

Yu-Hang Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

105
papers

3,184
citations

182225

30
h-index

206121

51
g-index

106
all docs

106
docs citations

106
times ranked

2391
citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting RNA 5-Methylcytosine Sites by Using Essential Sequence Features and Distributions. <i>BioMed Research International</i> , 2022, 2022, 1-11.	0.9	32
2	Identification of Novel Lung Cancer Driver Genes Connecting Different Omics Levels With a Heat Diffusion Algorithm. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 825272.	1.8	3
3	Editorial: Finding New Epigenomics and Epigenetics Biomarkers for Complex Diseases and Significant Developmental Events With Machine Learning Methods. <i>Frontiers in Genetics</i> , 2022, 13, 850367.	1.1	0
4	Screening gene signatures for clinical response subtypes of lung transplantation. <i>Molecular Genetics and Genomics</i> , 2022, 297, 1301-1313.	1.0	2
5	Identifying the Immunological Gene Signatures of Immune Cell Subtypes. <i>BioMed Research International</i> , 2021, 2021, 1-10.	0.9	1
6	Identifying the Signatures and Rules of Circulating Extracellular MicroRNA for Distinguishing Cancer Subtypes. <i>Frontiers in Genetics</i> , 2021, 12, 651610.	1.1	14
7	Investigating gene methylation signatures for fetal intolerance prediction. <i>PLoS ONE</i> , 2021, 16, e0250032.	1.1	1
8	Predicting gene phenotype by multi-label multi-class model based on essential functional features. <i>Molecular Genetics and Genomics</i> , 2021, 296, 905-918.	1.0	11
9	Identifying Infliximab- (IFX-) Responsive Blood Signatures for the Treatment of Rheumatoid Arthritis. <i>BioMed Research International</i> , 2021, 2021, 1-10.	0.9	1
10	Determining protein-protein functional associations by functional rules based on gene ontology and KEGG pathway. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021, 1869, 140621.	1.1	58
11	Analysis of the Sequence Characteristics of Antifreeze Protein. <i>Life</i> , 2021, 11, 520.	1.1	4
12	Characterization of the Blood and Cerebrospinal Fluid Microbiome in Children with Bacterial Meningitis and Its Potential Correlation with Inflammation. <i>MSystems</i> , 2021, 6, e0004921.	1.7	10
13	Identifying COVID-19-Specific Transcriptomic Biomarkers with Machine Learning Methods. <i>BioMed Research International</i> , 2021, 2021, 1-11.	0.9	17
14	Identification of Microbiota Biomarkers With Orthologous Gene Annotation for Type 2 Diabetes. <i>Frontiers in Microbiology</i> , 2021, 12, 711244.	1.5	7
15	Recognizing Pattern and Rule of Mutation Signatures Corresponding to Cancer Types. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 712931.	1.8	0
16	Tumor microbiome contributes to an aggressive phenotype in the basal-like subtype of pancreatic cancer. <i>Communications Biology</i> , 2021, 4, 1019.	2.0	57
17	Identifying Lung Cancer Cell Markers with Machine Learning Methods and Single-Cell RNA-Seq Data. <i>Life</i> , 2021, 11, 940.	1.1	8
18	Lung proteomic biomarkers associated with chronic obstructive pulmonary disease. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2021, 321, L1119-L1130.	1.3	14

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19	Predicting Human Protein Subcellular Locations by Using a Combination of Network and Function Features. <i>Frontiers in Genetics</i> , 2021, 12, 783128.	1.1	8
20	Identification of Pan-Cancer Biomarkers Based on the Gene Expression Profiles of Cancer Cell Lines. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 781285.	1.8	13
21	Identification of leukemia stem cell expression signatures through Monte Carlo feature selection strategy and support vector machine. <i>Cancer Gene Therapy</i> , 2020, 27, 56-69.	2.2	62
22	Screening Dys-Methylation Genes and Rules for Cancer Diagnosis by Using the Pan-Cancer Study. <i>IEEE Access</i> , 2020, 8, 489-501.	2.6	8
23	Identifying Robust Microbiota Signatures and Interpretable Rules to Distinguish Cancer Subtypes. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 604794.	1.6	13
24	Identifying the RNA signatures of coronary artery disease from combined lncRNA and mRNA expression profiles. <i>Genomics</i> , 2020, 112, 4945-4958.	1.3	11
25	Investigation and Prediction of Human Interactome Based on Quantitative Features. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 730.	2.0	11
26	Identification of COVID-19 Infection-Related Human Genes Based on a Random Walk Model in a Virus-Human Protein Interaction Network. <i>BioMed Research International</i> , 2020, 2020, 1-7.	0.9	16
27	Natural Selection on Exonic SNPs Shapes Allelic Expression Imbalance (AEI) Adaptability in Lung Cancer Progression. <i>Frontiers in Genetics</i> , 2020, 11, 665.	1.1	1
28	Distinguishing Glioblastoma Subtypes by Methylation Signatures. <i>Frontiers in Genetics</i> , 2020, 11, 604336.	1.1	29
29	Identifying Cell-Type Specific Genes and Expression Rules Based on Single-Cell Transcriptomic Atlas Data. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 350.	2.0	13
30	Identifying circulating miRNA biomarkers for early diagnosis and monitoring of lung cancer. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2020, 1866, 165847.	1.8	27
31	Discriminating Origin Tissues of Tumor Cell Lines by Methylation Signatures and Dys-Methylated Rules. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 507.	2.0	11
32	Alternative Polyadenylation Modification Patterns Reveal Essential Posttranscription Regulatory Mechanisms of Tumorigenesis in Multiple Tumor Types. <i>BioMed Research International</i> , 2020, 2020, 1-9.	0.9	5
33	Investigating the gene expression profiles of cells in seven embryonic stages with machine learning algorithms. <i>Genomics</i> , 2020, 112, 2524-2534.	1.3	28
34	Detecting the Multiomics Signatures of Factor-Specific Inflammatory Effects on Airway Smooth Muscles. <i>Frontiers in Genetics</i> , 2020, 11, 599970.	1.1	31
35	Identification of Gene Signatures and Expression Patterns During Epithelial-to-Mesenchymal Transition From Single-Cell Expression Atlas. <i>Frontiers in Genetics</i> , 2020, 11, 605012.	1.1	5
36	Identifying Transcriptomic Signatures and Rules for SARS-CoV-2 Infection. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 627302.	1.8	57

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37	Computational Method for Identifying Malonylation Sites by Using Random Forest Algorithm. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2020, 23, 304-312.	0.6	1
38	Analysis of Four Types of Leukemia Using Gene Ontology Term and Kyoto Encyclopedia of Genes and Genomes Pathway Enrichment Scores. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2020, 23, 295-303.	0.6	2
39	New Computational Tool Based on Machine-learning Algorithms for the Identification of Rhinovirus Infection-Related Genes. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2020, 22, 665-674.	0.6	11
40	Identification of synthetic lethality based on a functional network by using machine learning algorithms. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 405-416.	1.2	102
41	Analysis of Protein-Protein Functional Associations by Using Gene Ontology and KEGG Pathway. <i>BioMed Research International</i> , 2019, 2019, 1-10.	0.9	18
42	Gene Expression Difference Between Primary and Metastatic Renal Cell Carcinoma Using Patient-Derived Xenografts. <i>IEEE Access</i> , 2019, 7, 142586-142594.	2.6	12
43	Identifying Methylation Pattern and Genes Associated with Breast Cancer Subtypes. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4269.	1.8	37
44	Identifying Essential Signature Genes and Expression Rules Associated With Distinctive Development Stages of Early Embryonic Cells. <i>IEEE Access</i> , 2019, 7, 128570-128578.	2.6	20
45	Inferring novel genes related to oral cancer with a network embedding method and one-class learning algorithms. <i>Gene Therapy</i> , 2019, 26, 465-478.	2.3	14
46	Primary Tumor Site Specificity is Preserved in Patient-Derived Tumor Xenograft Models. <i>Frontiers in Genetics</i> , 2019, 10, 738.	1.1	23
47	Analysis of Expression Pattern of snoRNAs in Different Cancer Types with Machine Learning Algorithms. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2185.	1.8	44
48	Analysis of Gene Expression Differences between Different Pancreatic Cells. <i>ACS Omega</i> , 2019, 4, 6421-6435.	1.6	11
49	Copy Number Variation Pattern for Discriminating MACROD2 States of Colorectal Cancer Subtypes. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 407.	2.0	18
50	Screening of Methylation Signature and Gene Functions Associated With the Subtypes of Isocitrate Dehydrogenase-Mutation Gliomas. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 339.	2.0	20
51	Immunosignature Screening for Multiple Cancer Subtypes Based on Expression Rule. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 370.	2.0	9
52	Identification of the copy number variant biomarkers for breast cancer subtypes. <i>Molecular Genetics and Genomics</i> , 2019, 294, 95-110.	1.0	81
53	Classification of Widely and Rarely Expressed Genes with Recurrent Neural Network. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 49-60.	1.9	49
54	HIV infection alters the human epigenetic landscape. <i>Gene Therapy</i> , 2019, 26, 29-39.	2.3	39

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55	Tissue differences revealed by gene expression profiles of various cell lines. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 7068-7081.	1.2	59
56	Computational Method for the Identification of Molecular Metabolites Involved in Cereal Hull Color Variations. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2019, 21, 760-770.	0.6	3
57	Distinguishing three subtypes of hematopoietic cells based on gene expression profiles using a support vector machine. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018, 1864, 2255-2265.	1.8	13
58	Gene expression differences among different MSI statuses in colorectal cancer. <i>International Journal of Cancer</i> , 2018, 143, 1731-1740.	2.3	137
59	Discriminating cirRNAs from other lncRNAs using a hierarchical extreme learning machine (H-ELM) algorithm with feature selection. <i>Molecular Genetics and Genomics</i> , 2018, 293, 137-149.	1.0	65
60	Identification of gene expression signatures across different types of neural stem cells with the Monte Carlo feature selection method. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 3394-3403.	1.2	78
61	A computational method using the random walk with restart algorithm for identifying novel epigenetic factors. <i>Molecular Genetics and Genomics</i> , 2018, 293, 293-301.	1.0	32
62	A Computational Method for Classifying Different Human Tissues with Quantitatively Tissue-Specific Expressed Genes. <i>Genes</i> , 2018, 9, 449.	1.0	23
63	Tissue Expression Difference between mRNAs and lncRNAs. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3416.	1.8	64
64	Identification of the Gene Expression Rules That Define the Subtypes in Glioma. <i>Journal of Clinical Medicine</i> , 2018, 7, 350.	1.0	74
65	Identification of Differentially Expressed Genes between Original Breast Cancer and Xenograft Using Machine Learning Algorithms. <i>Genes</i> , 2018, 9, 155.	1.0	83
66	Identifying Patients with Atrioventricular Septal Defect in Down Syndrome Populations by Using Self-Normalizing Neural Networks and Feature Selection. <i>Genes</i> , 2018, 9, 208.	1.0	65
67	Inferring Novel Tumor Suppressor Genes with a Protein-Protein Interaction Network and Network Diffusion Algorithms. <i>Molecular Therapy - Methods and Clinical Development</i> , 2018, 10, 57-67.	1.8	41
68	Prediction of Protein-Peptide Interactions with a Nearest Neighbor Algorithm. <i>Current Bioinformatics</i> , 2018, 13, 14-24.	0.7	20
69	Data mining of the cancer-related lncRNAs GO terms and KEGG pathways by using mRMR method. <i>Mathematical Biosciences</i> , 2018, 304, 1-8.	0.9	29
70	Prediction of Nitrated Tyrosine Residues in Protein Sequences by Extreme Learning Machine and Feature Selection Methods. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2018, 21, 393-402.	0.6	29
71	Identifying the Characteristics of the Hypusination Sites Using SMOTE and SVM Algorithm with Feature Selection. <i>Current Proteomics</i> , 2018, 15, 111-118.	0.1	9
72	Analysis and prediction of drug-drug interaction by minimum redundancy maximum relevance and incremental feature selection. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 312-329.	2.0	81

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73	Identification of Genes Associated with Breast Cancer Metastasis to Bone on a Protein-Protein Interaction Network with a Shortest Path Algorithm. <i>Journal of Proteome Research</i> , 2017, 16, 1027-1038.	1.8	34
74	Identification of the core regulators of the HLA I-peptide binding process. <i>Scientific Reports</i> , 2017, 7, 42768.	1.6	15
75	Analysis of cancer-related lncRNAs using gene ontology and KEGG pathways. <i>Artificial Intelligence in Medicine</i> , 2017, 76, 27-36.	3.8	136
76	Identification of transcription factors that may reprogram lung adenocarcinoma. <i>Artificial Intelligence in Medicine</i> , 2017, 83, 52-57.	3.8	25
77	Identify Key Sequence Features to Improve CRISPR sgRNA Efficacy. <i>IEEE Access</i> , 2017, 5, 26582-26590.	2.6	153
78	Network-Based Method for Identifying Co-Regeneration Genes in Bone, Dentin, Nerve and Vessel Tissues. <i>Genes</i> , 2017, 8, 252.	1.0	11
79	Deciphering the Relationship between Obesity and Various Diseases from a Network Perspective. <i>Genes</i> , 2017, 8, 392.	1.0	5
80	Network-Based Method for Identifying Co-Regeneration Genes in Bone, Dentin, Nerve and Vessel Tissues. <i>Genes</i> , 2017, 8, 252.	1.0	1
81	Identification of Candidate Genes Related to Inflammatory Bowel Disease Using Minimum Redundancy Maximum Relevance, Incremental Feature Selection, and the Shortest-Path Approach. <i>BioMed Research International</i> , 2017, 2017, 1-15.	0.9	21
82	Cancer-Related Triplets of mRNA-lncRNA-miRNA Revealed by Integrative Network in Uterine Corpus Endometrial Carcinoma. <i>BioMed Research International</i> , 2017, 2017, 1-7.	0.9	30
83	Prediction and analysis of essential genes using the enrichments of gene ontology and KEGG pathways. <i>PLoS ONE</i> , 2017, 12, e0184129.	1.1	202
84	Identifying and analyzing different cancer subtypes using RNA-seq data of blood platelets. <i>Oncotarget</i> , 2017, 8, 87494-87511.	0.8	47
85	Determination of Genes Related to Uveitis by Utilization of the Random Walk with Restart Algorithm on a Protein-Protein Interaction Network. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1045.	1.8	23
86	Identifying novel fruit-related genes in <i>Arabidopsis thaliana</i> based on the random walk with restart algorithm. <i>PLoS ONE</i> , 2017, 12, e0177017.	1.1	10
87	Analysis and Prediction of Myristoylation Sites Using the mRMR Method, the IFS Method and an Extreme Learning Machine Algorithm. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2017, 20, 96-106.	0.6	12
88	Predicting Citrullination Sites in Protein Sequences Using mRMR Method and Random Forest Algorithm. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2017, 20, 164-173.	0.6	29
89	Prediction of the Ebola Virus Infection Related Human Genes Using Protein-Protein Interaction Network. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2017, 20, 638-646.	0.6	14
90	Recognizing and Predicting Thioether Bridges Formed by Lanthionine and β -Methylanthionine in Lantibiotics Using a Random Forest Approach with Feature Selection. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2017, 20, 582-593.	0.6	7

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91	Identification of Drug-Drug Interactions Using Chemical Interactions. <i>Current Bioinformatics</i> , 2017, 12, .	0.7	92
92	Analysis of Important Gene Ontology Terms and Biological Pathways Related to Pancreatic Cancer. <i>BioMed Research International</i> , 2016, 2016, 1-10.	0.9	12
93	Analysis and Identification of Aptamer-Compound Interactions with a Maximum Relevance Minimum Redundancy and Nearest Neighbor Algorithm. <i>BioMed Research International</i> , 2016, 2016, 1-9.	0.9	15
94	The Use of Gene Ontology Term and KEGG Pathway Enrichment for Analysis of Drug Half-Life. <i>PLoS ONE</i> , 2016, 11, e0165496.	1.1	9
95	Gene expression profiling gut microbiota in different races of humans. <i>Scientific Reports</i> , 2016, 6, 23075.	1.6	86
96	Identification of novel candidate drivers connecting different dysfunctional levels for lung adenocarcinoma using protein-protein interactions and a shortest path approach. <i>Scientific Reports</i> , 2016, 6, 29849.	1.6	28
97	Analysis of the chemical toxicity effects using the enrichment of Gene Ontology terms and KEGG pathways. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 2619-2626.	1.1	15
98	Identification of compound-protein interactions through the analysis of gene ontology, KEGG enrichment for proteins and molecular fragments of compounds. <i>Molecular Genetics and Genomics</i> , 2016, 291, 2065-2079.	1.0	62
99	Mining for genes related to choroidal neovascularization based on the shortest path algorithm and protein interaction information. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 2740-2749.	1.1	6
100	Identifying novel protein phenotype annotations by hybridizing protein-protein interactions and protein sequence similarities. <i>Molecular Genetics and Genomics</i> , 2016, 291, 913-934.	1.0	23
101	Analysis of Gene Expression Profiles in the Human Brain Stem, Cerebellum and Cerebral Cortex. <i>PLoS ONE</i> , 2016, 11, e0159395.	1.1	13
102	A Shortest-Path-Based Method for the Analysis and Prediction of Fruit-Related Genes in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2016, 11, e0159519.	1.1	7
103	Exploring Mouse Protein Function via Multiple Approaches. <i>PLoS ONE</i> , 2016, 11, e0166580.	1.1	22
104	Mining for Candidate Genes Related to Pancreatic Cancer Using Protein-Protein Interactions and a Shortest Path Approach. <i>BioMed Research International</i> , 2015, 2015, 1-12.	0.9	10
105	Identification of cortical interneuron cell markers in mouse embryos based on machine learning analysis of single-cell transcriptomics. <i>Frontiers in Neuroscience</i> , 0, 16, .	1.4	2