

# Zhi Wei

## List of Publications by Year in descending order

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Version: 2024-02-01

170  
papers

13,392  
citations

44042

48  
h-index

25770

108  
g-index

179  
all docs

179  
docs citations

179  
times ranked

28590  
citing authors

#	ARTICLE	IF	CITATIONS
1	Host-microbe interactions have shaped the genetic architecture of inflammatory bowel disease. <i>Nature</i> , 2012, 491, 119-124.	13.7	4,038
2	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018, 360, .	6.0	1,085
3	Robust prediction of response to immune checkpoint blockade therapy in metastatic melanoma. <i>Nature Medicine</i> , 2018, 24, 1545-1549.	15.2	473
4	Ex Vivo Profiling of PD-1 Blockade Using Organotypic Tumor Spheroids. <i>Cancer Discovery</i> , 2018, 8, 196-215.	7.7	392
5	Low concordance of multiple variant-calling pipelines: practical implications for exome and genome sequencing. <i>Genome Medicine</i> , 2013, 5, 28.	3.6	381
6	Suppression of Nucleotide Metabolism Underlies the Establishment and Maintenance of Oncogene-Induced Senescence. <i>Cell Reports</i> , 2013, 3, 1252-1265.	2.9	228
7	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
8	A Markov random field model for network-based analysis of genomic data. <i>Bioinformatics</i> , 2007, 23, 1537-1544.	1.8	222
9	Targeting mitochondrial biogenesis to overcome drug resistance to MAPK inhibitors. <i>Journal of Clinical Investigation</i> , 2016, 126, 1834-1856.	3.9	219
10	Meta-analysis of shared genetic architecture across ten pediatric autoimmune diseases. <i>Nature Medicine</i> , 2015, 21, 1018-1027.	15.2	212
11	Tumor innate immunity primed by specific interferon-stimulated endogenous retroviruses. <i>Nature Medicine</i> , 2018, 24, 1143-1150.	15.2	212
12	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
13	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
14	Distinct Microbial Signatures Associated With Different Breast Cancer Types. <i>Frontiers in Microbiology</i> , 2018, 9, 951.	1.5	170
15	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
16	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
17	A Unified Approach to Targeting the Lysosome's Degradative and Growth Signaling Roles. <i>Cancer Discovery</i> , 2017, 7, 1266-1283.	7.7	159
18	PAK signalling drives acquired drug resistance to MAPK inhibitors in BRAF-mutant melanomas. <i>Nature</i> , 2017, 550, 133-136.	13.7	146

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19	The ovarian cancer oncobiome. <i>Oncotarget</i> , 2017, 8, 36225-36245.	0.8	129
20	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
21	A Distance-Based Weighted Undersampling Scheme for Support Vector Machines and its Application to Imbalanced Classification. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2018, 29, 4152-4165.	7.2	111
22	Tumor-associated B-cells induce tumor heterogeneity and therapy resistance. <i>Nature Communications</i> , 2017, 8, 607.	5.8	109
23	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
24	Twitter sentiment classification for measuring public health concerns. <i>Social Network Analysis and Mining</i> , 2015, 5, 13.	1.9	101
25	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
26	Generation of folliculogenic human epithelial stem cells from induced pluripotent stem cells. <i>Nature Communications</i> , 2014, 5, 3071.	5.8	96
27	GAME: detecting cis-regulatory elements using a genetic algorithm. <i>Bioinformatics</i> , 2006, 22, 1577-1584.	1.8	94
28	Distinct microbiological signatures associated with triple negative breast cancer. <i>Scientific Reports</i> , 2015, 5, 15162.	1.6	92
29	Minor introns are embedded molecular switches regulated by highly unstable U6atac snRNA. <i>ELife</i> , 2013, 2, e00780.	2.8	91
30	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
31	Co-targeting <i>BET</i> and <i>MEK</i> as salvage therapy for <i>MAPK</i> and checkpoint inhibitor-resistant melanoma. <i>EMBO Molecular Medicine</i> , 2018, 10, .	3.3	79
32	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
33	Nonparametric pathway-based regression models for analysis of genomic data. <i>Biostatistics</i> , 2007, 8, 265-284.	0.9	74
34	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
35	Pharmacological Targeting of STK19 Inhibits Oncogenic NRAS-Driven Melanomagenesis. <i>Cell</i> , 2019, 176, 1113-1127.e16.	13.5	74
36	ER Translocation of the MAPK Pathway Drives Therapy Resistance in BRAF-Mutant Melanoma. <i>Cancer Discovery</i> , 2019, 9, 396-415.	7.7	71

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37	An omnibus test for differential distribution analysis of microbiome sequencing data. <i>Bioinformatics</i> , 2018, 34, 643-651.	1.8	69
38	Microbiome signatures in prostate cancer. <i>Carcinogenesis</i> , 2019, 40, 749-764.	1.3	69
39	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
40	The protective role of DOT1L in UV-induced melanomagenesis. <i>Nature Communications</i> , 2018, 9, 259.	5.8	63
41	Direct conversion of mouse and human fibroblasts to functional melanocytes by defined factors. <i>Nature Communications</i> , 2014, 5, 5807.	5.8	61
42	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
43	Genetic sharing and heritability of paediatric age of onset autoimmune diseases. <i>Nature Communications</i> , 2015, 6, 8442.	5.8	58
44	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
45	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
46	Microbial Signatures Associated with Oropharyngeal and Oral Squamous Cell Carcinomas. <i>Scientific Reports</i> , 2017, 7, 4036.	1.6	55
47	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
48	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
49	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
50	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
51	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
52	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
53	A link prediction approach to cancer drug sensitivity prediction. <i>BMC Systems Biology</i> , 2017, 11, 94.	3.0	47
54	Transfer Learning Approaches to Improve Drug Sensitivity Prediction in Multiple Myeloma Patients. <i>IEEE Access</i> , 2017, 5, 7381-7393.	2.6	46

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55	Model-based deep embedding for constrained clustering analysis of single cell RNA-seq data. Nature Communications, 2021, 12, 1873.	5.8	46
56	Multiple testing in genome-wide association studies via hidden Markov models. Bioinformatics, 2009, 25, 2802-2808.	1.8	45
57	Robust-yet-fragile nature of interdependent networks. Physical Review E, 2015, 91, 052809.	0.8	45
58	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
59	A change-point model for identifying 3' UTR switching by next-generation RNA sequencing. Bioinformatics, 2014, 30, 2162-2170.	1.8	43
60	A distance-based approach for testing the mediation effect of the human microbiome. Bioinformatics, 2018, 34, 1875-1883.	1.8	43
61	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
62	Prognostic correlations with the microbiome of breast cancer subtypes. Cell Death and Disease, 2021, 12, 831.	2.7	42
63	A hidden Markov random field model for genome-wide association studies. Biostatistics, 2010, 11, 139-150.	0.9	41
64	miR-200c/Bmi1 axis and epithelial-mesenchymal transition contribute to acquired resistance to BRAF inhibitor treatment. Pigment Cell and Melanoma Research, 2015, 28, 431-441.	1.5	41
65	Distinct gene-expression profiles associated with the susceptibility of pathogen-specific CD4 T cells to HIV-1 infection. Blood, 2013, 121, 1136-1144.	0.6	38
66	Multiple Testing for Pattern Identification, With Applications to Microarray Time-Course Experiments. Journal of the American Statistical Association, 2011, 106, 73-88.	1.8	35
67	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
68	Boosting support vector machines for cancer discrimination tasks. Computers in Biology and Medicine, 2018, 101, 236-249.	3.9	35
69	Oncogenic RAS Regulates Long Noncoding RNA <i>Orilnc1</i> in Human Cancer. Cancer Research, 2017, 77, 3745-3757.	0.4	34
70	DeepPolyA: A Convolutional Neural Network Approach for Polyadenylation Site Prediction. IEEE Access, 2018, 6, 24340-24349.	2.6	34
71	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
72	Enhancing KDM5A and TLR activity improves the response to immune checkpoint blockade. Science Translational Medicine, 2020, 12, .	5.8	34

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73	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
74	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
75	U-Statistics-based Tests for Multiple Genes in Genetic Association Studies. <i>Annals of Human Genetics</i> , 2008, 72, 821-833.	0.3	32
76	The Long Noncoding RNA Landscape in Amygdala Tissues from Schizophrenia Patients. <i>EBioMedicine</i> , 2018, 34, 171-181.	2.7	32
77	Inhibition of stress-inducible HSP70 impairs mitochondrial proteostasis and function. <i>Oncotarget</i> , 2017, 8, 45656-45669.	0.8	32
78	Induction of Telomere Dysfunction Prolongs Disease Control of Therapy-Resistant Melanoma. <i>Clinical Cancer Research</i> , 2018, 24, 4771-4784.	3.2	29
79	MSX1-Induced Neural Crest-Like Reprogramming Promotes Melanoma Progression. <i>Journal of Investigative Dermatology</i> , 2018, 138, 141-149.	0.3	29
80	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
81	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
82	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
83	Genome-wide prediction of synthetic rescue mediators of resistance to targeted and immunotherapy. <i>Molecular Systems Biology</i> , 2019, 15, e8323.	3.2	25
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	Gene Network Analysis in a Pediatric Cohort Identifies Novel Lung Function Genes. <i>PLoS ONE</i> , 2013, 8, e72899.	1.1	23
86	Rare variants at 16p11.2 are associated with common variable immunodeficiency. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 135, 1569-1577.	1.5	22
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	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
89	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
90	Copy Number Variations in CTNNA3 and RBFOX1 Associate with Pediatric Food Allergy. <i>Journal of Immunology</i> , 2015, 195, 1599-1607.	0.4	20

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91	Variants in CXCR4 associate with juvenile idiopathic arthritis susceptibility. BMC Medical Genetics, 2016, 17, 24.	2.1	20
92	CNV Analysis Associates AKNAD1 with Type-2 Diabetes in Jordan Subpopulations. Scientific Reports, 2015, 5, 13391.	1.6	18
93	Machine learning derived risk prediction of anorexia nervosa. BMC Medical Genomics, 2015, 9, 4.	0.7	18
94	UV-Induced Wnt7a in the Human Skin Microenvironment Specifies the Fate of Neural Crest-Like Cells via Suppression of Notch. Journal of Investigative Dermatology, 2015, 135, 1521-1532.	0.3	18
95	Online Change-Point Detection in Sparse Time Series With Application to Online Advertising. IEEE Transactions on Systems, Man, and Cybernetics: Systems, 2019, 49, 1141-1151.	5.9	18
96	Candidate gene analyses for acute pain and morphine analgesia after pediatric day surgery: African American versus European Caucasian ancestry and dose prediction limits. Pharmacogenomics Journal, 2019, 19, 570-581.	0.9	17
97	Target Genes of Autism Risk Loci in Brain Frontal Cortex. Frontiers in Genetics, 2019, 10, 707.	1.1	16
98	PIM kinases as therapeutic targets against advanced melanoma. Oncotarget, 2016, 7, 54897-54912.	0.8	16
99	A convolutional neural network model for survival prediction based on prognosis-related cascaded Wx feature selection. Laboratory Investigation, 2022, 102, 1064-1074.	1.7	16
100	SNVerGUI: a desktop tool for variant analysis of next-generation sequencing data. Journal of Medical Genetics, 2012, 49, 753-755.	1.5	15
101	Risk-Based Multi-Objective Optimization of Distributed Generation Based on GPSO-BFA Algorithm. IEEE Access, 2019, 7, 30563-30572.	2.6	15
102	DeepCNV: a deep learning approach for authenticating copy number variations. Briefings in Bioinformatics, 2021, 22, .	3.2	15
103	Weighted Gene Co-Expression Network Analysis Reveals Dysregulation of Mitochondrial Oxidative Phosphorylation in Eating Disorders. Genes, 2018, 9, 325.	1.0	14
104	A Reinforcement Learning Model Based on Temporal Difference Algorithm. IEEE Access, 2019, 7, 121922-121930.	2.6	14
105	The microbiome of HPV-positive tonsil squamous cell carcinoma and neck metastasis. Oral Oncology, 2021, 117, 105305.	0.8	14
106	Learning approaches to improve prediction of drug sensitivity in breast cancer patients. , 2016, 2016, 3314-3320.		13
107	An empirical Bayes change-point model for identifying 3 <sup>â€²</sup> and 5 <sup>â€²</sup> alternative splicing by next-generation RNA sequencing. Bioinformatics, 2016, 32, 1823-1831.	1.8	13
108	Dynamic surface control for a class of nonlinearly parameterized systems with input time delay using neural network. Journal of the Franklin Institute, 2020, 357, 1961-1986.	1.9	13

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109	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
110	Antitumor Activity of a Mitochondrial-Targeted HSP90 Inhibitor in Gliomas. <i>Clinical Cancer Research</i> , 2022, 28, 2180-2195.	3.2	12
111	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
112	Loss of Phd2 cooperates with BRAFV600E to drive melanomagenesis. <i>Nature Communications</i> , 2018, 9, 5426.	5.8	11
113	Time-Aware Latent Hierarchical Model for Predicting House Prices. , 2017, , .		10
114	Deep learning for sequence pattern recognition. , 2018, , .		10
115	Model-based autoencoders for imputing discrete single-cell RNA-seq data. <i>Methods</i> , 2021, 192, 112-119.	1.9	10
116	A Modified Nucleoside 6-Thio-2-Deoxyguanosine Exhibits Antitumor Activity in Gliomas. <i>Clinical Cancer Research</i> , 2021, 27, 6800-6814.	3.2	10
117	Genome-Wide Association Study of Serum Minerals Levels in Children of Different Ethnic Background. <i>PLoS ONE</i> , 2015, 10, e0123499.	1.1	9
118	A novel under-sampling algorithm based on Iterative-Partitioning Filters for imbalanced classification. , 2016, , .		9
119	Epistasis Detection in Genome-Wide Screening for Complex Human Diseases in Structured Populations. <i>Systems Medicine (New Rochelle, N Y)</i> , 2019, 2, 19-27.	1.4	9
120	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
121	Genome-wide association study identifies novel type II diabetes risk loci in Jordan subpopulations. <i>PeerJ</i> , 2017, 5, e3618.	0.9	9
122	Colonic healing requires Wnt produced by epithelium as well as Tagln+ and Acta2+ stromal cells. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	9
123	Genome-wide linkage and association analysis of rheumatoid arthritis in a Canadian population. <i>BMC Proceedings</i> , 2007, 1, S19.	1.8	8
124	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
125	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
126	Reliable Gender Prediction Based on Usersâ€™ Video Viewing Behavior. , 2016, , .		8



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127	A Blended Deep Learning Approach for Predicting User Intended Actions. , 2018, , .		8
128	An active learning approach for clustering single-cell RNA-seq data. Laboratory Investigation, 2022, 102, 227-235.	1.7	8
129	Targeted gene expression profiling of inverted papilloma and squamous cell carcinoma. International Forum of Allergy and Rhinology, 2022, 12, 200-209.	1.5	8
130	Transcriptome Profiling of Human Ulcerative Colitis Mucosa Reveals Altered Expression of Pathways Enriched in Genetic Susceptibility Loci. PLoS ONE, 2014, 9, e96153.	1.1	8
131	tRNA-DL: A Deep Learning Approach to Improve tRNAscan-SE Prediction Results. Human Heredity, 2018, 83, 163-172.	0.4	7
132	Multiple Epistasis Interactions Within MHC Are Associated With Ulcerative Colitis. Frontiers in Genetics, 2019, 10, 257.	1.1	7
133	Elucidation of DNA methylation on N6-adenine with deep learning. Nature Machine Intelligence, 2020, 2, 466-475.	8.3	7
134	An Enriched Time-Series Forecasting Framework for Long-Short Portfolio Strategy. IEEE Access, 2020, 8, 31992-32002.	2.6	7
135	Genetic Variation in PADI6-PADI4 on 1p36.13 Is Associated with Common Forms of Human Generalized Epilepsy. Genes, 2021, 12, 1441.	1.0	7
136	Fa-Mb-ResNet for Grounding Fault Identification and Line Selection in the Distribution Networks. IEEE Internet of Things Journal, 2022, 9, 11115-11125.	5.5	7
137	Collaborated Online Change-Point Detection in Sparse Time Series for Online Advertising. , 2015, , .		6
138	Application of computational methods in genetic study of inflammatory bowel disease. World Journal of Gastroenterology, 2016, 22, 949.	1.4	6
139	The virome of HPV-positive tonsil squamous cell carcinoma and neck metastasis. Oncotarget, 2020, 11, 282-293.	0.8	6
140	Improved Deep Convolutional Neural Networks via Boosting for Predicting the Quality of In Vitro Bovine Embryos. Electronics (Switzerland), 2022, 11, 1363.	1.8	6
141	Modeling Real Estate for School District Identification. , 2016, , .		5
142	A greedy-based oversampling approach to improve the prediction of mortality in MERS patients. , 2016, , .		5
143	Epstein-Barr Virus Facilitates Expression of KLF14 by Regulating the Cooperative Binding of the E2F-Rb-HDAC Complex in Latent Infection. Journal of Virology, 2020, 94, .	1.5	5
144	Regulation of Janus Kinase 2 by an Inflammatory Bowel Disease Causal Non-coding Single Nucleotide Polymorphism. Journal of Crohn's and Colitis, 2020, 14, 646-653.	0.6	5

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145	NUMB as a Therapeutic Target for Melanoma. <i>Journal of Investigative Dermatology</i> , 2022, 142, 1882-1892.e5.	0.3	5
146	Induction of metallothionein expression during monocyte to melanoma-associated macrophage differentiation. <i>Frontiers in Biology</i> , 2012, 7, 359-367.	0.7	4
147	Tissue-Specific Differential Expression of Novel Genes and Long Intergenic Noncoding RNAs in Humans With Extreme Response to Evoked Endotoxemia. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e001907.	1.6	4
148	A Comprehensive Survey of Immune Cytolytic Activity-Associated Gene Co-Expression Networks across 17 Tumor and Normal Tissue Types. <i>Cancers</i> , 2018, 10, 307.	1.7	4
149	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
150	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
151	Collapsing singletons may boost signal for associating rare variants in sequencing study. <i>BMC Proceedings</i> , 2014, 8, S50.	1.8	3
152	REMOLD: An Efficient Model-Based Clustering Algorithm for Large Datasets with Spark. , 2017, , .		3
153	Modeling Item-specific Effects for Video Click. , 2018, , 639-647.		3
154	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
155	A Middle Game Search Algorithm Applicable to Low-Cost Personal Computer for Go. <i>IEEE Access</i> , 2019, 7, 121719-121727.	2.6	3
156	Modeling and elucidation of housing price. <i>Data Mining and Knowledge Discovery</i> , 2019, 33, 636-662.	2.4	3
157	Top-k Parametrized Boost. <i>Lecture Notes in Computer Science</i> , 2014, , 91-98.	1.0	3
158	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
159	Hierarchical recognition of sparse patterns in large-scale simultaneous inference. <i>Biometrika</i> , 2015, 102, 267-280.	1.3	2
160	Annealed Sparsity via Adaptive and Dynamic Shrinking. , 2016, , .		2
161	User Response Driven Content Understanding with Causal Inference. , 2019, , .		2
162	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

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163	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
164	Genome-wide association study reveals two loci for serum magnesium concentrations in European-American children. <i>Scientific Reports</i> , 2015, 5, 18792.	1.6	1
165	Advanced Computational Approaches for Medical Genetics and Genomics. <i>BioMed Research International</i> , 2015, 2015, 1-2.	0.9	0
166	Dual $\ell_1$ - $\ell_2$ Convex Variable Subsets Family and Extremum Analysis for the OPF Problem. <i>IEEE Access</i> , 2018, 6, 27018-27027.	2.6	0
167	An Omnibus Test for Differential Distribution Analysis of Continuous Microbiome Data. <i>IEEE Access</i> , 2021, 9, 100029-100039.	2.6	0
168	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
169	Genetics of Inflammatory Bowel Diseases. , 2013, , 3-12.		0
170	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