

Zhi Wei

List of Publications by Year in descending order

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Version: 2024-02-01

170
papers

13,392
citations

50566

48
h-index

29333

108
g-index

179
all docs

179
docs citations

179
times ranked

31449
citing authors

#	ARTICLE	IF	CITATIONS
1	An active learning approach for clustering single-cell RNA-seq data. <i>Laboratory Investigation</i> , 2022, 102, 227-235.	1.7	8
2	Targeted gene expression profiling of inverted papilloma and squamous cell carcinoma. <i>International Forum of Allergy and Rhinology</i> , 2022, 12, 200-209.	1.5	8
3	Fa-Mb-ResNet for Grounding Fault Identification and Line Selection in the Distribution Networks. <i>IEEE Internet of Things Journal</i> , 2022, 9, 11115-11125.	5.5	7
4	Colonic healing requires Wnt produced by epithelium as well as Tagln+ and Acta2+ stromal cells. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	9
5	MGEL: Multigrained Representation Analysis and Ensemble Learning for Text Moderation. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2022, PP, 1-10.	7.2	0
6	Identification of Novel Loci Shared by Juvenile Idiopathic Arthritis Subtypes Through Integrative Genetic Analysis. <i>Arthritis and Rheumatology</i> , 2022, 74, 1420-1429.	2.9	4
7	NUMB as a Therapeutic Target for Melanoma. <i>Journal of Investigative Dermatology</i> , 2022, 142, 1882-1892.e5.	0.3	5
8	Antitumor Activity of a Mitochondrial-Targeted HSP90 Inhibitor in Gliomas. <i>Clinical Cancer Research</i> , 2022, 28, 2180-2195.	3.2	12
9	Improved Deep Convolutional Neural Networks via Boosting for Predicting the Quality of In Vitro Bovine Embryos. <i>Electronics (Switzerland)</i> , 2022, 11, 1363.	1.8	6
10	A convolutional neural network model for survival prediction based on prognosis-related cascaded Wx feature selection. <i>Laboratory Investigation</i> , 2022, 102, 1064-1074.	1.7	16
11	Model-based autoencoders for imputing discrete single-cell RNA-seq data. <i>Methods</i> , 2021, 192, 112-119.	1.9	10
12	An Omnibus Test for Differential Distribution Analysis of Continuous Microbiome Data. <i>IEEE Access</i> , 2021, 9, 100029-100039.	2.6	0
13	Very low mutation burden is a feature of inflamed recurrent glioblastomas responsive to cancer immunotherapy. <i>Nature Communications</i> , 2021, 12, 352.	5.8	77
14	Performance of model-based multifactor dimensionality reduction methods for epistasis detection by controlling population structure. <i>BioData Mining</i> , 2021, 14, 16.	2.2	2
15	Detection of Microbial Agents in Oropharyngeal and Nasopharyngeal Samples of SARS-CoV-2 Patients. <i>Frontiers in Microbiology</i> , 2021, 12, 637202.	1.5	0
16	Model-based deep embedding for constrained clustering analysis of single cell RNA-seq data. <i>Nature Communications</i> , 2021, 12, 1873.	5.8	46
17	ST-Trader: A Spatial-Temporal Deep Neural Network for Modeling Stock Market Movement. <i>IEEE/CAA Journal of Automatica Sinica</i> , 2021, 8, 1015-1024.	8.5	56
18	The microbiome of HPV-positive tonsil squamous cell carcinoma and neck metastasis. <i>Oral Oncology</i> , 2021, 117, 105305.	0.8	14

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19	Targeting mTOR signaling overcomes acquired resistance to combined BRAF and MEK inhibition in BRAF-mutant melanoma. <i>Oncogene</i> , 2021, 40, 5590-5599.	2.6	33
20	Neural Crest-Like Stem Cell Transcriptome Analysis Identifies LPAR1 in Melanoma Progression and Therapy Resistance. <i>Cancer Research</i> , 2021, 81, 5230-5241.	0.4	9
21	A Modified Nucleoside 6-Thio-2-Deoxyguanosine Exhibits Antitumor Activity in Gliomas. <i>Clinical Cancer Research</i> , 2021, 27, 6800-6814.	3.2	10
22	Prognostic correlations with the microbiome of breast cancer subtypes. <i>Cell Death and Disease</i> , 2021, 12, 831.	2.7	42
23	Genetic Variation in PADI6-PADI4 on 1p36.13 Is Associated with Common Forms of Human Generalized Epilepsy. <i>Genes</i> , 2021, 12, 1441.	1.0	7
24	DeepCNV: a deep learning approach for authenticating copy number variations. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	15
25	Pathway signatures derived from on-treatment tumor specimens predict response to anti-PD1 blockade in metastatic melanoma. <i>Nature Communications</i> , 2021, 12, 6023.	5.8	21
26	Dynamic surface control for a class of nonlinearly parameterized systems with input time delay using neural network. <i>Journal of the Franklin Institute</i> , 2020, 357, 1961-1986.	1.9	13
27	Paneth Cell-Derived Lysozyme Defines the Composition of Mucolytic Microbiota and the Inflammatory Tone of the Intestine. <i>Immunity</i> , 2020, 53, 398-416.e8.	6.6	97
28	Elucidation of DNA methylation on N6-adenine with deep learning. <i>Nature Machine Intelligence</i> , 2020, 2, 466-475.	8.3	7
29	Epstein-Barr Virus Facilitates Expression of KLF14 by Regulating the Cooperative Binding of the E2F-Rb-HDAC Complex in Latent Infection. <i>Journal of Virology</i> , 2020, 94, .	1.5	5
30	Enhancing KDM5A and TLR activity improves the response to immune checkpoint blockade. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	34
31	Fully Automated Bone Age Assessment on Large-Scale Hand X-Ray Dataset. <i>International Journal of Biomedical Imaging</i> , 2020, 2020, 1-12.	3.0	29
32	An Enriched Time-Series Forecasting Framework for Long-Short Portfolio Strategy. <i>IEEE Access</i> , 2020, 8, 31992-32002.	2.6	7
33	Rare copy number variants in over 100,000 European ancestry subjects reveal multiple disease associations. <i>Nature Communications</i> , 2020, 11, 255.	5.8	48
34	Regulation of Janus Kinase 2 by an Inflammatory Bowel Disease Causal Non-coding Single Nucleotide Polymorphism. <i>Journal of Crohn's and Colitis</i> , 2020, 14, 646-653.	0.6	5
35	The virome of HPV-positive tonsil squamous cell carcinoma and neck metastasis. <i>Oncotarget</i> , 2020, 11, 282-293.	0.8	6
36	A Feature Sampling Strategy for Analysis of High Dimensional Genomic Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 434-441.	1.9	3

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37	A Fatty Acid Oxidation-dependent Metabolic Shift Regulates the Adaptation of <i>BRAF</i> -mutated Melanoma to MAPK Inhibitors. <i>Clinical Cancer Research</i> , 2019, 25, 6852-6867.	3.2	74
38	Epistasis Detection in Genome-Wide Screening for Complex Human Diseases in Structured Populations. <i>Systems Medicine (New Rochelle, NY)</i> , 2019, 2, 19-27.	1.4	9
39	Improved Online Sequential Extreme Learning Machine: A New Intelligent Evaluation Method for AZ-Style Algorithms. <i>IEEE Access</i> , 2019, 7, 124891-124901.	2.6	4
40	A Middle Game Search Algorithm Applicable to Low-Cost Personal Computer for Go. <i>IEEE Access</i> , 2019, 7, 121719-121727.	2.6	3
41	Target Genes of Autism Risk Loci in Brain Frontal Cortex. <i>Frontiers in Genetics</i> , 2019, 10, 707.	1.1	16
42	A Reinforcement Learning Model Based on Temporal Difference Algorithm. <i>IEEE Access</i> , 2019, 7, 121922-121930.	2.6	14
43	Pharmacological Targeting of STK19 Inhibits Oncogenic NRAS-Driven Melanomagenesis. <i>Cell</i> , 2019, 176, 1113-1127.e16.	13.5	74
44	Multiple Epistasis Interactions Within MHC Are Associated With Ulcerative Colitis. <i>Frontiers in Genetics</i> , 2019, 10, 257.	1.1	7
45	Risk-Based Multi-Objective Optimization of Distributed Generation Based on GPSO-BFA Algorithm. <i>IEEE Access</i> , 2019, 7, 30563-30572.	2.6	15
46	Genome-wide prediction of synthetic rescue mediators of resistance to targeted and immunotherapy. <i>Molecular Systems Biology</i> , 2019, 15, e8323.	3.2	25
47	Clustering single-cell RNA-seq data with a model-based deep learning approach. <i>Nature Machine Intelligence</i> , 2019, 1, 191-198.	8.3	189
48	Microbiome signatures in prostate cancer. <i>Carcinogenesis</i> , 2019, 40, 749-764.	1.3	69
49	Modeling and elucidation of housing price. <i>Data Mining and Knowledge Discovery</i> , 2019, 33, 636-662.	2.4	3
50	Candidate gene analyses for acute pain and morphine analgesia after pediatric day surgery: African American versus European Caucasian ancestry and dose prediction limits. <i>Pharmacogenomics Journal</i> , 2019, 19, 570-581.	0.9	17
51	User Response Driven Content Understanding with Causal Inference. , 2019, , .		2
52	ER Translocation of the MAPK Pathway Drives Therapy Resistance in BRAF-Mutant Melanoma. <i>Cancer Discovery</i> , 2019, 9, 396-415.	7.7	71
53	A Deep Learning Approach to Competing Risks Representation in Peer-to-Peer Lending. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2019, 30, 1565-1574.	7.2	27
54	Online Change-Point Detection in Sparse Time Series With Application to Online Advertising. <i>IEEE Transactions on Systems, Man, and Cybernetics: Systems</i> , 2019, 49, 1141-1151.	5.9	18

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55	DeepPolyA: A Convolutional Neural Network Approach for Polyadenylation Site Prediction. IEEE Access, 2018, 6, 24340-24349.	2.6	34
56	Co-targeting BET and MEK as salvage therapy for $MAPK$ and checkpoint inhibitor-resistant melanoma. EMBO Molecular Medicine, 2018, 10, .	3.3	79
57	A distance-based approach for testing the mediation effect of the human microbiome. Bioinformatics, 2018, 34, 1875-1883.	1.8	43
58	The protective role of DOT1L in UV-induced melanomagenesis. Nature Communications, 2018, 9, 259.	5.8	63
59	Coexpression network analysis identifies transcriptional modules associated with genomic alterations in neuroblastoma. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 2341-2348.	1.8	35
60	A transfer learning approach via procrustes analysis and mean shift for cancer drug sensitivity prediction. Journal of Bioinformatics and Computational Biology, 2018, 16, 1840014.	0.3	34
61	A Distance-Based Weighted Undersampling Scheme for Support Vector Machines and its Application to Imbalanced Classification. IEEE Transactions on Neural Networks and Learning Systems, 2018, 29, 4152-4165.	7.2	111
62	Induction of Telomere Dysfunction Prolongs Disease Control of Therapy-Resistant Melanoma. Clinical Cancer Research, 2018, 24, 4771-4784.	3.2	29
63	An omnibus test for differential distribution analysis of microbiome sequencing data. Bioinformatics, 2018, 34, 643-651.	1.8	69
64	MSX1-Induced Neural Crest-Like Reprogramming Promotes Melanoma Progression. Journal of Investigative Dermatology, 2018, 138, 141-149.	0.3	29
65	<i>Ex Vivo</i> Profiling of PD-1 Blockade Using Organotypic Tumor Spheroids. Cancer Discovery, 2018, 8, 196-215.	7.7	392
66	Dual ℓ_1 and ℓ_2 Convex Variable Subsets Family and Extremum Analysis for the OPF Problem. IEEE Access, 2018, 6, 27018-27027.	2.6	0
67	tRNA-DL: A Deep Learning Approach to Improve tRNAscan-SE Prediction Results. Human Heredity, 2018, 83, 163-172.	0.4	7
68	Tissue-Specific Differential Expression of Novel Genes and Long Intergenic Noncoding RNAs in Humans With Extreme Response to Evoked Endotoxemia. Circulation Genomic and Precision Medicine, 2018, 11, e001907.	1.6	4
69	Loss of Phd2 cooperates with BRAFV600E to drive melanomagenesis. Nature Communications, 2018, 9, 5426.	5.8	11
70	A Blended Deep Learning Approach for Predicting User Intended Actions. , 2018, , .		8
71	A Comprehensive Survey of Immune Cytolytic Activity-Associated Gene Co-Expression Networks across 17 Tumor and Normal Tissue Types. Cancers, 2018, 10, 307.	1.7	4
72	Deep learning for sequence pattern recognition. , 2018, , .		10

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73	Dual Src and MEK Inhibition Decreases Ovarian Cancer Growth and Targets Tumor Initiating Stem-Like Cells. <i>Clinical Cancer Research</i> , 2018, 24, 4874-4886.	3.2	60
74	Modeling Item-specific Effects for Video Click. , 2018, , 639-647.		3
75	Tumor innate immunity primed by specific interferon-stimulated endogenous retroviruses. <i>Nature Medicine</i> , 2018, 24, 1143-1150.	15.2	212
76	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018, 360, .	6.0	1,085
77	Distinct Microbial Signatures Associated With Different Breast Cancer Types. <i>Frontiers in Microbiology</i> , 2018, 9, 951.	1.5	170
78	Weighted Gene Co-Expression Network Analysis Reveals Dysregulation of Mitochondrial Oxidative Phosphorylation in Eating Disorders. <i>Genes</i> , 2018, 9, 325.	1.0	14
79	Robust prediction of response to immune checkpoint blockade therapy in metastatic melanoma. <i>Nature Medicine</i> , 2018, 24, 1545-1549.	15.2	473
80	Boosting support vector machines for cancer discrimination tasks. <i>Computers in Biology and Medicine</i> , 2018, 101, 236-249.	3.9	35
81	The Long Noncoding RNA Landscape in Amygdala Tissues from Schizophrenia Patients. <i>EBioMedicine</i> , 2018, 34, 171-181.	2.7	32
82	Transfer Learning Approaches to Improve Drug Sensitivity Prediction in Multiple Myeloma Patients. <i>IEEE Access</i> , 2017, 5, 7381-7393.	2.6	46
83	Oncogenic RAS Regulates Long Noncoding RNA <i>Orilnc1</i> in Human Cancer. <i>Cancer Research</i> , 2017, 77, 3745-3757.	0.4	34
84	A genome-wide association study of anorexia nervosa suggests a risk locus implicated in dysregulated leptin signaling. <i>Scientific Reports</i> , 2017, 7, 3847.	1.6	23
85	PAK signalling drives acquired drug resistance to MAPK inhibitors in BRAF-mutant melanomas. <i>Nature</i> , 2017, 550, 133-136.	13.7	146
86	Priming and Activation of Inflammasome by Canarypox Virus Vector ALVAC via the cGAS/IFI16-“STING”-Type I IFN Pathway and AIM2 Sensor. <i>Journal of Immunology</i> , 2017, 199, 3293-3305.	0.4	33
87	Common variants in MMP20 at 11q22.2 predispose to 11q deletion and neuroblastoma risk. <i>Nature Communications</i> , 2017, 8, 569.	5.8	22
88	Tumor-associated B-cells induce tumor heterogeneity and therapy resistance. <i>Nature Communications</i> , 2017, 8, 607.	5.8	109
89	A Unified Approach to Targeting the Lysosome’s Degradative and Growth Signaling Roles. <i>Cancer Discovery</i> , 2017, 7, 1266-1283.	7.7	159
90	Microbial Signatures Associated with Oropharyngeal and Oral Squamous Cell Carcinomas. <i>Scientific Reports</i> , 2017, 7, 4036.	1.6	55

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91	Genome-Wide Association Study Identifies African-Specific Susceptibility Loci in African Americans With Inflammatory Bowel Disease. <i>Gastroenterology</i> , 2017, 152, 206-217.e2.	0.6	120
92	Time-Aware Latent Hierarchical Model for Predicting House Prices. , 2017, , .		10
93	REMOLD: An Efficient Model-Based Clustering Algorithm for Large Datasets with Spark. , 2017, , .		3
94	The ovarian cancer oncobiome. <i>Oncotarget</i> , 2017, 8, 36225-36245.	0.8	129
95	A link prediction approach to cancer drug sensitivity prediction. <i>BMC Systems Biology</i> , 2017, 11, 94.	3.0	47
96	Inhibition of stress-inducible HSP70 impairs mitochondrial proteostasis and function. <i>Oncotarget</i> , 2017, 8, 45656-45669.	0.8	32
97	Genome-wide association study identifies novel type II diabetes risk loci in Jordan subpopulations. <i>PeerJ</i> , 2017, 5, e3618.	0.9	9
98	Targeting mitochondrial biogenesis to overcome drug resistance to MAPK inhibitors. <i>Journal of Clinical Investigation</i> , 2016, 126, 1834-1856.	3.9	219
99	Application of computational methods in genetic study of inflammatory bowel disease. <i>World Journal of Gastroenterology</i> , 2016, 22, 949.	1.4	6
100	Pathway-based Genome-wide Association Studies Reveal the Association Between Growth Factor Activity and Inflammatory Bowel Disease. <i>Inflammatory Bowel Diseases</i> , 2016, 22, 1540-1551.	0.9	8
101	Reliable Gender Prediction Based on Usersâ€™ Video Viewing Behavior. , 2016, , .		8
102	Modeling Real Estate for School District Identification. , 2016, , .		5
103	Annealed Sparsity via Adaptive and Dynamic Shrinking. , 2016, , .		2
104	A novel under-sampling algorithm based on Iterative-Partitioning Filters for imbalanced classification. , 2016, , .		9
105	Learning approaches to improve prediction of drug sensitivity in breast cancer patients. , 2016, 2016, 3314-3320.		13
106	Genome-wide association study for acute otitis media in children identifies FNDC1 as disease contributing gene. <i>Nature Communications</i> , 2016, 7, 12792.	5.8	50
107	Understanding the genetic and epigenetic basis of common variable immunodeficiency disorder through omics approaches. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 2656-2663.	1.1	21
108	Variants in CXCR4 associate with juvenile idiopathic arthritis susceptibility. <i>BMC Medical Genetics</i> , 2016, 17, 24.	2.1	20

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109	A greedy-based oversampling approach to improve the prediction of mortality in MERS patients. , 2016, ,		5
110	An empirical Bayes change-point model for identifying 3â€² and 5â€² alternative splicing by next-generation RNA sequencing. Bioinformatics, 2016, 32, 1823-1831.	1.8	13
111	MAPK Activation Predicts Poor Outcome and the MEK Inhibitor, Selumetinib, Reverses Antiestrogen Resistance in ER-Positive High-Grade Serous Ovarian Cancer. Clinical Cancer Research, 2016, 22, 935-947.	3.2	42
112	PIM kinases as therapeutic targets against advanced melanoma. Oncotarget, 2016, 7, 54897-54912.	0.8	16
113	Distinct microbiological signatures associated with triple negative breast cancer. Scientific Reports, 2015, 5, 15162.	1.6	92
114	Genome-wide association study reveals two loci for serum magnesium concentrations in European-American children. Scientific Reports, 2015, 5, 18792.	1.6	1
115	CNV Analysis Associates AKNAD1 with Type-2 Diabetes in Jordan Subpopulations. Scientific Reports, 2015, 5, 13391.	1.6	18
116	Machine learning derived risk prediction of anorexia nervosa. BMC Medical Genomics, 2015, 9, 4.	0.7	18
117	Genome-Wide Association Study of Serum Minerals Levels in Children of Different Ethnic Background. PLoS ONE, 2015, 10, e0123499.	1.1	9
118	Advanced Computational Approaches for Medical Genetics and Genomics. BioMed Research International, 2015, 2015, 1-2.	0.9	0
119	Robust-yet-fragile nature of interdependent networks. Physical Review E, 2015, 91, 052809.	0.8	45
120	Rare variants at 16p11.2 are associated with common variable immunodeficiency. Journal of Allergy and Clinical Immunology, 2015, 135, 1569-1577.	1.5	22
121	Collaborated Online Change-Point Detection in Sparse Time Series for Online Advertising. , 2015, ,		6
122	UV-Induced Wnt7a in the Human Skin Microenvironment Specifies the Fate of Neural Crestâ€œLike Cells via Suppression of Notch. Journal of Investigative Dermatology, 2015, 135, 1521-1532.	0.3	18
123	miRâ€œ200c/Bmi1 axis and epithelialâ€œmesenchymal transition contribute to acquired resistance to <sc>BRAF</sc> inhibitor treatment. Pigment Cell and Melanoma Research, 2015, 28, 431-441.	1.5	41
124	Hierarchical recognition of sparse patterns in large-scale simultaneous inference. Biometrika, 2015, 102, 267-280.	1.3	2
125	Twitter sentiment classification for measuring public health concerns. Social Network Analysis and Mining, 2015, 5, 13.	1.9	101
126	Scalable quality assurance for large SNOMED CT hierarchies using subject-based subtaxonomies. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 507-518.	2.2	44

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127	Genetic sharing and heritability of paediatric age of onset autoimmune diseases. <i>Nature Communications</i> , 2015, 6, 8442.	5.8	58
128	Meta-analysis of shared genetic architecture across ten pediatric autoimmune diseases. <i>Nature Medicine</i> , 2015, 21, 1018-1027.	15.2	212
129	Copy Number Variations in CTNNA3 and RBFOX1 Associate with Pediatric Food Allergy. <i>Journal of Immunology</i> , 2015, 195, 1599-1607.	0.4	20
130	Direct conversion of mouse and human fibroblasts to functional melanocytes by defined factors. <i>Nature Communications</i> , 2014, 5, 5807.	5.8	61
131	Generation of folliculogenic human epithelial stem cells from induced pluripotent stem cells. <i>Nature Communications</i> , 2014, 5, 3071.	5.8	96
132	A change-point model for identifying 3'UTR switching by next-generation RNA sequencing. <i>Bioinformatics</i> , 2014, 30, 2162-2170.	1.8	43
133	Preferential infection of human Ad5-specific CD4 T cells by HIV in Ad5 naturally exposed and recombinant Ad5-HIV vaccinated individuals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13439-13444.	3.3	49
134	Collapsing singletons may boost signal for associating rare variants in sequencing study. <i>BMC Proceedings</i> , 2014, 8, S50.	1.8	3
135	Top-k Parametrized Boost. <i>Lecture Notes in Computer Science</i> , 2014, , 91-98.	1.0	3
136	The SLE Transcriptome Exhibits Evidence of Chronic Endotoxin Exposure and Has Widespread Dysregulation of Non-Coding and Coding RNAs. <i>PLoS ONE</i> , 2014, 9, e93846.	1.1	109
137	Transcriptome Profiling of Human Ulcerative Colitis Mucosa Reveals Altered Expression of Pathways Enriched in Genetic Susceptibility Loci. <i>PLoS ONE</i> , 2014, 9, e96153.	1.1	8
138	Low concordance of multiple variant-calling pipelines: practical implications for exome and genome sequencing. <i>Genome Medicine</i> , 2013, 5, 28.	3.6	381
139	Suppression of Nucleotide Metabolism Underlies the Establishment and Maintenance of Oncogene-Induced Senescence. <i>Cell Reports</i> , 2013, 3, 1252-1265.	2.9	228
140	Large Sample Size, Wide Variant Spectrum, and Advanced Machine-Learning Technique Boost Risk Prediction for Inflammatory Bowel Disease. <i>American Journal of Human Genetics</i> , 2013, 92, 1008-1012.	2.6	162
141	A High-Content Screening Assay for Small-Molecule Modulators of Oncogene-Induced Senescence. <i>Journal of Biomolecular Screening</i> , 2013, 18, 1054-1061.	2.6	11
142	GWAS of blood cell traits identifies novel associated loci and epistatic interactions in Caucasian and African-American children. <i>Human Molecular Genetics</i> , 2013, 22, 1457-1464.	1.4	82
143	Dysregulation of synaptogenesis genes antecedes motor neuron pathology in spinal muscular atrophy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19348-19353.	3.3	161
144	Distinct gene-expression profiles associated with the susceptibility of pathogen-specific CD4 T cells to HIV-1 infection. <i>Blood</i> , 2013, 121, 1136-1144.	0.6	38

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145	An empirical Bayes testing procedure for detecting variants in analysis of next generation sequencing data. <i>Annals of Applied Statistics</i> , 2013, 7, .	0.5	12
146	Minor introns are embedded molecular switches regulated by highly unstable U6atac snRNA. <i>ELife</i> , 2013, 2, e00780.	2.8	91
147	Gene Network Analysis in a Pediatric Cohort Identifies Novel Lung Function Genes. <i>PLoS ONE</i> , 2013, 8, e72899.	1.1	23
148	Genetics of Inflammatory Bowel Diseases. , 2013, , 3-12.		0
149	A powerful test for multiple rare variants association studies that incorporates sequencing qualities. <i>Nucleic Acids Research</i> , 2012, 40, e60-e60.	6.5	26
150	SNVerGUI: a desktop tool for variant analysis of next-generation sequencing data. <i>Journal of Medical Genetics</i> , 2012, 49, 753-755.	1.5	15
151	Host-microbe interactions have shaped the genetic architecture of inflammatory bowel disease. <i>Nature</i> , 2012, 491, 119-124.	13.7	4,038
152	Hidden Markov Models for Controlling False Discovery Rate in Genome-Wide Association Analysis. <i>Methods in Molecular Biology</i> , 2012, 802, 337-344.	0.4	2
153	Induction of metallothionein expression during monocyte to melanoma-associated macrophage differentiation. <i>Frontiers in Biology</i> , 2012, 7, 359-367.	0.7	4
154	Melanoma-derived conditioned media efficiently induce the differentiation of monocytes to macrophages that display a highly invasive gene signature. <i>Pigment Cell and Melanoma Research</i> , 2012, 25, 493-505.	1.5	57
155	Multiple Testing for Pattern Identification, With Applications to Microarray Time-Course Experiments. <i>Journal of the American Statistical Association</i> , 2011, 106, 73-88.	1.8	35
156	Next generation sequencing has lower sequence coverage and poorer SNP-detection capability in the regulatory regions. <i>Scientific Reports</i> , 2011, 1, 55.	1.6	67
157	SNVer: a statistical tool for variant calling in analysis of pooled or individual next-generation sequencing data. <i>Nucleic Acids Research</i> , 2011, 39, e132-e132.	6.5	225
158	Ranking causal variants and associated regions in genome-wide association studies by the support vector machine and random forest. <i>Nucleic Acids Research</i> , 2011, 39, e62-e62.	6.5	49
159	Exome sequencing and unrelated findings in the context of complex disease research: ethical and clinical implications. <i>Discovery Medicine</i> , 2011, 12, 41-55.	0.5	49
160	Network-Based Empirical Bayes Methods for Linear Models with Applications to Genomic Data. <i>Journal of Biopharmaceutical Statistics</i> , 2010, 20, 209-222.	0.4	8
161	A hidden Markov random field model for genome-wide association studies. <i>Biostatistics</i> , 2010, 11, 139-150.	0.9	41
162	Simultaneous set-wise testing under dependence, with applications to genome-wide association studies. <i>Statistics and Its Interface</i> , 2010, 3, 501-511.	0.2	2

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163	Multiple testing in genome-wide association studies via hidden Markov models. <i>Bioinformatics</i> , 2009, 25, 2802-2808.	1.8	45
164	From Disease Association to Risk Assessment: An Optimistic View from Genome-Wide Association Studies on Type 1 Diabetes. <i>PLoS Genetics</i> , 2009, 5, e1000678.	1.5	186
165	U-statistics-based Tests for Multiple Genes in Genetic Association Studies. <i>Annals of Human Genetics</i> , 2008, 72, 821-833.	0.3	32
166	A hidden spatial-temporal Markov random field model for network-based analysis of time course gene expression data. <i>Annals of Applied Statistics</i> , 2008, 2, .	0.5	51
167	A Markov random field model for network-based analysis of genomic data. <i>Bioinformatics</i> , 2007, 23, 1537-1544.	1.8	222
168	Nonparametric pathway-based regression models for analysis of genomic data. <i>Biostatistics</i> , 2007, 8, 265-284.	0.9	74
169	Genome-wide linkage and association analysis of rheumatoid arthritis in a Canadian population. <i>BMC Proceedings</i> , 2007, 1, S19.	1.8	8
170	GAME: detecting cis-regulatory elements using a genetic algorithm. <i>Bioinformatics</i> , 2006, 22, 1577-1584.	1.8	94