7.2	21
131	Rescue of Fragile X Syndrome Neurons by DNA Methylation Editing of the FMR1 Gene. <i>Cell</i> , 2018 , 172, 979-992.e6	56.2	239
130	Epitranscriptomic m ⁶ A Regulation of Axon Regeneration in the Adult Mammalian Nervous System. <i>Neuron</i> , 2018 , 97, 313-325.e6	13.9	171
129	The nuclear matrix protein HNRNPU maintains 3D genome architecture globally in mouse hepatocytes. <i>Genome Research</i> , 2018 , 28, 192-202	9.7	57
128	InfiniumPurify: An R package for estimating and accounting for tumor purity in cancer methylation research. <i>Genes and Diseases</i> , 2018 , 5, 43-45	6.6	23
127	A High Throughput Whole Blood Assay for Analysis of Multiple Antigen-Specific T Cell Responses in Human Infection. <i>Journal of Immunology</i> , 2018 , 200, 3008-3019	5.3	4
126	Active N-Methyladenine Demethylation by DMAD Regulates Gene Expression by Coordinating with Polycomb Protein in Neurons. <i>Molecular Cell</i> , 2018 , 71, 848-857.e6	17.6	40
125	Fragile X mental retardation protein modulates the stability of its m ⁶ A-marked messenger RNA targets. <i>Human Molecular Genetics</i> , 2018 , 27, 3936-3950	5.6	89
124	A comprehensive review of computational prediction of genome-wide features. <i>Briefings in Bioinformatics</i> , 2018 ,	13.4	8
123	Ten-Eleven Translocation Proteins Modulate the Response to Environmental Stress in Mice. <i>Cell Reports</i> , 2018 , 25, 3194-3203.e4	10.6	27
122	Nondestructive, base-resolution sequencing of 5-hydroxymethylcytosine using a DNA deaminase. <i>Nature Biotechnology</i> , 2018 ,	44.5	91

121	5-Hydroxymethylcytosine alterations in the human postmortem brains of autism spectrum disorder. <i>Human Molecular Genetics</i> , 2018 , 27, 2955-2964	5.6	16
120	A genome-wide profiling of brain DNA hydroxymethylation in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2017 , 13, 674-688	1.2	61
119	Epigenomic reprogramming during pancreatic cancer progression links anabolic glucose metabolism to distant metastasis. <i>Nature Genetics</i> , 2017 , 49, 367-376	36.3	250
118	PLMET: 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	2.8	6
117	Open-ringed structure of the Cdt1-Mcm2-7 complex as a precursor of the MCM double hexamer. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 300-308	17.6	56
116	Fat mass and obesity-associated (FTO) protein regulates adult neurogenesis. <i>Human Molecular Genetics</i> , 2017 , 26, 2398-2411	5.6	134
115	Accounting for tumor purity improves cancer subtype classification from DNA methylation data. <i>Bioinformatics</i> , 2017 , 33, 2651-2657	7.2	17
114	Differential gene network analysis from single cell RNA-seq. <i>Journal of Genetics and Genomics</i> , 2017 , 44, 331-334	4	6
113	DNA N6-methyladenine is dynamically regulated in the mouse brain following environmental stress. <i>Nature Communications</i> , 2017 , 8, 1122	17.4	123
112	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	5.6	28
111	Zika virus directly infects peripheral neurons and induces cell death. <i>Nature Neuroscience</i> , 2017 , 20, 1209-1212	23.5	49
110	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	0.9	34
109	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	17.6	81
108	Estimating and accounting for tumor purity in the analysis of DNA methylation data from cancer studies. <i>Genome Biology</i> , 2017 , 18, 17	18.3	78
107	Ten-eleven translocation 2 interacts with forkhead box O3 and regulates adult neurogenesis. <i>Nature Communications</i> , 2017 , 8, 15903	17.4	65
106	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	3.1	15
105	ROC Curve Analysis in the Presence of Imperfect Reference Standards. <i>Statistics in Biosciences</i> , 2017 , 9, 91-104	1.5	10
104	High glucose microenvironments inhibit the proliferation and migration of bone mesenchymal stem cells by activating GSK3 β . <i>Journal of Bone and Mineral Metabolism</i> , 2016 , 34, 140-50	2.9	34

103	Molecular signatures associated with ZIKV exposure in human cortical neural progenitors. <i>Nucleic Acids Research</i> , 2016 , 44, 8610-8620	20.1	119
102	Negative Allosteric Modulation of mGluR5 Partially Corrects Pathophysiology in a Mouse Model of Rett Syndrome. <i>Journal of Neuroscience</i> , 2016 , 36, 11946-11958	6.6	29
101	Editing DNA Methylation in the Mammalian Genome. <i>Cell</i> , 2016 , 167, 233-247.e17	56.2	690
100	Endothelin-1 supports clonal derivation and expansion of cardiovascular progenitors derived from human embryonic stem cells. <i>Nature Communications</i> , 2016 , 7, 10774	17.4	17
99	NanoStringDiff: a novel statistical method for differential expression analysis based on NanoString nCounter data. <i>Nucleic Acids Research</i> , 2016 , 44, e151	20.1	67
98	Inhibition of ileal bile acid uptake protects against nonalcoholic fatty liver disease in high-fat diet-fed mice. <i>Science Translational Medicine</i> , 2016 , 8, 357ra122	17.5	106
97	Lin28A Binds Active Promoters and Recruits Tet1 to Regulate Gene Expression. <i>Molecular Cell</i> , 2016 , 61, 153-60	17.6	55
96	Statistical challenges in analyzing methylation and long-range chromosomal interaction data. <i>Statistics in Biosciences</i> , 2016 , 8, 284-309	1.5	7
95	Experimental Design and Power Calculation for RNA-seq Experiments. <i>Methods in Molecular Biology</i> , 2016 , 1418, 379-90	1.4	8
94	Measuring the spatial correlations of protein binding sites. <i>Bioinformatics</i> , 2016 , 32, 1766-72	7.2	2
93	Differential methylation analysis for BS-seq data under general experimental design. <i>Bioinformatics</i> , 2016 , 32, 1446-53	7.2	183
92	Tumor purity and differential methylation in cancer epigenomics. <i>Briefings in Functional Genomics</i> , 2016 , 15, 408-419	4.9	9
91	Brain-Region-Specific Organoids Using Mini-bioreactors for Modeling ZIKV Exposure. <i>Cell</i> , 2016 , 165, 1238-1254	56.2	1165
90	A robust approach for ECG-based analysis of cardiopulmonary coupling. <i>Medical Engineering and Physics</i> , 2016 , 38, 671-678	2.4	5
89	Base-resolution profiling of active DNA demethylation using MAB-seq and caMAB-seq. <i>Nature Protocols</i> , 2016 , 11, 1081-100	18.8	22
88	Long-Lived Plasma Cells Are Contained within the CD19(-)CD38(hi)CD138(+) Subset in Human Bone Marrow. <i>Immunity</i> , 2015 , 43, 132-45	32.3	258
87	Plasmodium knowlesi gene expression differs in ex vivo compared to in vitro blood-stage cultures. <i>Malaria Journal</i> , 2015 , 14, 110	3.6	21
86	A novel statistical method for quantitative comparison of multiple ChIP-seq datasets. <i>Bioinformatics</i> , 2015 , 31, 1889-96	7.2	32

85	Predicting tumor purity from methylation microarray data. <i>Bioinformatics</i> , 2015 , 31, 3401-5	7.2	35
84	Charting oxidized methylcytosines at base resolution. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 656-61	17.6	47
83	Detection of differentially methylated regions from whole-genome bisulfite sequencing data without replicates. <i>Nucleic Acids Research</i> , 2015 , 43, e141	20.1	144
82	PROPER: comprehensive power evaluation for differential expression using RNA-seq. <i>Bioinformatics</i> , 2015 , 31, 233-41	7.2	48
81	Network-based survival-associated module biomarker and its crosstalk with cell death genes in ovarian cancer. <i>Scientific Reports</i> , 2015 , 5, 11566	4.9	31
80	Local false discovery rate estimation using feature reliability in LC/MS metabolomics data. <i>Scientific Reports</i> , 2015 , 5, 17221	4.9	17
79	MacroH2A1 associates with nuclear lamina and maintains chromatin architecture in mouse liver cells. <i>Scientific Reports</i> , 2015 , 5, 17186	4.9	36
78	Computer Simulation, Bioinformatics, and Statistical Analysis of Cancer Data and Processes. <i>Cancer Informatics</i> , 2015 , 14, 247-51	2.4	
77	Base-resolution methylation patterns accurately predict transcription factor bindings in vivo. <i>Nucleic Acids Research</i> , 2015 , 43, 2757-66	20.1	33
76	SynBioLGDB: a resource for experimentally validated logic gates in synthetic biology. <i>Scientific Reports</i> , 2015 , 5, 8090	4.9	12
75	ViRBase: a resource for virus-host ncRNA-associated interactions. <i>Nucleic Acids Research</i> , 2015 , 43, D578-821	20.1	68
74	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	1.4	15
73	Cellular resolution maps of X chromosome inactivation: implications for neural development, function, and disease. <i>Neuron</i> , 2014 , 81, 103-19	13.9	139
72	Reversing DNA methylation: mechanisms, genomics, and biological functions. <i>Cell</i> , 2014 , 156, 45-68	56.2	738
71	Single-base resolution analysis of active DNA demethylation using methylase-assisted bisulfite sequencing. <i>Nature Biotechnology</i> , 2014 , 32, 1231-40	44.5	107
70	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> , 2014 , 16, 377-89	6.4	28
69	HMMR maintains the stemness and tumorigenicity of glioblastoma stem-like cells. <i>Cancer Research</i> , 2014 , 74, 3168-79	10.1	73
68	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	1.6	10

67	PolyaPeak: detecting transcription factor binding sites from ChIP-seq using peak shape information. <i>PLoS ONE</i> , 2014 , 9, e89694	3.7	9
66	N-cadherin prevents the premature differentiation of anterior heart field progenitors in the pharyngeal mesodermal microenvironment. <i>Cell Research</i> , 2014 , 24, 1420-32	24.7	27
65	A Bayesian hierarchical model to detect differentially methylated loci from single nucleotide resolution sequencing data. <i>Nucleic Acids Research</i> , 2014 , 42, e69	20.1	245
64	Genome-wide alteration of 5-hydroxymethylcytosine in a mouse model of fragile X-associated tremor/ataxia syndrome. <i>Human Molecular Genetics</i> , 2014 , 23, 1095-107	5.6	49
63	Modeling Parkinson's disease in monkeys for translational studies, a critical analysis. <i>Experimental Neurology</i> , 2014 , 256, 133-43	5.7	57
62	Complete morphologies of basal forebrain cholinergic neurons in the mouse. <i>ELife</i> , 2014 , 3, e02444	8.9	87
61	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, 16562-7	11.5	200
60	Cell-cycle control of developmentally regulated transcription factors accounts for heterogeneity in human pluripotent cells. <i>Stem Cell Reports</i> , 2013 , 1, 532-44	8	98
59	Kdm2b maintains murine embryonic stem cell status by recruiting PRC1 complex to CpG islands of developmental genes. <i>Nature Cell Biology</i> , 2013 , 15, 373-84	23.4	225
58	A new shrinkage estimator for dispersion improves differential expression detection in RNA-seq data. <i>Biostatistics</i> , 2013 , 14, 232-43	3.7	139
57	Genome-wide profiling of 5-formylcytosine reveals its roles in epigenetic priming. <i>Cell</i> , 2013 , 153, 678-91	56.2	453
56	Genome-wide analysis reveals TET- and TDG-dependent 5-methylcytosine oxidation dynamics. <i>Cell</i> , 2013 , 153, 692-706	56.2	390
55	Subtelomeric hotspots of aberrant 5-hydroxymethylcytosine-mediated epigenetic modifications during reprogramming to pluripotency. <i>Nature Cell Biology</i> , 2013 , 15, 700-11	23.4	80
54	Exploring the cooccurrence patterns of multiple sets of genomic intervals. <i>BioMed Research International</i> , 2013 , 2013, 617545	3	1
53	Early embryos reprogram DNA methylation in two steps. <i>Cell Stem Cell</i> , 2012 , 10, 487-9	18	11
52	Fragile X premutation RNA is sufficient to cause primary ovarian insufficiency in mice. <i>Human Molecular Genetics</i> , 2012 , 21, 5039-47	5.6	65
51	Genome-wide DNA hydroxymethylation changes are associated with neurodevelopmental genes in the developing human cerebellum. <i>Human Molecular Genetics</i> , 2012 , 21, 5500-10	5.6	135
50	Euchromatin islands in large heterochromatin domains are enriched for CTCF binding and differentially DNA-methylated regions. <i>BMC Genomics</i> , 2012 , 13, 566	4.5	33

49	Statistics for next generation sequencing - meeting report. <i>Frontiers in Genetics</i> , 2012 , 3, 128	4.5	
48	Regulation and function of mammalian DNA methylation patterns: a genomic perspective. <i>Briefings in Functional Genomics</i> , 2012 , 11, 240-50	4.9	24
47	Highly efficient derivation of ventricular cardiomyocytes from induced pluripotent stem cells with a distinct epigenetic signature. <i>Cell Research</i> , 2012 , 22, 142-54	24.7	70
46	Morphologic diversity of cutaneous sensory afferents revealed by genetically directed sparse labeling. <i>ELife</i> , 2012 , 1, e00181	8.9	43
45	JAMIE: A software tool for jointly analyzing multiple ChIP-chip experiments. <i>Methods in Molecular Biology</i> , 2012 , 802, 363-75	1.4	1
44	Tet1 and 5-hydroxymethylation: a genome-wide view in mouse embryonic stem cells. <i>Cell Cycle</i> , 2011 , 10, 2428-36	4.7	113
43	Increased methylation variation in epigenetic domains across cancer types. <i>Nature Genetics</i> , 2011 , 43, 768-75	36.3	825
42	5-hmC-mediated epigenetic dynamics during postnatal neurodevelopment and aging. <i>Nature Neuroscience</i> , 2011 , 14, 1607-16	25.5	639
41	Genome-scale epigenetic reprogramming during epithelial-to-mesenchymal transition. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 867-74	17.6	297
40	Dual functions of Tet1 in transcriptional regulation in mouse embryonic stem cells. <i>Nature</i> , 2011 , 473, 389-93	50.4	496
39	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, 679-84	12.6	431
38	Mechanisms and functions of Tet protein-mediated 5-methylcytosine oxidation. <i>Genes and Development</i> , 2011 , 25, 2436-52	12.6	487
37	Deletion of astroglial Dicer causes non-cell-autonomous neuronal dysfunction and degeneration. <i>Journal of Neuroscience</i> , 2011 , 31, 8306-19	6.6	135
36	Reply to Reassessing the abundance of H3K9me2 chromatin domains in embryonic stem cells□ <i>Nature Genetics</i> , 2010 , 42, 5-6	36.3	22
35	Intensity normalization improves color calling in SOLiD sequencing. <i>Nature Methods</i> , 2010 , 7, 336-7	21.6	22
34	JAMIE: joint analysis of multiple ChIP-chip experiments. <i>Bioinformatics</i> , 2010 , 26, 1864-70	7.2	12
33	Building the Quality Control System for Medical Equipments in Hospital 2010 ,		3
32	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> , 2010 , 107, 18161-6	11.5	140

31	Redefining CpG islands using hidden Markov models. <i>Biostatistics</i> , 2010 , 11, 499-514	3.7	122
30	A smartphone based respiratory biofeedback system 2010 ,		14
29	Dnmt3a-dependent nonpromoter DNA methylation facilitates transcription of neurogenic genes. <i>Science</i> , 2010 , 329, 444-8	33.3	480
28	A Prototype of Wearable Respiration Biofeedback Platform and Its Preliminary Evaluation on Cardiovascular Variability 2009 ,		9
27	Deciphering Rett syndrome with mouse genetics, epigenomics, and human neurons. <i>International Review of Neurobiology</i> , 2009 , 89, 147-60	4.4	8
26	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, 4882-7	11.5	171
25	Reversing DNA methylation: new insights from neuronal activity-induced Gadd45b in adult neurogenesis. <i>Science Signaling</i> , 2009 , 2, pe17	8.8	31
24	Ago2 immunoprecipitation identifies predicted microRNAs in human embryonic stem cells and neural precursors. <i>PLoS ONE</i> , 2009 , 4, e7192	3.7	94
23	A species-generalized probabilistic model-based definition of CpG islands. <i>Mammalian Genome</i> , 2009 , 20, 674-80	3.2	47
22	Large histone H3 lysine 9 dimethylated chromatin blocks distinguish differentiated from embryonic stem cells. <i>Nature Genetics</i> , 2009 , 41, 246-50	36.3	469
21	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> , 2008 , 105, 1026-31	11.5	266
20	Comprehensive high-throughput arrays for relative methylation (CHARM). <i>Genome Research</i> , 2008 , 18, 780-90	9.7	350
19	Copy number variant analysis of human embryonic stem cells. <i>Stem Cells</i> , 2008 , 26, 1484-9	5.8	42
18	Overlapping euchromatin/heterochromatin-associated marks are enriched in imprinted gene regions and predict allele-specific modification. <i>Genome Research</i> , 2008 , 18, 1806-13	9.7	27
17	R/qtlbim: QTL with Bayesian Interval Mapping in experimental crosses. <i>Bioinformatics</i> , 2007 , 23, 641-3	7.2	92
16	A phenotypic small-molecule screen identifies an orphan ligand-receptor pair that regulates neural stem cell differentiation. <i>Chemistry and Biology</i> , 2007 , 14, 1019-30		61
15	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, 13821-6	11.5	112
14	Histone modifications around individual BDNF gene promoters in prefrontal cortex are associated with extinction of conditioned fear. <i>Learning and Memory</i> , 2007 , 14, 268-76	2.8	441

13	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, 1319-24	11.5	177
12	Epigenetic regulation of stem cell differentiation. <i>Pediatric Research</i> , 2006 , 59, 21R-5R	3.2	111
11	Neural progenitors populate the cerebrospinal fluid of preterm patients with hydrocephalus. <i>Journal of Pediatrics</i> , 2006 , 148, 337-340	3.6	21
10	The ups and downs of BDNF in Rett syndrome. <i>Neuron</i> , 2006 , 49, 321-3	13.9	36
9	A positive autoregulatory loop of Jak-STAT signaling controls the onset of astroglialogenesis. <i>Nature Neuroscience</i> , 2005 , 8, 616-25	25.5	302
8	DNA methylation controls the timing of astroglialogenesis through regulation of JAK-STAT signaling. <i>Development (Cambridge)</i> , 2005 , 132, 3345-56	6.6	334
7	Crystal structure of human coactosin-like protein at 1.9 Å resolution. <i>Protein Science</i> , 2004 , 13, 2845-51	6.3	9
6	MAANOVA: A Software Package for the Analysis of Spotted cDNA Microarray Experiments 2003 , 313-341		131
5	R/qtl: QTL mapping in experimental crosses. <i>Bioinformatics</i> , 2003 , 19, 889-90	7.2	2292
4	DNA methylation-related chromatin remodeling in activity-dependent BDNF gene regulation. <i>Science</i> , 2003 , 302, 890-3	33.3	1187
3	Massively parallel, time-resolved single-cell RNA sequencing with scNT-Seq		2
2	Dissecting differential signals in high-throughput data from complex tissues		2
1	Penalized Latent Dirichlet Allocation Model in Single-Cell RNA Sequencing. <i>Statistics in Biosciences</i> , 1	1.5	1