

# Yu-Hang Zhang

## List of Publications by Year in descending order

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Version: 2024-02-01

105  
papers

3,184  
citations

159573

30  
h-index

182417

51  
g-index

106  
all docs

106  
docs citations

106  
times ranked

2230  
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction and analysis of essential genes using the enrichments of gene ontology and KEGG pathways. PLoS ONE, 2017, 12, e0184129.	2.5	202
2	Identify Key Sequence Features to Improve CRISPR sgRNA Efficacy. IEEE Access, 2017, 5, 26582-26590.	4.2	153
3	<scp>G</scp>ene expression differences among different <scp>MSI</scp> statuses in colorectal cancer. International Journal of Cancer, 2018, 143, 1731-1740.	5.1	137
4	Analysis of cancer-related lncRNAs using gene ontology and KEGG pathways. Artificial Intelligence in Medicine, 2017, 76, 27-36.	6.5	136
5	Identification of synthetic lethality based on a functional network by using machine learning algorithms. Journal of Cellular Biochemistry, 2019, 120, 405-416.	2.6	102
6	Identification of Drug-Drug Interactions Using Chemical Interactions. Current Bioinformatics, 2017, 12, .	1.5	92
7	Gene expression profiling gut microbiota in different races of humans. Scientific Reports, 2016, 6, 23075.	3.3	86
8	Identification of Differentially Expressed Genes between Original Breast Cancer and Xenograft Using Machine Learning Algorithms. Genes, 2018, 9, 155.	2.4	83
9	Analysis and prediction of drug-drug interaction by minimum redundancy maximum relevance and incremental feature selection. Journal of Biomolecular Structure and Dynamics, 2017, 35, 312-329.	3.5	81
10	Identification of the copy number variant biomarkers for breast cancer subtypes. Molecular Genetics and Genomics, 2019, 294, 95-110.	2.1	81
11	Identification of gene expression signatures across different types of neural stem cells with the Monte-Carlo feature selection method. Journal of Cellular Biochemistry, 2018, 119, 3394-3403.	2.6	78
12	Identification of the Gene Expression Rules That Define the Subtypes in Glioma. Journal of Clinical Medicine, 2018, 7, 350.	2.4	74
13	Discriminating cirRNAs from other lncRNAs using a hierarchical extreme learning machine (H-ELM) algorithm with feature selection. Molecular Genetics and Genomics, 2018, 293, 137-149.	2.1	65
14	Identifying Patients with Atrioventricular Septal Defect in Down Syndrome Populations by Using Self-Normalizing Neural Networks and Feature Selection. Genes, 2018, 9, 208.	2.4	65
15	Tissue Expression Difference between mRNAs and lncRNAs. International Journal of Molecular Sciences, 2018, 19, 3416.	4.1	64
16	Identification of compound-protein interactions through the analysis of gene ontology, KEGG enrichment for proteins and molecular fragments of compounds. Molecular Genetics and Genomics, 2016, 291, 2065-2079.	2.1	62
17	Identification of leukemia stem cell expression signatures through Monte Carlo feature selection strategy and support vector machine. Cancer Gene Therapy, 2020, 27, 56-69.	4.6	62
18	Tissue differences revealed by gene expression profiles of various cell lines. Journal of Cellular Biochemistry, 2019, 120, 7068-7081.	2.6	59

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19	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.	2.3	58
20	Identifying Transcriptomic Signatures and Rules for SARS-CoV-2 Infection. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 627302.	3.7	57
21	Tumor microbiome contributes to an aggressive phenotype in the basal-like subtype of pancreatic cancer. <i>Communications Biology</i> , 2021, 4, 1019.	4.4	57
22	Classification of Widely and Rarely Expressed Genes with Recurrent Neural Network. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 49-60.	4.1	49
23	Identifying and analyzing different cancer subtypes using RNA-seq data of blood platelets. <i>Oncotarget</i> , 2017, 8, 87494-87511.	1.8	47
24	Analysis of Expression Pattern of snoRNAs in Different Cancer Types with Machine Learning Algorithms. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2185.	4.1	44
25	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.	4.1	41
26	HIV infection alters the human epigenetic landscape. <i>Gene Therapy</i> , 2019, 26, 29-39.	4.5	39
27	Identifying Methylation Pattern and Genes Associated with Breast Cancer Subtypes. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4269.	4.1	37
28	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.	3.7	34
29	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.	2.1	32
30	Predicting RNA 5-Methylcytosine Sites by Using Essential Sequence Features and Distributions. <i>BioMed Research International</i> , 2022, 2022, 1-11.	1.9	32
31	Detecting the Multiomics Signatures of Factor-Specific Inflammatory Effects on Airway Smooth Muscles. <i>Frontiers in Genetics</i> , 2020, 11, 599970.	2.3	31
32	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.	1.9	30
33	Data mining of the cancer-related lncRNAs GO terms and KEGG pathways by using mRMR method. <i>Mathematical Biosciences</i> , 2018, 304, 1-8.	1.9	29
34	Distinguishing Glioblastoma Subtypes by Methylation Signatures. <i>Frontiers in Genetics</i> , 2020, 11, 604336.	2.3	29
35	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.	1.1	29
36	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.	1.1	29

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37	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.	3.3	28
38	Investigating the gene expression profiles of cells in seven embryonic stages with machine learning algorithms. <i>Genomics</i> , 2020, 112, 2524-2534.	2.9	28
39	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.	3.8	27
40	Identification of transcription factors that may reprogram lung adenocarcinoma. <i>Artificial Intelligence in Medicine</i> , 2017, 83, 52-57.	6.5	25
41	Identifying novel protein phenotype annotations by hybridizing protein-protein interactions and protein sequence similarities. <i>Molecular Genetics and Genomics</i> , 2016, 291, 913-934.	2.1	23
42	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.	4.1	23
43	A Computational Method for Classifying Different Human Tissues with Quantitatively Tissue-Specific Expressed Genes. <i>Genes</i> , 2018, 9, 449.	2.4	23
44	Primary Tumor Site Specificity is Preserved in Patient-Derived Tumor Xenograft Models. <i>Frontiers in Genetics</i> , 2019, 10, 738.	2.3	23
45	Exploring Mouse Protein Function via Multiple Approaches. <i>PLoS ONE</i> , 2016, 11, e0166580.	2.5	22
46	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.	1.9	21
47	Prediction of Protein-Peptide Interactions with a Nearest Neighbor Algorithm. <i>Current Bioinformatics</i> , 2018, 13, 14-24.	1.5	20
48	Identifying Essential Signature Genes and Expression Rules Associated With Distinctive Development Stages of Early Embryonic Cells. <i>IEEE Access</i> , 2019, 7, 128570-128578.	4.2	20
49	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.	4.1	20
50	Analysis of Protein-Protein Functional Associations by Using Gene Ontology and KEGG Pathway. <i>BioMed Research International</i> , 2019, 2019, 1-10.	1.9	18
51	Copy Number Variation Pattern for Discriminating MACROD2 States of Colorectal Cancer Subtypes. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 407.	4.1	18
52	Identifying COVID-19-Specific Transcriptomic Biomarkers with Machine Learning Methods. <i>BioMed Research International</i> , 2021, 2021, 1-11.	1.9	17
53	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.	1.9	16
54	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.	1.9	15

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55	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.	2.4	15
56	Identification of the core regulators of the HLA I-peptide binding process. <i>Scientific Reports</i> , 2017, 7, 42768.	3.3	15
57	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.	4.5	14
58	Identifying the Signatures and Rules of Circulating Extracellular MicroRNA for Distinguishing Cancer Subtypes. <i>Frontiers in Genetics</i> , 2021, 12, 651610.	2.3	14
59	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.	1.1	14
60	Lung proteomic biomarkers associated with chronic obstructive pulmonary disease. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2021, 321, L1119-L1130.	2.9	14
61	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.	3.8	13
62	Identifying Robust Microbiota Signatures and Interpretable Rules to Distinguish Cancer Subtypes. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 604794.	3.5	13
63	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.	4.1	13
64	Analysis of Gene Expression Profiles in the Human Brain Stem, Cerebellum and Cerebral Cortex. <i>PLoS ONE</i> , 2016, 11, e0159395.	2.5	13
65	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.	3.7	13
66	Analysis of Important Gene Ontology Terms and Biological Pathways Related to Pancreatic Cancer. <i>BioMed Research International</i> , 2016, 2016, 1-10.	1.9	12
67	Gene Expression Difference Between Primary and Metastatic Renal Cell Carcinoma Using Patient-Derived Xenografts. <i>IEEE Access</i> , 2019, 7, 142586-142594.	4.2	12
68	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.	1.1	12
69	Network-Based Method for Identifying Co-Regeneration Genes in Bone, Dentin, Nerve and Vessel Tissues. <i>Genes</i> , 2017, 8, 252.	2.4	11
70	Analysis of Gene Expression Differences between Different Pancreatic Cells. <i>ACS Omega</i> , 2019, 4, 6421-6435.	3.5	11
71	Identifying the RNA signatures of coronary artery disease from combined lncRNA and mRNA expression profiles. <i>Genomics</i> , 2020, 112, 4945-4958.	2.9	11
72	Investigation and Prediction of Human Interactome Based on Quantitative Features. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 730.	4.1	11

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73	Discriminating Origin Tissues of Tumor Cell Lines by Methylation Signatures and Dys-Methylated Rules. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 507.	4.1	11
74	Predicting gene phenotype by multi-label multi-class model based on essential functional features. <i>Molecular Genetics and Genomics</i> , 2021, 296, 905-918.	2.1	11
75	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.	1.1	11
76	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.	1.9	10
77	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.	3.8	10
78	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.	2.5	10
79	The Use of Gene Ontology Term and KEGG Pathway Enrichment for Analysis of Drug Half-Life. <i>PLoS ONE</i> , 2016, 11, e0165496.	2.5	9
80	Immunosignature Screening for Multiple Cancer Subtypes Based on Expression Rule. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 370.	4.1	9
81	Identifying the Characteristics of the Hypusination Sites Using SMOTE and SVM Algorithm with Feature Selection. <i>Current Proteomics</i> , 2018, 15, 111-118.	0.3	9
82	Screening Dys-Methylation Genes and Rules for Cancer Diagnosis by Using the Pan-Cancer Study. <i>IEEE Access</i> , 2020, 8, 489-501.	4.2	8
83	Identifying Lung Cancer Cell Markers with Machine Learning Methods and Single-Cell RNA-Seq Data. <i>Life</i> , 2021, 11, 940.	2.4	8
84	Predicting Human Protein Subcellular Locations by Using a Combination of Network and Function Features. <i>Frontiers in Genetics</i> , 2021, 12, 783128.	2.3	8
85	Identification of Microbiota Biomarkers With Orthologous Gene Annotation for Type 2 Diabetes. <i>Frontiers in Microbiology</i> , 2021, 12, 711244.	3.5	7
86	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.	2.5	7
87	Recognizing and Predicting Thioether Bridges Formed by Lanthionine and $\hat{\gamma}$ -Methylanthionine in Lantibiotics Using a Random Forest Approach with Feature Selection. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2017, 20, 582-593.	1.1	7
88	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.	2.4	6
89	Deciphering the Relationship between Obesity and Various Diseases from a Network Perspective. <i>Genes</i> , 2017, 8, 392.	2.4	5
90	Alternative Polyadenylation Modification Patterns Reveal Essential Posttranscription Regulatory Mechanisms of Tumorigenesis in Multiple Tumor Types. <i>BioMed Research International</i> , 2020, 2020, 1-9.	1.9	5

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91	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.	2.3	5
92	Analysis of the Sequence Characteristics of Antifreeze Protein. <i>Life</i> , 2021, 11, 520.	2.4	4
93	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.	1.1	3
94	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.	3.7	3
95	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.	1.1	2
96	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, .	2.8	2
97	Screening gene signatures for clinical response subtypes of lung transplantation. <i>Molecular Genetics and Genomics</i> , 2022, 297, 1301-1313.	2.1	2
98	Network-Based Method for Identifying Co-Regeneration Genes in Bone, Dentin, Nerve and Vessel Tissues. <i>Genes</i> , 2017, 8, 252.	2.4	1
99	Natural Selection on Exonic SNPs Shapes Allelic Expression Imbalance (AEI) Adaptability in Lung Cancer Progression. <i>Frontiers in Genetics</i> , 2020, 11, 665.	2.3	1
100	Identifying the Immunological Gene Signatures of Immune Cell Subtypes. <i>BioMed Research International</i> , 2021, 2021, 1-10.	1.9	1
101	Investigating gene methylation signatures for fetal intolerance prediction. <i>PLoS ONE</i> , 2021, 16, e0250032.	2.5	1
102	Identifying Infliximab- (IFX-) Responsive Blood Signatures for the Treatment of Rheumatoid Arthritis. <i>BioMed Research International</i> , 2021, 2021, 1-10.	1.9	1
103	Computational Method for Identifying Malonylation Sites by Using Random Forest Algorithm. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2020, 23, 304-312.	1.1	1
104	Recognizing Pattern and Rule of Mutation Signatures Corresponding to Cancer Types. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 712931.	3.7	0
105	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.	2.3	0