

Pingzhao Hu

List of Publications by Year in descending order

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Version: 2024-02-01

140
papers

5,773
citations

101384

36
h-index

85405

71
g-index

142
all docs

142
docs citations

142
times ranked

12294
citing authors

#	ARTICLE	IF	CITATIONS
1	Mesenchymal stromal (stem) cell therapy modulates miR-193b-5p expression to attenuate sepsis-induced acute lung injury. <i>European Respiratory Journal</i> , 2022, 59, 2004216.	3.1	36
2	A pathogenic deletion in Forkhead Box L1 (FOXL1) identifies the first otosclerosis (OTSC) gene. <i>Human Genetics</i> , 2022, 141, 965-979.	1.8	7
3	Bayesian tensor factorization-drive breast cancer subtyping by integrating multi-omics data. <i>Journal of Biomedical Informatics</i> , 2022, 125, 103958.	2.5	10
4	Extendable and explainable deep learning for pan-cancer radiogenomics research. <i>Current Opinion in Chemical Biology</i> , 2022, 66, 102111.	2.8	11
5	MicroRNA regulatory networks associated with abnormal muscle repair in survivors of critical illness. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2022, 13, 1262-1276.	2.9	6
6	Multimic Metabolic Enrichment Network Analysis Reveals Metabolite-Protein Physical Interaction Subnetworks Altered in Cancer. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100189.	2.5	4
7	Polygenic risk and causal inference of psychiatric comorbidity in inflammatory bowel disease among patients with European ancestry. <i>Journal of Translational Medicine</i> , 2022, 20, 43.	1.8	1
8	Deep learning-driven prediction of drug mechanism of action from large-scale chemical-genetic interaction profiles. <i>Journal of Cheminformatics</i> , 2022, 14, 12.	2.8	9
9	Transitions between versions of the International Classification of Diseases and chronic disease prevalence estimates from administrative health data: a population-based study. <i>BMC Public Health</i> , 2022, 22, 701.	1.2	2
10	Deep clustering of small molecules at large-scale via variational autoencoder embedding and K-means. <i>BMC Bioinformatics</i> , 2022, 23, 132.	1.2	5
11	Tightly integrated multiomics-based deep tensor survival model for time-to-event prediction. <i>Bioinformatics</i> , 2022, 38, 3259-3266.	1.8	3
12	YOLO-LOGO: A transformer-based YOLO segmentation model for breast mass detection and segmentation in digital mammograms. <i>Computer Methods and Programs in Biomedicine</i> , 2022, 221, 106903.	2.6	36
13	Comprehensive multi-cohort transcriptional meta-analysis of muscle diseases identifies a signature of disease severity. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
14	Mapping Three Versions of the International Classification of Diseases to Categories of Chronic Conditions. <i>International Journal of Population Data Science</i> , 2021, 6, 1406.	0.1	2
15	Predicting breast cancer drug response using a multiple-layer cell line drug response network model. <i>BMC Cancer</i> , 2021, 21, 648.	1.1	8
16	Genetic predictors of gene expression associated with psychiatric comorbidity in patients with inflammatory bowel disease – A pilot study. <i>Genomics</i> , 2021, 113, 919-932.	1.3	4
17	Computational Drug Repurposing for Alzheimer's Disease Using Risk Genes From GWAS and Single-Cell RNA Sequencing Studies. <i>Frontiers in Pharmacology</i> , 2021, 12, 617537.	1.6	16
18	Characterization of Supragingival Plaque and Oral Swab Microbiomes in Children With Severe Early Childhood Caries. <i>Frontiers in Microbiology</i> , 2021, 12, 683685.	1.5	19

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19	ChrNet: A re-trainable chromosome-based 1D convolutional neural network for predicting immune cell types. <i>Genomics</i> , 2021, 113, 2023-2031.	1.3	5
20	Self-supervised deep learning model for COVID-19 lung CT image segmentation highlighting putative causal relationship among age, underlying disease and COVID-19. <i>Journal of Translational Medicine</i> , 2021, 19, 318.	1.8	70
21	Mitogen-induced transcriptional programming in human fibroblasts. <i>Gene</i> , 2021, 800, 145842.	1.0	4
22	Identification of significantly mutated subnetworks in the breast cancer genome. <i>Scientific Reports</i> , 2021, 11, 642.	1.6	0
23	A Novel Matrix Profile-Guided Attention LSTM Model for Forecasting COVID-19 Cases in USA. <i>Frontiers in Public Health</i> , 2021, 9, 741030.	1.3	7
24	A Maximum Flow-Based Approach to Prioritize Drugs for Drug Repurposing of Chronic Diseases. <i>Life</i> , 2021, 11, 1115.	1.1	3
25	Computational Prediction of the Pathogenic Status of Cancer-Specific Somatic Variants. <i>Frontiers in Genetics</i> , 2021, 12, 805656.	1.1	1
26	Proteomic Approaches to Defining Remission and the Risk of Relapse in Rheumatoid Arthritis. <i>Frontiers in Immunology</i> , 2021, 12, 729681.	2.2	4
27	Copy number variation-based gene set analysis reveals cytokine signalling pathways associated with psychiatric comorbidity in patients with inflammatory bowel disease. <i>Genomics</i> , 2020, 112, 683-693.	1.3	8
28	Epigenetic Profiling in Severe Sepsis: A Pilot Study of DNA Methylation Profiles in Critical Illness*. <i>Critical Care Medicine</i> , 2020, 48, 142-150.	0.4	42
29	Integrative Data Augmentation with U-Net Segmentation Masks Improves Detection of Lymph Node Metastases in Breast Cancer Patients. <i>Cancers</i> , 2020, 12, 2934.	1.7	28
30	A machine learning-based clinical tool for diagnosing myopathy using multi-cohort microarray expression profiles. <i>Journal of Translational Medicine</i> , 2020, 18, 454.	1.8	7
31	An integrative deep learning framework for classifying molecular subtypes of breast cancer. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2185-2199.	1.9	40
32	Dynamics of the cell-free DNA methylome of metastatic prostate cancer during androgen-targeting treatment. <i>Epigenomics</i> , 2020, 12, 1317-1332.	1.0	15
33	A Two-Dimensional Sparse Matrix Profile DenseNet for COVID-19 Diagnosis Using Chest CT Images. <i>IEEE Access</i> , 2020, 8, 213718-213728.	2.6	60
34	Incidence, Characteristics, and Outcomes of Interval Breast Cancers Compared With Screening-Detected Breast Cancers. <i>JAMA Network Open</i> , 2020, 3, e2018179.	2.8	48
35	Tumor-Infiltrating CD8 T Cells Predict Clinical Breast Cancer Outcomes in Young Women. <i>Cancers</i> , 2020, 12, 1076.	1.7	31
36	DTF: Deep Tensor Factorization for predicting anticancer drug synergy. <i>Bioinformatics</i> , 2020, 36, 4483-4489.	1.8	34

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37	Mesenchymal stromal/stem cells modulate response to experimental sepsis-induced lung injury via regulation of miR-27a-5p in recipient mice. <i>Thorax</i> , 2020, 75, 556-567.	2.7	17
38	Sex-Based Diverse Plaque Microbiota in Children with Severe Caries. <i>Journal of Dental Research</i> , 2020, 99, 703-712.	2.5	37
39	Deep graph embedding for prioritizing synergistic anticancer drug combinations. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 427-438.	1.9	64
40	Discovery of inflammatory bowel disease-associated miRNAs using a novel bipartite clustering approach. <i>BMC Medical Genomics</i> , 2020, 13, 10.	0.7	11
41	Epigenetics of Sepsis. <i>Critical Care Medicine</i> , 2020, 48, 745-756.	0.4	41
42	Mesenchymal Stem/Stromal Cells Increase Cardiac MIR-187-3P Expression in Polymicrobial Animal Model of Sepsis. <i>Shock</i> , 2020, Publish Ahead of Print, 133-141.	1.0	12
43	Development of a machine learning-based multimode diagnosis system for lung cancer. <i>Aging</i> , 2020, 12, 9840-9854.	1.4	8
44	Genome-wide copy number variant data for inflammatory bowel disease in a caucasian population. <i>Data in Brief</i> , 2019, 25, 104203.	0.5	0
45	Predicting Drug-Drug Interactions Using Deep Neural Network. , 2019, , .		11
46	A Novel Convolutional Regression Network for Cell Counting. , 2019, , .		5
47	Isolation and characterization of a new basal-like luminal progenitor in human breast tissue. <i>Stem Cell Research and Therapy</i> , 2019, 10, 269.	2.4	4
48	MiR-490-3p and MiR-744-5p Are Increased in ICU Acquired Weakness (ICUAW) and Regulate Myoblast Differentiation and Proliferation. , 2019, , .		0
49	Automated Counting of Cancer Cells by Ensembling Deep Features. <i>Cells</i> , 2019, 8, 1019.	1.8	12
50	Modeling Gene-Environment Interaction for the Risk of Non-hodgkin Lymphoma. <i>Frontiers in Oncology</i> , 2019, 8, 657.	1.3	3
51	Genome-Wide Canonical Correlation Analysis-Based Computational Methods for Mining Information from Microbiome and Gene Expression Data. <i>Lecture Notes in Computer Science</i> , 2019, , 511-517.	1.0	1
52	Genome-wide analysis identifies rare copy number variations associated with inflammatory bowel disease. <i>PLoS ONE</i> , 2019, 14, e0217846.	1.1	16
53	Association Analysis of Deep Genomic Features Extracted by Denoising Autoencoders in Breast Cancer. <i>Cancers</i> , 2019, 11, 494.	1.7	15
54	An OpenMP-based tool for finding longest common subsequence in bioinformatics. <i>BMC Research Notes</i> , 2019, 12, 220.	0.6	11

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55	Predicting drug-target interaction network using deep learning model. <i>Computational Biology and Chemistry</i> , 2019, 80, 90-101.	1.1	89
56	Chromatin organization of transcribed genes in chicken polychromatic erythrocytes. <i>Gene</i> , 2019, 699, 80-87.	1.0	8
57	Integrative Analysis Reveals Subtype-Specific Regulatory Determinants in Triple Negative Breast Cancer. <i>Cancers</i> , 2019, 11, 507.	1.7	10
58	Computational drug repurposing for inflammatory bowel disease using genetic information. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 127-135.	1.9	19
59	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	15
60	Epigenome-wide DNA methylation profiling of periprostatic adipose tissue in prostate cancer patients with excess adiposity—a pilot study. <i>Clinical Epigenetics</i> , 2018, 10, 54.	1.8	22
61	Long Non-Coding RNA H19 Acts as an Estrogen Receptor Modulator that is Required for Endocrine Therapy Resistance in ER+ Breast Cancer Cells. <i>Cellular Physiology and Biochemistry</i> , 2018, 51, 1518-1532.	1.1	57
62	Recurrent copy number alterations in young women with breast cancer. <i>Oncotarget</i> , 2018, 9, 11541-11558.	0.8	12
63	A deep neural network based regression model for triglyceride concentrations prediction using epigenome-wide DNA methylation profiles. <i>BMC Proceedings</i> , 2018, 12, 21.	1.8	7
64	Association Analysis of Somatic Copy Number Alteration Burden With Breast Cancer Survival. <i>Frontiers in Genetics</i> , 2018, 9, 421.	1.1	38
65	An integrative network-based approach to identify novel disease genes and pathways: a case study in the context of inflammatory bowel disease. <i>BMC Bioinformatics</i> , 2018, 19, 264.	1.2	22
66	Drug-Target Interaction Network Predictions for Drug Repurposing Using LASSO-Based Regularized Linear Classification Model. <i>Lecture Notes in Computer Science</i> , 2018, , 272-278.	1.0	1
67	Somatic Copy Number Alteration-Based Prediction of Molecular Subtypes of Breast Cancer Using Deep Learning Model. <i>Lecture Notes in Computer Science</i> , 2017, , 57-63.	1.0	4
68	Protein complexes, big data, machine learning and integrative proteomics: lessons learned over a decade of systematic analysis of protein interaction networks. <i>Expert Review of Proteomics</i> , 2017, 14, 845-855.	1.3	19
69	DJ-1/PARK7 Impairs Bacterial Clearance in Sepsis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 195, 889-905.	2.5	55
70	Associations between genetic variants in immunoregulatory genes and risk of non-Hodgkin lymphoma in a Chinese population. <i>Oncotarget</i> , 2017, 8, 10450-10457.	0.8	10
71	Discovering MicroRNA-Regulatory Modules in Multi-Dimensional Cancer Genomic Data: A Survey of Computational Methods. <i>Cancer Informatics</i> , 2016, 15s2, CIN.S39369.	0.9	8
72	A Novel Graph-based Algorithm to Infer Recurrent Copy Number Variations in Cancer. <i>Cancer Informatics</i> , 2016, 15s2, CIN.S39368.	0.9	1

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73	Transcriptomic analysis reveals abnormal muscle repair and remodeling in survivors of critical illness with sustained weakness. <i>Scientific Reports</i> , 2016, 6, 29334.	1.6	32
74	The genetic diversity of Epstein-Barr virus in the setting of transplantation relative to non-transplant settings: A feasibility study. <i>Pediatric Transplantation</i> , 2016, 20, 124-129.	0.5	5
75	Chlamydial Protease-Like Activity Factor and Type III Secreted Effectors Cooperate in Inhibition of p65 Nuclear Translocation. <i>MBio</i> , 2016, 7, .	1.8	26
76	Identity-by-descent mapping for diastolic blood pressure in unrelated Mexican Americans. <i>BMC Proceedings</i> , 2016, 10, 263-267.	1.8	4
77	The Histone Methyltransferase Enzyme Enhancer of Zeste Homolog 2 Protects against Podocyte Oxidative Stress and Renal Injury in Diabetes. <i>Journal of the American Society of Nephrology: JASN</i> , 2016, 27, 2021-2034.	3.0	72
78	Microarray Meta-Analysis and Cross-Platform Normalization: Integrative Genomics for Robust Biomarker Discovery. <i>Microarrays (Basel, Switzerland)</i> , 2015, 4, 389-406.	1.4	93
79	Identification of genomic signatures in circulating tumor cells from breast cancer. <i>International Journal of Cancer</i> , 2015, 137, 332-344.	2.3	54
80	A high-resolution copy-number variation resource for clinical and population genetics. <i>Genetics in Medicine</i> , 2015, 17, 747-752.	1.1	73
81	Prenatal Exposure to Maternal Cigarette Smoking and DNA Methylation: Epigenome-Wide Association in a Discovery Sample of Adolescents and Replication in an Independent Cohort at Birth through 17 Years of Age. <i>Environmental Health Perspectives</i> , 2015, 123, 193-199.	2.8	178
82	Ras Signaling Is a Key Determinant for Metastatic Dissemination and Poor Survival of Luminal Breast Cancer Patients. <i>Cancer Research</i> , 2015, 75, 4960-4972.	0.4	48
83	Highly Pathogenic H5N1 and Novel H7N9 Influenza A Viruses Induce More Profound Proteomic Host Responses than Seasonal and Pandemic H1N1 Strains. <i>Journal of Proteome Research</i> , 2015, 14, 4511-4523.	1.8	55
84	Discriminative learning of generative models: large margin multinomial mixture models for document classification. <i>Pattern Analysis and Applications</i> , 2015, 18, 535-551.	3.1	2
85	RelB deficiency causes combined immunodeficiency. <i>LymphoSign Journal</i> , 2015, 2, 147-155.	0.1	21
86	Gene expression in young adult type breast cancer: a retrospective analysis. <i>Oncotarget</i> , 2015, 6, 13688-13702.	0.8	39
87	Genome-wide association study of bipolar disorder in Canadian and UK populations corroborates disease loci including SYNE1 and CSMD1. <i>BMC Medical Genetics</i> , 2014, 15, 2.	2.1	106
88	Brain-expressed exons under purifying selection are enriched for de novo mutations in autism spectrum disorder. <i>Nature Genetics</i> , 2014, 46, 742-747.	9.4	149
89	Dynamic pathway analysis of genes associated with blood pressure using whole genome sequence data. <i>BMC Proceedings</i> , 2014, 8, S106.	1.8	3
90	MicroRNA-144 is a circulating effector of remote ischemic preconditioning. <i>Basic Research in Cardiology</i> , 2014, 109, 423.	2.5	201

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91	Neuregulin 1-alpha regulates phosphorylation, acetylation, and alternative splicing in lymphoblastoid cells. <i>Genome</i> , 2013, 56, 619-625.	0.9	5
92	RNA-Seq analysis of the parietal cortex in Alzheimer's disease reveals alternatively spliced isoforms related to lipid metabolism. <i>Neuroscience Letters</i> , 2013, 536, 90-95.	1.0	77
93	Metaphyseal Dysplasia with Maxillary Hypoplasia and Brachydactyly Is Caused by a Duplication in RUNX2. <i>American Journal of Human Genetics</i> , 2013, 92, 252-258.	2.6	29
94	Association between a Multi-Locus Genetic Risk Score and Inflammatory Bowel Disease. <i>Bioinformatics and Biology Insights</i> , 2013, 7, BBI.S11601.	1.0	9
95	NADPH oxidase complex and IBD candidate gene studies: identification of a rare variant in <i>NCF2</i> that results in reduced binding to RAC2. <i>Gut</i> , 2012, 61, 1028-1035.	6.1	158
96	Salutary effect of resveratrol on sepsis-induced myocardial depression*. <i>Critical Care Medicine</i> , 2012, 40, 1896-1907.	0.4	42
97	A Census of Human Soluble Protein Complexes. <i>Cell</i> , 2012, 150, 1068-1081.	13.5	781
98	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
99	Markers of survival and metastatic potential in childhood CNS primitive neuro-ectodermal brain tumours: an integrative genomic analysis. <i>Lancet Oncology</i> , The, 2012, 13, 838-848.	5.1	148
100	Obesity and prostate cancer: gene expression signature of human periprostatic adipose tissue. <i>BMC Medicine</i> , 2012, 10, 108.	2.3	74
101	Network Analysis of Transcriptional Responses Induced by Mesenchymal Stem Cell Treatment of Experimental Sepsis. <i>American Journal of Pathology</i> , 2012, 181, 1681-1692.	1.9	76
102	Microarray Meta-Analysis Identifies Acute Lung Injury Biomarkers in Donor Lungs That Predict Development of Primary Graft Failure in Recipients. <i>PLoS ONE</i> , 2012, 7, e45506.	1.1	17
103	Gene network modular-based classification of microarray samples. <i>BMC Bioinformatics</i> , 2012, 13, S17.	1.2	6
104	Gene and miRNA expression profiles in autism spectrum disorders. <i>Brain Research</i> , 2011, 1380, 85-97.	1.1	165
105	A genotype resource for postmortem brain samples from the Autism Tissue Program. <i>Autism Research</i> , 2011, 4, 89-97.	2.1	23
106	Genome-wide association study of type 2 diabetes in a sample from Mexico City and a meta-analysis of a Mexican-American sample from Starr County, Texas. <i>Diabetologia</i> , 2011, 54, 2038-2046.	2.9	114
107	Pathway-based joint effects analysis of rare genetic variants using Genetic Analysis Workshop 17 exon sequence data. <i>BMC Proceedings</i> , 2011, 5, S45.	1.8	7
108	A pathway-based association analysis model using common and rare variants. <i>BMC Proceedings</i> , 2011, 5, S85.	1.8	1

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109	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
110	Gene Network Modules-Based Linear Discriminant Analysis of Microarray Gene Expression Data. <i>Lecture Notes in Computer Science</i> , 2011, , 286-296.	1.0	2
111	Incorporating Correlations among Gene Ontology Terms into Predicting Protein Functions. , 2011, , 154-173.		0
112	Predicting protein functions by relaxation labelling protein interaction network. <i>BMC Bioinformatics</i> , 2010, 11, S64.	1.2	16
113	Transcriptomic analysis of dystrophin RNAi knockdown reveals a central role for dystrophin in muscle differentiation and contractile apparatus organization. <i>BMC Genomics</i> , 2010, 11, 345.	1.2	26
114	Gene Expression Changes Associated with Resistance to Intravenous Corticosteroid Therapy in Children with Severe Ulcerative Colitis. <i>PLoS ONE</i> , 2010, 5, e13085.	1.1	37
115	Prkar1a is an osteosarcoma tumor suppressor that defines a molecular subclass in mice. <i>Journal of Clinical Investigation</i> , 2010, 120, 3310-3325.	3.9	89
116	A topology-sharing based method for protein function prediction via analysis of protein functional association networks. , 2009, , .		2
117	Data Integration in Genetics and Genomics: Methods and Challenges. <i>Human Genomics and Proteomics</i> , 2009, 1, .	1.5	105
118	Pathway-based analysis of a genome-wide case-control association study of rheumatoid arthritis. <i>BMC Proceedings</i> , 2009, 3, S128.	1.8	13
119	Global Functional Atlas of Escherichia coli Encompassing Previously Uncharacterized Proteins. <i>PLoS Biology</i> , 2009, 7, e1000096.	2.6	331
120	IL-23R Polymorphisms in Patients with Ankylosing Spondylitis in Korea: Table 1.. <i>Journal of Rheumatology</i> , 2009, 36, 1003-1005.	1.0	42
121	Using the ratio of means as the effect size measure in combining results of microarray experiments. <i>BMC Systems Biology</i> , 2009, 3, 106.	3.0	10
122	Gene expression using microarrays in transplant recipients at risk of EBV lymphoproliferation after organ transplantation: Preliminary proof-of-concept. <i>Pediatric Transplantation</i> , 2009, 13, 990-998.	0.5	12
123	A flexible approximate likelihood ratio test for detecting differential expression in microarray data. <i>Computational Statistics and Data Analysis</i> , 2009, 53, 3685-3695.	0.7	3
124	Bioinformatics Application: Predicting Protein Subcellular Localization by Applying Machine Learning. , 2009, , 163-174.		0
125	Differential gene profiling in acute lung injury identifies injury-specific gene expression*. <i>Critical Care Medicine</i> , 2008, 36, 855-865.	0.4	56
126	Interleukin 1 polymorphisms in patients with ankylosing spondylitis in Korea. <i>Journal of Rheumatology</i> , 2008, 35, 1603-8.	1.0	19

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127	Identifying cis- and trans-acting single-nucleotide polymorphisms controlling lymphocyte gene expression in humans. BMC Proceedings, 2007, 1, S7.	1.8	7
128	Computational prediction of cancer-gene function. Nature Reviews Cancer, 2007, 7, 23-34.	12.8	81
129	Impact of normalization and filtering on linkage analysis of gene expression data. BMC Proceedings, 2007, 1, S150.	1.8	2
130	Chromosomal Clustering of Periodically Expressed Genes in Plasmodium falciparum. , 2007, , 103-119.		0
131	Integrative analysis of gene expression data including an assessment of pathway enrichment for predicting prostate cancer. Cancer Informatics, 2007, 2, 289-300.	0.9	3
132	Integrating Affymetrix microarray data sets using probe-level test statistic for predicting prostate cancer. , 2006, , .		3
133	Global Survey of Organ and Organelle Protein Expression in Mouse: Combined Proteomic and Transcriptomic Profiling. Cell, 2006, 125, 173-186.	13.5	429
134	Integrative Analysis of Gene Expression Data Including an Assessment of Pathway Enrichment for Predicting Prostate Cancer. Cancer Informatics, 2006, 2, 117693510600200.	0.9	1
135	Statistical Methods for Meta-Analysis of Microarray Data: A Comparative Study. Information Systems Frontiers, 2006, 8, 9-20.	4.1	19
136	Tests for differential gene expression using weights in oligonucleotide microarray experiments. BMC Genomics, 2006, 7, 33.	1.2	9
137	Integrative analysis of multiple gene expression profiles with quality-adjusted effect size models. BMC Bioinformatics, 2005, 6, 128.	1.2	45
138	An empirical test of the competing destinations model. Journal of Geographical Systems, 2002, 4, 301-323.	1.9	21
139	Deep Learning Models for Predicting Phenotypic Traits and Diseases from Omics Data. , 0, , .		3
140	Incorporating Correlations among Gene Ontology Terms into Predicting Protein Functions. , 0, , 831-850.		0