Pingzhao Hu

List of Publications by Year
in descending order

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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	A Census of Human Soluble Protein Complexes. Cell, 2012, 150, 1068-1081.	13.5	781
2	Global Survey of Organ and Organelle Protein Expression in Mouse: Combined Proteomic and Transcriptomic Profiling. Cell, 2006, 125, 173-186.	13.5	429
3	Global Functional Atlas of Escherichia coli Encompassing Previously Uncharacterized Proteins. PLoS Biology, 2009, 7, e1000096.	2.6	331
4	SNVer: a statistical tool for variant calling in analysis of pooled or individual next-generation sequencing data. Nucleic Acids Research, 2011, 39, e132-e132.	6.5	225
5	MicroRNA-144 is a circulating effector of remote ischemic preconditioning. Basic Research in Cardiology, 2014, 109, 423.	2.5	201
6	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. Environmental Health Perspectives, 2015, 123, 193-199.	2.8	178
7	Gene and miRNA expression profiles in autism spectrum disorders. Brain Research, 2011, 1380, 85-97.	1.1	165
8	NADPH oxidase complex and IBD candidate gene studies: identification of a rare variant inNCF2that results in reduced binding to RAC2. Gut, 2012, 61, 1028-1035.	6.1	158
9	Brain-expressed exons under purifying selection are enriched for de novo mutations in autism spectrum disorder. Nature Genetics, 2014, 46, 742-747.	9.4	149
10	Markers of survival and metastatic potential in childhood CNS primitive neuro-ectodermal brain tumours: an integrative genomic analysis. Lancet Oncology, The, 2012, 13, 838-848.	5.1	148
11	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. Diabetologia, 2011, 54, 2038-2046.	2.9	114
12	Genome-wide association study of bipolar disorder in Canadian and UK populations corroborates disease loci including SYNE1 and CSMD1. BMC Medical Genetics, 2014, 15, 2.	2.1	106
13	Data Integration in Genetics and Genomics: Methods and Challenges. Human Genomics and Proteomics, 2009, 1, .	1.5	105
14	Microarray Meta-Analysis and Cross-Platform Normalization: Integrative Genomics for Robust Biomarker Discovery. Microarrays (Basel, Switzerland), 2015, 4, 389-406.	1.4	93
15	Predicting drug-target interaction network using deep learning model. Computational Biology and Chemistry, 2019, 80, 90-101.	1.1	89
16	Prkar1a is an osteosarcoma tumor suppressor that defines a molecular subclass in mice. Journal of Clinical Investigation, 2010, 120, 3310-3325.	3.9	89
17	Computational prediction of cancer-gene function. Nature Reviews Cancer, 2007, 7, 23-34.	12.8	81
18	RNA-Seq analysis of the parietal cortex in Alzheimer's disease reveals alternatively spliced isoforms related to lipid metabolism. Neuroscience Letters, 2013, 536, 90-95.	1.0	77

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19	Network Analysis of Transcriptional Responses Induced by Mesenchymal Stem Cell Treatment of Experimental Sepsis. American Journal of Pathology, 2012, 181, 1681-1692.	1.9	76
20	Obesity and prostate cancer: gene expression signature of human periprostatic adipose tissue. BMC Medicine, 2012, 10, 108.	2.3	74
21	A high-resolution copy-number variation resource for clinical and population genetics. Genetics in Medicine, 2015, 17, 747-752.	1.1	73
22	The Histone Methyltransferase Enzyme Enhancer of Zeste Homolog 2 Protects against Podocyte Oxidative Stress and Renal Injury in Diabetes. Journal of the American Society of Nephrology: JASN, 2016, 27, 2021-2034.	3.0	72
23	Self-supervised deep learning model for COVID-19 lung CT image segmentation highlighting putative causal relationship among age, underlying disease and COVID-19. Journal of Translational Medicine, 2021, 19, 318.	1.8	70
24	Deep graph embedding for prioritizing synergistic anticancer drug combinations. Computational and Structural Biotechnology Journal, 2020, 18, 427-438.	1.9	64
25	A Two-Dimensional Sparse Matrix Profile DenseNet for COVID-19 Diagnosis Using Chest CT Images. IEEE Access, 2020, 8, 213718-213728.	2.6	60
26	Long Non-Coding RNA H19 Acts as an Estrogen Receptor Modulator that is Required for Endocrine Therapy Resistance in ER+ Breast Cancer Cells. Cellular Physiology and Biochemistry, 2018, 51, 1518-1532.	1.1	57
27	Differential gene profiling in acute lung injury identifies injury-specific gene expression*. Critical Care Medicine, 2008, 36, 855-865.	0.4	56
28	Highly Pathogenic H5N1 and Novel H7N9 Influenza A Viruses Induce More Profound Proteomic Host Responses than Seasonal and Pandemic H1N1 Strains. Journal of Proteome Research, 2015, 14, 4511-4523.	1.8	55
29	DJ-1/PARK7 Impairs Bacterial Clearance in Sepsis. American Journal of Respiratory and Critical Care Medicine, 2017, 195, 889-905.	2.5	55
30	Identification of genomic signatures in circulating tumor cells from breast cancer. International Journal of Cancer, 2015, 137, 332-344.	2.3	54
31	Ras Signaling Is a Key Determinant for Metastatic Dissemination and Poor Survival of Luminal Breast Cancer Patients. Cancer Research, 2015, 75, 4960-4972.	0.4	48
32	Incidence, Characteristics, and Outcomes of Interval Breast Cancers Compared With Screening-Detected Breast Cancers. JAMA Network Open, 2020, 3, e2018179.	2.8	48
33	Integrative analysis of multiple gene expression profiles with quality-adjusted effect size models. BMC Bioinformatics, 2005, 6, 128.	1.2	45
34	IL-23R Polymorphisms in Patients with Ankylosing Spondylitis in Korea: Table 1.. Journal of Rheumatology, 2009, 36, 1003-1005.	1.0	42
35	Salutary effect of resveratrol on sepsis-induced myocardial depression*. Critical Care Medicine, 2012, 40, 1896-1907.	0.4	42
36	Epigenetic Profiling in Severe Sepsis: A Pilot Study of DNA Methylation Profiles in Critical Illness*. Critical Care Medicine, 2020, 48, 142-150.	0.4	42

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37	Epigenetics of Sepsis. Critical Care Medicine, 2020, 48, 745-756.	0.4	41
38	An integrative deep learning framework for classifying molecular subtypes of breast cancer. Computational and Structural Biotechnology Journal, 2020, 18, 2185-2199.	1.9	40
39	Gene expression in â€œyoung adult typeâ€•breast cancer: a retrospective analysis. Oncotarget, 2015, 6, 13688-13702.	0.8	39
40	Association Analysis of Somatic Copy Number Alteration Burden With Breast Cancer Survival. Frontiers in Genetics, 2018, 9, 421.	1.1	38
41	Gene Expression Changes Associated with Resistance to Intravenous Corticosteroid Therapy in Children with Severe Ulcerative Colitis. PLoS ONE, 2010, 5, e13085.	1.1	37
42	Sex-Based Diverse Plaque Microbiota in Children with Severe Caries. Journal of Dental Research, 2020, 99, 703-712.	2.5	37
43	Mesenchymal stromal (stem) cell therapy modulates miR-193b-5p expression to attenuate sepsis-induced acute lung injury. European Respiratory Journal, 2022, 59, 2004216.	3.1	36
44	YOLO-LOGO: A transformer-based YOLO segmentation model for breast mass detection and segmentation in digital mammograms. Computer Methods and Programs in Biomedicine, 2022, 221, 106903.	2.6	36
45	DTF: Deep Tensor Factorization for predicting anticancer drug synergy. Bioinformatics, 2020, 36, 4483-4489.	1.8	34
46	Transcriptomic analysis reveals abnormal muscle repair and remodeling in survivors of critical illness with sustained weakness. Scientific Reports, 2016, 6, 29334.	1.6	32
47	Tumor-Infiltrating CD8 T Cells Predict Clinical Breast Cancer Outcomes in Young Women. Cancers, 2020, 12, 1076.	1.7	31
48	Metaphyseal Dysplasia with Maxillary Hypoplasia and Brachydactyly Is Caused by a Duplication in RUNX2. American Journal of Human Genetics, 2013, 92, 252-258.	2.6	29
49	Integrative Data Augmentation with U-Net Segmentation Masks Improves Detection of Lymph Node Metastases in Breast Cancer Patients. Cancers, 2020, 12, 2934.	1.7	28
50	Transcriptomic analysis of dystrophin RNAi knockdown reveals a central role for dystrophin in muscle differentiation and contractile apparatus organization. BMC Genomics, 2010, 11, 345.	1.2	26
51	Chlamydial Protease-Like Activity Factor and Type III Secreted Effectors Cooperate in Inhibition of p65 Nuclear Translocation. MBio, 2016, 7, .	1.8	26
52	A genotype resource for postmortem brain samples from the Autism Tissue Program. Autism Research, 2011, 4, 89-97.	2.1	23
53	Epigenome-wide DNA methylation profiling of periprostatic adipose tissue in prostate cancer patients with excess adiposityâ€”a pilot study. Clinical Epigenetics, 2018, 10, 54.	1.8	22
54	An integrative network-based approach to identify novel disease genes and pathways: a case study in the context of inflammatory bowel disease. BMC Bioinformatics, 2018, 19, 264.	1.2	22

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55	An empirical test of the competing destinations model. Journal of Geographical Systems, 2002, 4, 301-323.	1.9	21
56	RelB deficiency causes combined immunodeficiency. LymphoSign Journal, 2015, 2, 147-155.	0.1	21
57	Statistical Methods for Meta-Analysis of Microarray Data: A Comparative Study. Information Systems Frontiers, 2006, 8, 9-20.	4.1	19
58	Protein complexes, big data, machine learning and integrative proteomics: lessons learned over a decade of systematic analysis of protein interaction networks. Expert Review of Proteomics, 2017, 14, 845-855.	1.3	19
59	Computational drug repurposing for inflammatory bowel disease using genetic information. Computational and Structural Biotechnology Journal, 2019, 17, 127-135.	1.9	19
60	Characterization of Supragingival Plaque and Oral Swab Microbiomes in Children With Severe Early Childhood Caries. Frontiers in Microbiology, 2021, 12, 683685.	1.5	19
61	Interleukin 1 polymorphisms in patients with ankylosing spondylitis in Korea. Journal of Rheumatology, 2008, 35, 1603-8.	1.0	19
62	Microarray Meta-Analysis Identifies Acute Lung Injury Biomarkers in Donor Lungs That Predict Development of Primary Graft Failure in Recipients. PLoS ONE, 2012, 7, e45506.	1.1	17
63	Mesenchymal stromal/stem cells modulate response to experimental sepsis-induced lung injury via regulation of miR-27a-5p in recipient mice. Thorax, 2020, 75, 556-567.	2.7	17
64	Predicting protein functions by relaxation labelling protein interaction network. BMC Bioinformatics, 2010, 11, S64.	1.2	16
65	Genome-wide analysis identifies rare copy number variations associated with inflammatory bowel disease. PLoS ONE, 2019, 14, e0217846.	1.1	16
66	Computational Drug Repurposing for Alzheimerâ€™s Disease Using Risk Genes From GWAS and Single-Cell RNA Sequencing Studies. Frontiers in Pharmacology, 2021, 12, 617537.	1.6	16
67	SNVerGUI: a desktop tool for variant analysis of next-generation sequencing data. Journal of Medical Genetics, 2012, 49, 753-755.	1.5	15
68	Association Analysis of Deep Genomic Features Extracted by Denoising Autoencoders in Breast Cancer. Cancers, 2019, 11, 494.	1.7	15
69	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	15
70	Dynamics of the cell-free DNA methylome of metastatic prostate cancer during androgen-targeting treatment. Epigenomics, 2020, 12, 1317-1332.	1.0	15
71	Pathway-based analysis of a genome-wide case-control association study of rheumatoid arthritis. BMC Proceedings, 2009, 3, S128.	1.8	13
72	Gene expression using microarrays in transplant recipients at risk of EBV lymphoproliferation after organ transplantation: Preliminary proofâ€ofâ€concept. Pediatric Transplantation, 2009, 13, 990-998.	0.5	12

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73	Recurrent copy number alterations in young women with breast cancer. Oncotarget, 2018, 9, 11541-11558.	0.8	12
74	Automated Counting of Cancer Cells by Ensembling Deep Features. Cells, 2019, 8, 1019.	1.8	12
75	Mesenchymal Stem/Stromal Cells Increase Cardiac MIR-187-3P Expression in Polymicrobial Animal Model of Sepsis. Shock, 2020, Publish Ahead of Print, 133-141.	1.0	12
76	Predicting Drug-Drug Interactions Using Deep Neural Network. , 2019, , .		11
77	An OpenMP-based tool for finding longest common subsequence in bioinformatics. BMC Research Notes, 2019, 12, 220.	0.6	11
78	Discovery of inflammatory bowel disease-associated miRNAs using a novel bipartite clustering approach. BMC Medical Genomics, 2020, 13, 10.	0.7	11
79	Extendable and explainable deep learning for pan-cancer radiogenomics research. Current Opinion in Chemical Biology, 2022, 66, 102111.	2.8	11
80	Using the ratio of means as the effect size measure in combining results of microarray experiments. BMC Systems Biology, 2009, 3, 106.	3.0	10
81	Integrative Analysis Reveals Subtype-Specific Regulatory Determinants in Triple Negative Breast Cancer. Cancers, 2019, 11, 507.	1.7	10
82	Associations between genetic variants in immunoregulatory genes and risk of non-Hodgkin lymphoma in a Chinese population. Oncotarget, 2017, 8, 10450-10457.	0.8	10
83	Bayesian tensor factorization-drive breast cancer subtyping by integrating multi-omics data. Journal of Biomedical Informatics, 2022, 125, 103958.	2.5	10
84	Tests for differential gene expression using weights in oligonucleotide microarray experiments. BMC Genomics, 2006, 7, 33.	1.2	9
85	Association between a Multi-Locus Genetic Risk Score and Inflammatory Bowel Disease. Bioinformatics and Biology Insights, 2013, 7, BBI.S11601.	1.0	9
86	Deep learning-driven prediction of drug mechanism of action from large-scale chemical-genetic interaction profiles. Journal of Cheminformatics, 2022, 14, 12.	2.8	9
87	Discovering MicroRNA-Regulatory Modules in Multi-Dimensional Cancer Genomic Data: A Survey of Computational Methods. Cancer Informatics, 2016, 15s2, CIN.S39369.	0.9	8
88	Chromatin organization of transcribed genes in chicken polychromatic erythrocytes. Gene, 2019, 699, 80-87.	1.0	8
89	Copy number variation-based gene set analysis reveals cytokine signalling pathways associated with psychiatric comorbidity in patients with inflammatory bowel disease. Genomics, 2020, 112, 683-693.	1.3	8
90	Predicting breast cancer drug response using a multiple-layer cell line drug response network model. BMC Cancer, 2021, 21, 648.	1.1	8

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91	Development of a machine learning-based multimode diagnosis system for lung cancer. Aging, 2020, 12, 9840-9854.	1.4	8
92	Identifying cis- and trans-acting single-nucleotide polymorphisms controlling lymphocyte gene expression in humans. BMC Proceedings, 2007, 1, S7.	1.8	7
93	Pathway-based joint effects analysis of rare genetic variants using Genetic Analysis Workshop 17 exon sequence data. BMC Proceedings, 2011, 5, S45.	1.8	7
94	A deep neural network based regression model for triglyceride concentrations prediction using epigenome-wide DNA methylation profiles. BMC Proceedings, 2018, 12, 21.	1.8	7
95	A machine learning-based clinical tool for diagnosing myopathy using multi-cohort microarray expression profiles. Journal of Translational Medicine, 2020, 18, 454.	1.8	7
96	A Novel Matrix Profile-Guided Attention LSTM Model for Forecasting COVID-19 Cases in USA. Frontiers in Public Health, 2021, 9, 741030.	1.3	7
97	A pathogenic deletion in Forkhead Box L1 (FOXL1) identifies the first otosclerosis (OTSC) gene. Human Genetics, 2022, 141, 965-979.	1.8	7
98	Gene network modular-based classification of microarray samples. BMC Bioinformatics, 2012, 13, S17.	1.2	6
99	MicroRNA regulatory networks associated with abnormal muscle repair in survivors of critical illness. Journal of Cachexia, Sarcopenia and Muscle, 2022, 13, 1262-1276.	2.9	6
100	Neuregulin 1-alpha regulates phosphorylation, acetylation, and alternative splicing in lymphoblastoid cells. Genome, 2013, 56, 619-625.	0.9	5
101	The genetic diversity of Epsteinâ€“Barr virus in the setting of transplantation relative to nonâ€transplant settings: A feasibility study. Pediatric Transplantation, 2016, 20, 124-129.	0.5	5
102	A Novel Convolutional Regression Network for Cell Counting. , 2019, , .		5
103	ChrNet: A re-trainable chromosome-based 1D convolutional neural network for predicting immune cell types. Genomics, 2021, 113, 2023-2031.	1.3	5
104	Deep clustering of small molecules at large-scale via variational autoencoder embedding and K-means. BMC Bioinformatics, 2022, 23, 132.	1.2	5
105	Identity-by-descent mapping for diastolic blood pressure in unrelated Mexican Americans. BMC Proceedings, 2016, 10, 263-267.	1.8	4
106	Somatic Copy Number Alteration-Based Prediction of Molecular Subtypes of Breast Cancer Using Deep Learning Model. Lecture Notes in Computer Science, 2017, , 57-63.	1.0	4
107	Isolation and characterization of a new basal-like luminal progenitor in human breast tissue. Stem Cell Research and Therapy, 2019, 10, 269.	2.4	4
108	Genetic predictors of gene expression associated with psychiatric comorbidity in patients with inflammatory bowel disease â€“ A pilot study. Genomics, 2021, 113, 919-932.	1.3	4

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109	Mitogen-induced transcriptional programming in human fibroblasts. Gene, 2021, 800, 145842.	1.0	4
110	Multiomic Metabolic Enrichment Network Analysis Reveals Metaboliteâ€“Protein Physical Interaction Subnetworks Altered in Cancer. Molecular and Cellular Proteomics, 2022, 21, 100189.	2.5	4
111	Proteomic Approaches to Defining Remission and the Risk of Relapse in Rheumatoid Arthritis. Frontiers in Immunology, 2021, 12, 729681.	2.2	4
112	Integrating Affymetrix microarray data sets using probe-level test statistic for predicting prostate cancer. , 2006, , .		3
113	A flexible approximate likelihood ratio test for detecting differential expression in microarray data. Computational Statistics and Data Analysis, 2009, 53, 3685-3695.	0.7	3
114	Dynamic pathway analysis of genes associated with blood pressure using whole genome sequence data. BMC Proceedings, 2014, 8, S106.	1.8	3
115	Deep Learning Models for Predicting Phenotypic Traits and Diseases from Omics Data. , 0, , .		3
116	Modeling Gene-Environment Interaction for the Risk of Non-hodgkin Lymphoma. Frontiers in Oncology, 2019, 8, 657.	1.3	3
117	A Maximum Flow-Based Approach to Prioritize Drugs for Drug Repurposing of Chronic Diseases. Life, 2021, 11, 1115.	1.1	3
118	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
119	Tightly integrated multiomics-based deep tensor survival model for time-to-event prediction. Bioinformatics, 2022, 38, 3259-3266.	1.8	3
120	Impact of normalization and filtering on linkage analysis of gene expression data. BMC Proceedings, 2007, 1, S150.	1.8	2
121	A topology-sharing based method for protein function prediction via analysis of protein functional association networks. , 2009, , .		2
122	Gene Network Modules-Based Liner Discriminant Analysis of Microarray Gene Expression Data. Lecture Notes in Computer Science, 2011, , 286-296.	1.0	2
123	Discriminative learning of generative models: large margin multinomial mixture models for document classification. Pattern Analysis and Applications, 2015, 18, 535-551.	3.1	2
124	Mapping Three Versions of the International Classification of Diseases to Categories of Chronic Conditions. International Journal of Population Data Science, 2021, 6, 1406.	0.1	2
125	Transitions between versions of the International Classification of Diseases and chronic disease prevalence estimates from administrative health data: a population-based study. BMC Public Health, 2022, 22, 701.	1.2	2
126	Comprehensive multi-cohort transcriptional meta-analysis of muscle diseases identifies a signature of disease severity. Scientific Reports, 2022, 12, .	1.6	2

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127	Integrative Analysis of Gene Expression Data Including an Assessment of Pathway Enrichment for Predicting Prostate Cancer. Cancer Informatics, 2006, 2, 117693510600200.	0.9	1
128	A pathway-based association analysis model using common and rare variants. BMC Proceedings, 2011, 5, S85.	1.8	1
129	A Novel Graph-based Algorithm to Infer Recurrent Copy Number Variations in Cancer. Cancer Informatics, 2016, 15s2, CIN.S39368.	0.9	1
130	Drug-Target Interaction Network Predictions for Drug Repurposing Using LASSO-Based Regularized Linear Classification Model. Lecture Notes in Computer Science, 2018, , 272-278.	1.0	1
131	Genome-Wide Canonical Correlation Analysis-Based Computational Methods for Mining Information from Microbiome and Gene Expression Data. Lecture Notes in Computer Science, 2019, , 511-517.	1.0	1
132	Computational Prediction of the Pathogenic Status of Cancer-Specific Somatic Variants. Frontiers in Genetics, 2021, 12, 805656.	1.1	1
133	Polygenic risk and causal inference of psychiatric comorbidity in inflammatory bowel disease among patients with European ancestry. Journal of Translational Medicine, 2022, 20, 43.	1.8	1
134	Genome-wide copy number variant data for inflammatory bowel disease in a caucasian population. Data in Brief, 2019, 25, 104203.	0.5	0
135	MiR-490-3p and MiR-744-5p Are Increased in ICU Acquired Weakness (ICUAW) and Regulate Myoblast Differentiation and Proliferation. , 2019, , .		0
136	Identification of significantly mutated subnetworks in the breast cancer genome. Scientific Reports, 2021, 11, 642.	1.6	0
137	Incorporating Correlations among Gene Ontology Terms into Predicting Protein Functions. , 2011, , 154-173.		0
138	Incorporating Correlations among Gene Ontology Terms into Predicting Protein Functions. , 0, , 831-850.		0
139	Chromosomal Clustering of Periodically Expressed Genes in Plasmodium falciparum. , 2007, , 103-119.		0
140	Bioinformatics Application: Predicting Protein Subcellular Localization by Applying Machine Learning. , 2009, , 163-174.		0