Tao Huang

List of Publications by Year
in descending order

263 papers	13,326 citations	36303 51 h-index	32842 100 g-index
264 all docs	264 docs citations	264 times ranked	23091 citing authors

#	Article	IF	Citations
1	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	12.6	4,659
2	Prediction and analysis of essential genes using the enrichments of gene ontology and KEGG pathways. PLoS ONE, 2017, 12, e0184129.	2.5	202
3	Artificial intelligence: A powerful paradigm for scientific research. Innovation(China), 2021, 2, 100179.	9.1	200
4	Promises and Challenges of Big Data Computing in Health Sciences. Big Data Research, 2015, 2, 2-11.	4.2	185
5	Synchronized age-related gene expression changes across multiple tissues in human and the link to complex diseases. Scientific Reports, 2015, 5, 15145.	3.3	180
6	Genome-wide identification of mRNA 5-methylcytosine in mammals. Nature Structural and Molecular Biology, 2019, 26, 380-388.	8.2	176
7	Dynamic landscape and evolution of m6A methylation in human. Nucleic Acids Research, 2020, 48, 6251-6264.	14.5	173
8	Identify Key Sequence Features to Improve CRISPR sgRNA Efficacy. IEEE Access, 2017, 5, 26582-26590.	4.2	153
9	Identification of Colorectal Cancer Related Genes with mRMR and Shortest Path in Protein-Protein Interaction Network. PLoS ONE, 2012, 7, e33393.	2.5	149
10	Predicting Functions of Proteins in Mouse Based on Weighted Protein-Protein Interaction Network and Protein Hybrid Properties. PLoS ONE, 2011, 6, e14556.	2.5	144
11	<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
12	Analysis of cancer-related lncRNAs using gene ontology and KEGG pathways. Artificial Intelligence in Medicine, 2017, 76, 27-36.	6.5	136
13	Prediction of lysine ubiquitination with mRMR feature selection and analysis. Amino Acids, 2012, 42, 1387-1395.	2.7	129
14	Analysis and Prediction of the Metabolic Stability of Proteins Based on Their Sequential Features, Subcellular Locations and Interaction Networks. PLoS ONE, 2010, 5, e10972.	2.5	123
15	Genetic differences among ethnic groups. BMC Genomics, 2015, 16, 1093.	2.8	109
16	Genetic Modulation of RNA Splicing with a CRISPR-Guided Cytidine Deaminase. Molecular Cell, 2018, 72, 380-394.e7.	9.7	107
17	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
18	BMAL1 knockout macaque monkeys display reduced sleep and psychiatric disorders. National Science Review, 2019, 6, 87-100.	9.5	98

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19	Prediction of Protein-Protein Interaction Sites by Random Forest Algorithm with mRMR and IFS. PLoS ONE, 2012, 7, e43927.	2.5	92
20	Identification of Drug-Drug Interactions Using Chemical Interactions. Current Bioinformatics, 2017, 12, .	1.5	92
21	Gene expression profiling gut microbiota in different races of humans. Scientific Reports, 2016, 6, 23075.	3.3	86
22	Classification and Analysis of Regulatory Pathways Using Graph Property, Biochemical and Physicochemical Property, and Functional Property. PLoS ONE, 2011, 6, e25297.	2.5	84
23	Identification of Differentially Expressed Genes between Original Breast Cancer and Xenograft Using Machine Learning Algorithms. Genes, 2018, 9, 155.	2.4	83
24	Integrative Analysis of DNA Methylation and Gene Expression Data Identifies EPAS1 as a Key Regulator of COPD. PLoS Genetics, 2015, 11, e1004898.	3.5	82
25	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
26	Identification of the copy number variant biomarkers for breast cancer subtypes. Molecular Genetics and Genomics, 2019, 294, 95-110.	2.1	81
27	Mesenchymal stem cell treatment improves outcome of COVID-19 patients via multiple immunomodulatory mechanisms. Cell Research, 2021, 31, 1244-1262.	12.0	81
28	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
29	Prediction and analysis of cell-penetrating peptides using pseudo-amino acid composition and random forest models. Amino Acids, 2015, 47, 1485-1493.	2.7	77
30	Identification of the Gene Expression Rules That Define the Subtypes in Glioma. Journal of Clinical Medicine, 2018, 7, 350.	2.4	74
31	Prediction of Pharmacological and Xenobiotic Responses to Drugs Based on Time Course Gene Expression Profiles. PLoS ONE, 2009, 4, e8126.	2.5	74
32	Prediction of synergistic anti-cancer drug combinations based on drug target network and drug induced gene expression profiles. Artificial Intelligence in Medicine, 2017, 83, 35-43.	6.5	71
33	A hybrid method for prediction and repositioning of drug Anatomical Therapeutic Chemical classes. Molecular BioSystems, 2014, 10, 868.	2.9	70
34	Prediction of Deleterious Non-Synonymous SNPs Based on Protein Interaction Network and Hybrid Properties. PLoS ONE, 2010, 5, e11900.	2.5	70
35	RNA m6A Modification in Cancers: Molecular Mechanisms and Potential Clinical Applications. Innovation(China), 2020, 1, 100066.	9.1	69
36	Associations between Ionomic Profile and Metabolic Abnormalities in Human Population. PLoS ONE, 2012, 7, e38845.	2.5	69

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37	Deciphering the effects of gene deletion on yeast longevity using network and machine learning approaches. Biochimie, 2012, 94, 1017-1025.	2.6	67
38	Next-generation sequencing identifies novel genes with rare variants in total anomalous pulmonary venous connection. EBioMedicine, 2018, 38, 217-227.	6.1	67
39	Classification of cancers based on copy number variation landscapes. Biochimica Et Biophysica Acta - General Subjects, 2016, 1860, 2750-2755.	2.4	65
40	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
41	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
42	Predicting Biological Functions of Compounds Based on Chemical-Chemical Interactions. PLoS ONE, 2011, 6, e29491.	2.5	64
43	Tissue Expression Difference between mRNAs and lncRNAs. International Journal of Molecular Sciences, 2018, 19, 3416.	4.1	64
44	Implications of Newly Identified Brain eQTL Genes and Their Interactors in Schizophrenia. Molecular Therapy - Nucleic Acids, 2018, 12, 433-442.	5.1	63
45	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
46	Proteogenomic characterization and comprehensive integrative genomic analysis of human colorectal cancer liver metastasis. Molecular Cancer, 2018, 17, 139.	19.2	62
47	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
48	Tissue differences revealed by gene expression profiles of various cell lines. Journal of Cellular Biochemistry, 2019, 120, 7068-7081.	2.6	59
49	Classifying Ten Types of Major Cancers Based on Reverse Phase Protein Array Profiles. PLoS ONE, 2015, 10, e0123147.	2.5	58
50	Determining protein–protein functional associations by functional rules based on gene ontology and KEGG pathway. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2021, 1869, 140621.	2.3	58
51	Identifying Transcriptomic Signatures and Rules for SARS-CoV-2 Infection. Frontiers in Cell and Developmental Biology, 2020, 8, 627302.	3.7	57
52	Signal Propagation in Protein Interaction Network during Colorectal Cancer Progression. BioMed Research International, 2013, 2013, 1-9.	1.9	53
53	Hepatitis C Virus Network Based Classification of Hepatocellular Cirrhosis and Carcinoma. PLoS ONE, 2012, 7, e34460.	2.5	52
54	Analysis and Prediction of Translation Rate Based on Sequence and Functional Features of the mRNA. PLoS ONE, 2011, 6, e16036.	2.5	51

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55	Gene Ontology and KEGG Pathway Enrichment Analysis of a Drug Target-Based Classification System. PLoS ONE, 2015, 10, e0126492.	2.5	50
56	Classification of Widely and Rarely Expressed Genes with Recurrent Neural Network. Computational and Structural Biotechnology Journal, 2019, 17, 49-60.	4.1	49
57	Predicting Metabolic Pathways of Small Molecules and Enzymes Based on Interaction Information of Chemicals and Proteins. PLoS ONE, 2012, 7, e45944.	2.5	49
58	Identification of hepatocellular carcinoma related genes with k-th shortest paths in a protein–protein interaction network. Molecular BioSystems, 2013, 9, 2720.	2.9	47
59	Identifying and analyzing different cancer subtypes using RNA-seq data of blood platelets. Oncotarget, 2017, 8, 87494-87511.	1.8	47
60	Application of the Shortest Path Algorithm for the Discovery of Breast Cancer-Related Genes. Current Bioinformatics, 2016, 11, 51-58.	1.5	46
61	Predicting and analyzing early wake-up associated gene expressions by integrating GWAS and eQTL studies. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 2241-2246.	3.8	46
62	Air pollution and DNA methylation alterations in lung cancer: A systematic and comparative study. Oncotarget, 2017, 8, 1369-1391.	1.8	46
63	Predicting Protein Phenotypes Based on Protein-Protein Interaction Network. PLoS ONE, 2011, 6, e17668.	2.5	44
64	SNHG8 is identified as a key regulator of epstein-barr virus(EBV)-associated gastric cancer by an integrative analysis of lncRNA and mRNA expression. Oncotarget, 2016, 7, 80990-81002.	1.8	44
65	Analysis of Expression Pattern of snoRNAs in Different Cancer Types with Machine Learning Algorithms. International Journal of Molecular Sciences, 2019, 20, 2185.	4.1	44
66	MiR-139-5p/SLC7A11 inhibits the proliferation, invasion and metastasis of pancreatic carcinoma via PI3K/Akt signaling pathway. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2020, 1866, 165747.	3.8	44
67	Identification of Protein Subcellular Localization With Network and Functional Embeddings. Frontiers in Genetics, 2020, 11, 626500.	2.3	44
68	Analysis of Tumor Suppressor Genes Based on Gene Ontology and the KEGG Pathway. PLoS ONE, 2014, 9, e107202.	2.5	44
69	The prediction of interferon treatment effects based on time series microarray gene expression profiles. Journal of Translational Medicine, 2008, 6, 44.	4.4	42
70	A network-based method using a random walk with restart algorithm and screening tests to identify novel genes associated with Menière's disease. PLoS ONE, 2017, 12, e0182592.	2.5	41
71	Inferring Novel Tumor Suppressor Genes with a Protein-Protein Interaction Network and Network Diffusion Algorithms. Molecular Therapy - Methods and Clinical Development, 2018, 10, 57-67.	4.1	41
72	Prediction of Tyrosine Sulfation with mRMR Feature Selection and Analysis. Journal of Proteome Research, 2010, 9, 6490-6497.	3.7	40

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73	Discover the network mechanisms underlying the connections between aging and age-related diseases. Scientific Reports, 2016, 6, 32566.	3.3	40
74	HIV infection alters the human epigenetic landscape. Gene Therapy, 2019, 26, 29-39.	4.5	39
75	Genomic variation, origin tracing, and vaccine development of SARS-CoV-2: A systematic review. Innovation(China), 2021, 2, 100116.	9.1	39
76	Predicting Transcriptional Activity of Multiple Site p53 Mutants Based on Hybrid Properties. PLoS ONE, 2011, 6, e22940.	2.5	38
77	Predicting Heart Cell Types by Using Transcriptome Profiles and a Machine Learning Method. Life, 2022, 12, 228.	2.4	38
78	Predicting A-to-I RNA Editing by Feature Selection and Random Forest. PLoS ONE, 2014, 9, e110607.	2.5	37
79	Aneuploid Cell Survival Relies upon Sphingolipid Homeostasis. Cancer Research, 2017, 77, 5272-5286.	0.9	37
80	Identifying Methylation Pattern and Genes Associated with Breast Cancer Subtypes. International Journal of Molecular Sciences, 2019, 20, 4269.	4.1	37
81	Sequence- and structure-selective mRNA m5C methylation by NSUN6 in animals. National Science Review, 2021, 8, nwaa273.	9.5	36
82	MODMatcher: Multi-Omics Data Matcher for Integrative Genomic Analysis. PLoS Computational Biology, 2014, 10, e1003790.	3.2	35
83	Classification of Non-Small Cell Lung Cancer Based on Copy Number Alterations. PLoS ONE, 2014, 9, e88300.	2.5	35
84	Prediction of Human Genes' Regulatory Functions Based on Proteinprotein Interaction Network. Protein and Peptide Letters, 2012, 19, 910-916.	0.9	34
85	Identification of Genes Associated with Breast Cancer Metastasis to Bone on a Protein–Protein Interaction Network with a Shortest Path Algorithm. Journal of Proteome Research, 2017, 16, 1027-1038.	3.7	34
86	Using GeneReg to construct time delay gene regulatory networks. BMC Research Notes, 2010, 3, 142.	1.4	33
87	A method to distinguish between lysine acetylation and lysine ubiquitination with feature selection and analysis. Journal of Biomolecular Structure and Dynamics, 2015, 33, 2479-2490.	3.5	33
88	Identification of novel proliferative diabetic retinopathy related genes on protein–protein interaction network. Neurocomputing, 2016, 217, 63-72.	5.9	33
89	A computational method using the random walk with restart algorithm for identifying novel epigenetic factors. Molecular Genetics and Genomics, 2018, 293, 293-301.	2.1	32
90	Discovery of 4-(((4-(5-chloro-2-(((1s,4s)-4-((2-methoxyethyl)amino)cyclohexyl)amino)pyridin-4-yl)thiazol-2-yl)amino)methyl)tetrahydro-2H-pyran-4-car (JSH-150) as a novel highly selective and potent CDK9 kinase inhibitor. European Journal of Medicinal Chemistry, 2018, 158, 896-916.	5.5	32

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91	The transcriptome difference between colorectal tumor and normal tissues revealed by single-cell sequencing. Journal of Cancer, 2019, 10, 5883-5890.	2.5	32
92	Predicting RNA 5-Methylcytosine Sites by Using Essential Sequence Features and Distributions. BioMed Research International, 2022, 2022, 1-11.	1.9	32
93	Novel Candidate Key Drivers in the Integrative Network of Genes, MicroRNAs, Methylations, and Copy Number Variations in Squamous Cell Lung Carcinoma. BioMed Research International, 2015, 2015, 1-11.	1.9	31
94	Cross talk of chromosome instability, CpG island methylator phenotype and mismatch repair in colorectal cancer. Oncology Letters, 2018, 16, 1736-1746.	1.8	31
95	Detecting the Multiomics Signatures of Factor-Specific Inflammatory Effects on Airway Smooth Muscles. Frontiers in Genetics, 2020, 11, 599970.	2.3	31
96	Finding Candidate Drugs for Hepatitis C Based on Chemical-Chemical and Chemical-Protein Interactions. PLoS ONE, 2014, 9, e107767.	2.5	31
97	Prediction of Metabolic Pathway Using Graph Property, Chemical Functional Group and Chemical Structural Set. Current Bioinformatics, 2013, 8, 200-207.	1.5	30
98	Identification of new candidate drugs for lung cancer using chemical–chemical interactions, chemical–protein interactions and a K-means clustering algorithm. Journal of Biomolecular Structure and Dynamics, 2016, 34, 906-917.	3.5	30
99	Cancer-Related Triplets of mRNA-lncRNA-miRNA Revealed by Integrative Network in Uterine Corpus Endometrial Carcinoma. BioMed Research International, 2017, 2017, 1-7.	1.9	30
100	Mutational inactivation of mTORC1 repressor gene *DEPDC5* in human gastrointestinal stromal tumors. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 22746-22753.	7.1	29
101	The early detection of asthma based on blood gene expression. Molecular Biology Reports, 2019, 46, 217-223.	2.3	29
102	Distinguishing Glioblastoma Subtypes by Methylation Signatures. Frontiers in Genetics, 2020, 11, 604336.	2.3	29
103	Identification of Common Genes and Pathways in Eight Fibrosis Diseases. Frontiers in Genetics, 2020, 11, 627396.	2.3	29
104	Prediction of Nitrated Tyrosine Residues in Protein Sequences by Extreme Learning Machine and Feature Selection Methods. Combinatorial Chemistry and High Throughput Screening, 2018, 21, 393-402.	1.1	29
105	Analysis of Protein Pathway Networks Using Hybrid Properties. Molecules, 2010, 15, 8177-8192.	3.8	28
106	Identification of retinoblastoma related genes with shortest path in a protein–protein interaction network. Biochimie, 2012, 94, 1910-1917.	2.6	28
107	An Information-Theoretic Machine Learning Approach to Expression QTL Analysis. PLoS ONE, 2013, 8, e67899.	2.5	28
108	Discriminating between deleterious and neutral non-frameshifting indels based on protein interaction networks and hybrid properties. Molecular Genetics and Genomics, 2015, 290, 343-352.	2.1	28

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109	Identification of novel candidate drivers connecting different dysfunctional levels for lung adenocarcinoma using protein-protein interactions and a shortest path approach. Scientific Reports, 2016, 6, 29849.	3.3	28
110	Identification and analysis of the cleavage site in a signal peptide using SMOTE, dagging, and feature selection methods. Molecular Omics, 2018, 14, 64-73.	2.8	28
111	Investigating the gene expression profiles of cells in seven embryonic stages with machine learning algorithms. Genomics, 2020, 112, 2524-2534.	2.9	28
112	A Unified 35-Gene Signature for both Subtype Classification and Survival Prediction in Diffuse Large B-Cell Lymphomas. PLoS ONE, 2010, 5, e12726.	2.5	28
113	Computational Analysis of HIV-1 Resistance Based on Gene Expression Profiles and the Virus-Host Interaction Network. PLoS ONE, 2011, 6, e17291.	2.5	27
114	Identification of Lung-Cancer-Related Genes with the Shortest Path Approach in a Protein-Protein Interaction Network. BioMed Research International, 2013, 2013, 1-8.	1.9	26
115	The Identification and Analysis of mRNA–lncRNA–miRNA Cliques From the Integrative Network of Ovarian Cancer. Frontiers in Genetics, 2019, 10, 751.	2.3	26
116	Identifying protein subcellular locations with embeddings-based node2loc. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	26
117	Identification of transcription factors that may reprogram lung adenocarcinoma. Artificial Intelligence in Medicine, 2017, 83, 52-57.	6.5	25
118	Inter-tissue coexpression network analysis reveals DPP4 as an important gene in heart to blood communication. Genome Medicine, 2016, 8, 15.	8.2	24
119	Mining for novel tumor suppressor genes using a shortest path approach. Journal of Biomolecular Structure and Dynamics, 2016, 34, 664-675.	3.5	24
120	Identification of Cell Markers and Their Expression Patterns in Skin Based on Single-Cell RNA-Sequencing Profiles. Life, 2022, 12, 550.	2.4	24
121	Developmental mRNA m5C landscape and regulatory innovations of massive m5C modification of maternal mRNAs in animals. Nature Communications, 2022, 13, 2484.	12.8	24
122	Computationally identifying virulence factors based on KEGG pathways. Molecular BioSystems, 2013, 9, 1447.	2.9	23
123	A computational method for the identification of new candidate carcinogenic and non-carcinogenic chemicals. Molecular BioSystems, 2015, 11, 2541-2550.	2.9	23
124	Identifying novel protein phenotype annotations by hybridizing protein–protein interactions and protein sequence similarities. Molecular Genetics and Genomics, 2016, 291, 913-934.	2.1	23
125	An integrated method for the identification of novel genes related to oral cancer. PLoS ONE, 2017, 12, e0175185.	2.5	23
126	A Computational Method for Classifying Different Human Tissues with Quantitatively Tissue-Specific Expressed Genes. Genes, 2018, 9, 449.	2.4	23

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127	Primary Tumor Site Specificity is Preserved in Patient-Derived Tumor Xenograft Models. Frontiers in Genetics, 2019, 10, 738.	2.3	23
128	Exploring Mouse Protein Function via Multiple Approaches. PLoS ONE, 2016, 11, e0166580.	2.5	22
129	Predicting protein oxidation sites with feature selection and analysis approach. Journal of Biomolecular Structure and Dynamics, 2012, 29, 1154-1162.	3.5	21
130	Identification and Analysis of Blood Gene Expression Signature for Osteoarthritis With Advanced Feature Selection Methods. Frontiers in Genetics, 2018, 9, 246.	2.3	21
131	Thymine DNA glycosylase promotes transactivation of Î²-catenin/TCFs by cooperating with CBP. Journal of Molecular Cell Biology, 2014, 6, 231-239.	3.3	20
132	Prediction of protein N-formylation and comparison with N-acetylation based on a feature selection method. Neurocomputing, 2016, 217, 53-62.	5.9	20
133	Prediction of Protein-Peptide Interactions with a Nearest Neighbor Algorithm. Current Bioinformatics, 2018, 13, 14-24.	1.5	20
134	Identifying Essential Signature Genes and Expression Rules Associated With Distinctive Development Stages of Early Embryonic Cells. IEEE Access, 2019, 7, 128570-128578.	4.2	20
135	Screening of Methylation Signature and Gene Functions Associated With the Subtypes of Isocitrate Dehydrogenase-Mutation Gliomas. Frontiers in Bioengineering and Biotechnology, 2019, 7, 339.	4.1	20
136	A Sequence-based Approach for Predicting Protein Disordered Regions. Protein and Peptide Letters, 2013, 20, 243-248.	0.9	20
137	Functional association between influenza A (H1N1) virus and human. Biochemical and Biophysical Research Communications, 2009, 390, 1111-1113.	2.1	19
138	Integrative Analysis Reveals Enhanced Regulatory Effects of Human Long Intergenic Non-Coding RNAs in Lung Adenocarcinoma. Journal of Genetics and Genomics, 2015, 42, 423-436.	3.9	19
139	SySAP: a system-level predictor of deleterious single amino acid polymorphisms. Protein and Cell, 2012, 3, 38-43.	11.0	18
140	Prediction of Substrate-Enzyme-Product Interaction Based on Molecular Descriptors and Physicochemical Properties. BioMed Research International, 2013, 2013, 1-7.	1.9	18
141	Analysis of Proteinâ€"Protein Functional Associations by Using Gene Ontology and KEGG Pathway. BioMed Research International, 2019, 2019, 1-10.	1.9	18
142	Copy Number Variation Pattern for Discriminating MACROD2 States of Colorectal Cancer Subtypes. Frontiers in Bioengineering and Biotechnology, 2019, 7, 407.	4.1	18
143	E3 ligase MKRN3 is a tumor suppressor regulating PABPC1 ubiquitination in nonâ€"small cell lung cancer. Journal of Experimental Medicine, 2021, 218, .	8.5	18
144	Dysfunctions Associated with Methylation, MicroRNA Expression and Gene Expression in Lung Cancer. PLoS ONE, 2012, 7, e43441.	2.5	18

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145	A Novel Method of Predicting Protein Disordered Regions Based on Sequence Features. BioMed Research International, 2013, 2013, 1-8.	1.9	17
146	Computational Systems Biology Methods in Molecular Biology, Chemistry Biology, Molecular Biomedicine, and Biopharmacy. BioMed Research International, 2014, 2014, 1-2.	1.9	17
147	The Reconstruction and Analysis of Gene Regulatory Networks. Methods in Molecular Biology, 2018, 1754, 137-154.	0.9	17
148	Dual Regulatory Mechanisms of Expression and Mutation Involving Metabolism-Related Genes FDFT1 and UQCR5 during CLM. Molecular Therapy - Oncolytics, 2019, 14, 172-178.	4.4	17
149	Pan-Cancer Classification Based on Self-Normalizing Neural Networks and Feature Selection. Frontiers in Bioengineering and Biotechnology, 2020, 8, 766.	4.1	17
150	Identifying COVID-19-Specific Transcriptomic Biomarkers with Machine Learning Methods. BioMed Research International, 2021, 2021, 1-11.	1.9	17
151	A new method for identifying causal genes of schizophrenia and anti-tuberculosis drug-induced hepatotoxicity. Scientific Reports, 2016, 6, 32571.	3.3	16
152	Identification of COVID-19 Infection-Related Human Genes Based on a Random Walk Model in a Virus–Human Protein Interaction Network. BioMed Research International, 2020, 2020, 1-7.	1.9	16
153	Dyella telluris sp. nov. and Dyella acidiphila sp. nov., isolated from forest soil of Dinghushan Biosphere Reserve, China. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	1.7	16
154	Protein–protein interaction networks as miners of biological discovery. Proteomics, 2022, 22, e2100190.	2.2	16
155	The role of Hepatitis C Virus in the dynamic protein interaction networks of hepatocellular cirrhosis and carcinoma. International Journal of Computational Biology and Drug Design, 2011, 4, 5.	0.3	15
156	Identification of the core regulators of the HLA I-peptide binding process. Scientific Reports, 2017, 7, 42768.	3.3	15
157	Prediction of Multi-Type Membrane Proteins in Human by an Integrated Approach. PLoS ONE, 2014, 9, e93553.	2.5	15
158	An Ensemble Prognostic Model for Colorectal Cancer. PLoS ONE, 2013, 8, e63494.	2.5	14
159	Identification of <i>Influenza A</i>/H7N9 Virus Infection-Related Human Genes Based on Shortest Paths in a Virus-Human Protein Interaction Network. BioMed Research International, 2014, 2014, 1-11.	1.9	14
160	Inferring novel genes related to oral cancer with a network embedding method and one-class learning algorithms. Gene Therapy, 2019, 26, 465-478.	4.5	14
161	Identifying the Signatures and Rules of Circulating Extracellular MicroRNA for Distinguishing Cancer Subtypes. Frontiers in Genetics, 2021, 12, 651610.	2.3	14
162	Identification of Key Genes With Differential Correlations in Lung Adenocarcinoma. Frontiers in Cell and Developmental Biology, 2021, 9, 675438.	3.7	14

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163	Over-Expression and Prognostic Significance of FN1, Correlating With Immune Infiltrates in Thyroid Cancer. Frontiers in Medicine, 2021, 8, 812278.	2.6	14
164	Prediction and Analysis of Retinoblastoma Related Genes through Gene Ontology and KEGG. BioMed Research International, 2013, 2013, 1-8.	1.9	13
165	Identifying Robust Microbiota Signatures and Interpretable Rules to Distinguish Cancer Subtypes. Frontiers in Molecular Biosciences, 2020, 7, 604794.	3.5	13
166	Identifying Cell-Type Specific Genes and Expression Rules Based on Single-Cell Transcriptomic Atlas Data. Frontiers in Bioengineering and Biotechnology, 2020, 8, 350.	4.1	13
167	Investigation of miRNA and mRNA Co-expression Network in Ependymoma. Frontiers in Bioengineering and Biotechnology, 2020, 8, 177.	4.1	13
168	A Hybrid Computational Method for the Discovery of Novel Reproduction-Related Genes. PLoS ONE, 2015, 10, e0117090.	2.5	13
169	Analysis of Gene Expression Profiles in the Human Brain Stem, Cerebellum and Cerebral Cortex. PLoS ONE, 2016, 11, e0159395.	2.5	13
170	Identification of Pan-Cancer Biomarkers Based on the Gene Expression Profiles of Cancer Cell Lines. Frontiers in Cell and Developmental Biology, 2021, 9, 781285.	3.7	13
171	Gene Expression Difference Between Primary and Metastatic Renal Cell Carcinoma Using Patient-Derived Xenografts. IEEE Access, 2019, 7, 142586-142594.	4.2	12
172	Discriminating between Lysine Sumoylation and Lysine Acetylation Using mRMR Feature Selection and Analysis. PLoS ONE, 2014, 9, e107464.	2.5	12
173	Discovery of New Candidate Genes Related to Brain Development Using Protein Interaction Information. PLoS ONE, 2015, 10, e0118003.	2.5	12
174	OPMSP: A Computational Method Integrating Protein Interaction and Sequence Information for the Identification of Novel Putative Oncogenes. Protein and Peptide Letters, 2016, 23, 1081-1094.	0.9	12
175	Analysis of the preferences for splice codes across tissues. Protein and Cell, 2015, 6, 904-907.	11.0	11
176	Network-Based Method for Identifying Co-Regeneration Genes in Bone, Dentin, Nerve and Vessel Tissues. Genes, 2017, 8, 252.	2.4	11
177	Analysis of Gene Expression Differences between Different Pancreatic Cells. ACS Omega, 2019, 4, 6421-6435.	3.5	11
178	Identifying the RNA signatures of coronary artery disease from combined lncRNA and mRNA expression profiles. Genomics, 2020, 112, 4945-4958.	2.9	11
179	Investigation and Prediction of Human Interactome Based on Quantitative Features. Frontiers in Bioengineering and Biotechnology, 2020, 8, 730.	4.1	11
180	The Key Genes for Perineural Invasion in Pancreatic Ductal Adenocarcinoma Identified With Monte-Carlo Feature Selection Method. Frontiers in Genetics, 2020, 11, 554502.	2.3	11

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181	Discriminating Origin Tissues of Tumor Cell Lines by Methylation Signatures and Dys-Methylated Rules. Frontiers in Bioengineering and Biotechnology, 2020, 8, 507.	4.1	11
182	Predicting gene phenotype by multi-label multi-class model based on essential functional features. Molecular Genetics and Genomics, 2021, 296, 905-918.	2.1	11
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