

# Tao Huang

## List of Publications by Year in descending order

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263  
papers

13,326  
citations

41627

51  
h-index

37326

100  
g-index

264  
all docs

264  
docs citations

264  
times ranked

25636  
citing authors

#	ARTICLE	IF	CITATIONS
1	Editorial: RNA Modification in Human Cancers: Roles and Therapeutic Implications. <i>Frontiers in Genetics</i> , 2022, 13, 845744.	1.1	1
2	Predicting RNA 5-Methylcytosine Sites by Using Essential Sequence Features and Distributions. <i>BioMed Research International</i> , 2022, 2022, 1-11.	0.9	32
3	Inhibition of the Eubiquitinating enzyme USP47 as a novel targeted therapy for hematologic malignancies expressing mutant EZH2. <i>Leukemia</i> , 2022, 36, 1048-1057.	3.3	5
4	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
5	Predicting Heart Cell Types by Using Transcriptome Profiles and a Machine Learning Method. <i>Life</i> , 2022, 12, 228.	1.1	38
6	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
7	Inducible Regulatory T Cell Predicts Efficacy of PD-1 Blockade Therapy in Melanoma. <i>Advanced Therapeutics</i> , 2022, 5, .	1.6	2
8	Exploring the Genomic Patterns in Human and Mouse Cerebellums Via Single-Cell Sequencing and Machine Learning Method. <i>Frontiers in Genetics</i> , 2022, 13, 857851.	1.1	9
9	Identification of Cell Markers and Their Expression Patterns in Skin Based on Single-Cell RNA-Sequencing Profiles. <i>Life</i> , 2022, 12, 550.	1.1	24
10	Detecting Blood Methylation Signatures in Response to Childhood Cancer Radiotherapy via Machine Learning Methods. <i>Biology</i> , 2022, 11, 607.	1.3	0
11	Identifying Key MicroRNA Signatures for Neurodegenerative Diseases With Machine Learning Methods. <i>Frontiers in Genetics</i> , 2022, 13, 880997.	1.1	7
12	Identifying luminal and basal mammary cell specific genes and their expression patterns during pregnancy. <i>PLoS ONE</i> , 2022, 17, e0267211.	1.1	0
13	Developmental mRNA m5C landscape and regulatory innovations of massive m5C modification of maternal mRNAs in animals. <i>Nature Communications</i> , 2022, 13, 2484.	5.8	24
14	Detecting Brain Structure-Specific Methylation Signatures and Rules for Alzheimer's Disease. <i>Frontiers in Neuroscience</i> , 2022, 16, 895181.	1.4	1
15	Hsa_circ_0006692 Promotes Lung Cancer Progression via miR-205-5p/CDK19 Axis. <i>Genes</i> , 2022, 13, 846.	1.0	6
16	Identifying Methylation Signatures and Rules for COVID-19 With Machine Learning Methods. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, .	1.6	5
17	Recognition of Immune Cell Markers of COVID-19 Severity with Machine Learning Methods. <i>BioMed Research International</i> , 2022, 2022, 1-12.	0.9	3
18	Protein-protein interaction networks as miners of biological discovery. <i>Proteomics</i> , 2022, 22, e2100190.	1.3	16

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19	Identifying Functions of Proteins in Mice With Functional Embedding Features. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	6
20	Identifying COVID-19 Severity-Related SARS-CoV-2 Mutation Using a Machine Learning Method. <i>Life</i> , 2022, 12, 806.	1.1	11
21	Identifying In Vitro Cultured Human Hepatocytes Markers with Machine Learning Methods Based on Single-Cell RNA-Seq Data. <i>Frontiers in Bioengineering and Biotechnology</i> , 2022, 10, .	2.0	2
22	Screening gene signatures for clinical response subtypes of lung transplantation. <i>Molecular Genetics and Genomics</i> , 2022, 297, 1301-1313.	1.0	2
23	Applications of Deep Learning in Biomedicine. , 2021, , 29-39.		1
24	Sequence- and structure-selective mRNA m5C methylation by NSUN6 in animals. <i>National Science Review</i> , 2021, 8, nwaa273.	4.6	36
25	Identifying protein subcellular locations with embeddings-based node2loc. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, PP, 1-1.	1.9	26
26	Intermediate stage hepatocellular carcinoma: Comparison of the value of inflammation-based scores in predicting progression-free survival of patients receiving transarterial chemoembolization. <i>Journal of Cancer Research and Therapeutics</i> , 2021, 17, 740.	0.3	7
27	Prediction of Nitration Sites Based on FCBF Method and Stacking Ensemble Model. <i>Current Proteomics</i> , 2021, 18, .	0.1	1
28	Identifying the Immunological Gene Signatures of Immune Cell Subtypes. <i>BioMed Research International</i> , 2021, 2021, 1-10.	0.9	1
29	Identifying the Signatures and Rules of Circulating Extracellular MicroRNA for Distinguishing Cancer Subtypes. <i>Frontiers in Genetics</i> , 2021, 12, 651610.	1.1	14
30	Investigating gene methylation signatures for fetal intolerance prediction. <i>PLoS ONE</i> , 2021, 16, e0250032.	1.1	1
31	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
32	Editorial: Computational Methods in Predicting Complex Disease Associated Genes and Environmental Factors. <i>Frontiers in Genetics</i> , 2021, 12, 679651.	1.1	2
33	Identifying Infliximab- (IFX-) Responsive Blood Signatures for the Treatment of Rheumatoid Arthritis. <i>BioMed Research International</i> , 2021, 2021, 1-10.	0.9	1
34	Genomic variation, origin tracing, and vaccine development of SARS-CoV-2: A systematic review. <i>Innovation(China)</i> , 2021, 2, 100116.	5.2	39
35	Identification of Key Genes With Differential Correlations in Lung Adenocarcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 675438.	1.8	14
36	Determining proteinâ€™ 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

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37	E3 ligase MKRN3 is a tumor suppressor regulating PABPC1 ubiquitination in non-small cell lung cancer. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	18
38	Analysis of the Sequence Characteristics of Antifreeze Protein. <i>Life</i> , 2021, 11, 520.	1.1	4
39	Identifying COVID-19-Specific Transcriptomic Biomarkers with Machine Learning Methods. <i>BioMed Research International</i> , 2021, 2021, 1-11.	0.9	17
40	Identification of Microbiota Biomarkers With Orthologous Gene Annotation for Type 2 Diabetes. <i>Frontiers in Microbiology</i> , 2021, 12, 711244.	1.5	7
41	Editorial: Cross-Domain Analysis for All of Us Precision Medicine. <i>Frontiers in Genetics</i> , 2021, 12, 713771.	1.1	2
42	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
43	<i>Dyella telluris</i> sp. nov. and <i>Dyella acidiphila</i> sp. nov., isolated from forest soil of Dinghushan Biosphere Reserve, China. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	16
44	Identifying Lung Cancer Cell Markers with Machine Learning Methods and Single-Cell RNA-Seq Data. <i>Life</i> , 2021, 11, 940.	1.1	8
45	Identification of Chronic Hypersensitivity Pneumonitis Biomarkers with Machine Learning and Differential Co-expression Analysis. <i>Current Gene Therapy</i> , 2021, 21, 299-303.	0.9	11
46	Mesenchymal stem cell treatment improves outcome of COVID-19 patients via multiple immunomodulatory mechanisms. <i>Cell Research</i> , 2021, 31, 1244-1262.	5.7	81
47	SNHG8 Promotes the Progression of Epstein-Barr Virus-Associated Gastric Cancer via Sponging miR-512-5p and Targeting TRIM28. <i>Frontiers in Oncology</i> , 2021, 11, 734694.	1.3	10
48	Artificial intelligence: A powerful paradigm for scientific research. <i>Innovation(China)</i> , 2021, 2, 100179.	5.2	200
49	Competitive Endogenous RNA Landscape in Epstein-Barr Virus Associated Nasopharyngeal Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 782473.	1.8	7
50	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
51	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
52	The Therapeutic Targets Revealed by Integrative Network Analysis of Noncoding RNAs. <i>Current Gene Therapy</i> , 2021, 21, 279-279.	0.9	1
53	Over-Expression and Prognostic Significance of FN1, Correlating With Immune Infiltrates in Thyroid Cancer. <i>Frontiers in Medicine</i> , 2021, 8, 812278.	1.2	14
54	Integrative Analysis of Bulk and Single-Cell RNA Sequencing Data Reveals Cell Types Involved in Heart Failure. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 779225.	2.0	10

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55	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
56	Cripto-1 promotes tumor invasion and predicts poor outcomes in hepatocellular carcinoma. <i>Carcinogenesis</i> , 2020, 41, 571-581.	1.3	5
57	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
58	Identifying Robust Microbiota Signatures and Interpretable Rules to Distinguish Cancer Subtypes. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 604794.	1.6	13
59	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
60	Investigation and Prediction of Human Interactome Based on Quantitative Features. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 730.	2.0	11
61	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
62	The Methylation Pattern for Knee and Hip Osteoarthritis. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 602024.	1.8	7
63	Distinguishing Glioblastoma Subtypes by Methylation Signatures. <i>Frontiers in Genetics</i> , 2020, 11, 604336.	1.1	29
64	Editorial: Advanced Interpretable Machine Learning Methods for Clinical NGS Big Data of Complex Hereditary Diseases. <i>Frontiers in Genetics</i> , 2020, 11, 600902.	1.1	2
65	Decipher the connections between proteins and phenotypes. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020, 1868, 140503.	1.1	8
66	Pan-Cancer Classification Based on Self-Normalizing Neural Networks and Feature Selection. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 766.	2.0	17
67	The Role of ARL4C in Erlotinib Resistance: Activation of the Jak2/Stat 5/β-Catenin Signaling Pathway. <i>Frontiers in Oncology</i> , 2020, 10, 585292.	1.3	5
68	Disease Cluster Detection and Functional Characterization. <i>IEEE Access</i> , 2020, 8, 141958-141966.	2.6	5
69	The Key Genes for Perineural Invasion in Pancreatic Ductal Adenocarcinoma Identified With Monte-Carlo Feature Selection Method. <i>Frontiers in Genetics</i> , 2020, 11, 554502.	1.1	11
70	RNA m6A Modification in Cancers: Molecular Mechanisms and Potential Clinical Applications. <i>Innovation(China)</i> , 2020, 1, 100066.	5.2	69
71	Dynamic landscape and evolution of m6A methylation in human. <i>Nucleic Acids Research</i> , 2020, 48, 6251-6264.	6.5	173
72	Identification and Analysis of Dysfunctional Genes and Pathways in CD8+ T Cells of Non-Small Cell Lung Cancer Based on RNA Sequencing. <i>Frontiers in Genetics</i> , 2020, 11, 352.	1.1	6

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73	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
74	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
75	The self-organization model reveals systematic characteristics of aging. <i>Theoretical Biology and Medical Modelling</i> , 2020, 17, 4.	2.1	1
76	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
77	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
78	MiR-139-5p/SLC7A11 inhibits the proliferation, invasion and metastasis of pancreatic carcinoma via PI3K/Akt signaling pathway. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2020, 1866, 165747.	1.8	44
79	Investigation of miRNA and mRNA Co-expression Network in Ependymoma. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 177.	2.0	13
80	Detecting the Multiomics Signatures of Factor-Specific Inflammatory Effects on Airway Smooth Muscles. <i>Frontiers in Genetics</i> , 2020, 11, 599970.	1.1	31
81	Identification of Common Genes and Pathways in Eight Fibrosis Diseases. <i>Frontiers in Genetics</i> , 2020, 11, 627396.	1.1	29
82	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
83	Identifying Transcriptomic Signatures and Rules for SARS-CoV-2 Infection. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 627302.	1.8	57
84	Identification of Protein Subcellular Localization With Network and Functional Embeddings. <i>Frontiers in Genetics</i> , 2020, 11, 626500.	1.1	44
85	Applications of Network Analysis in Biomedicine. <i>Methods in Molecular Biology</i> , 2020, 2204, 39-50.	0.4	1
86	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
87	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
88	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
89	The Innovation: A Journal to See the Unseen and Change the Unchanged. <i>Innovation(China)</i> , 2020, 1, 100014.	5.2	1
90	Network-based analysis with primary cells reveals drug response landscape of acute myeloid leukemia. <i>Experimental Cell Research</i> , 2020, 393, 112054.	1.2	2

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91	Meet our Editor (Genetics). Current Chinese Science, 2020, 1, 6-6.	0.2	0
92	Identification of synthetic lethality based on a functional network by using machine learning algorithms. Journal of Cellular Biochemistry, 2019, 120, 405-416.	1.2	102
93	Analysis of Protein-Protein Functional Associations by Using Gene Ontology and KEGG Pathway. BioMed Research International, 2019, 2019, 1-10.	0.9	18
94	Dual Regulatory Mechanisms of Expression and Mutation Involving Metabolism-Related Genes FDFT1 and UQCR5 during CLM. Molecular Therapy - Oncolytics, 2019, 14, 172-178.	2.0	17
95	Mutational inactivation of mTORC1 repressor gene <i>DEPDC5</i> in human gastrointestinal stromal tumors. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 22746-22753.	3.3	29
96	Gene Expression Difference Between Primary and Metastatic Renal Cell Carcinoma Using Patient-Derived Xenografts. IEEE Access, 2019, 7, 142586-142594.	2.6	12
97	Identifying Methylation Pattern and Genes Associated with Breast Cancer Subtypes. International Journal of Molecular Sciences, 2019, 20, 4269.	1.8	37
98	Identifying Essential Signature Genes and Expression Rules Associated With Distinctive Development Stages of Early Embryonic Cells. IEEE Access, 2019, 7, 128570-128578.	2.6	20
99	Inferring novel genes related to oral cancer with a network embedding method and one-class learning algorithms. Gene Therapy, 2019, 26, 465-478.	2.3	14
100	Primary Tumor Site Specificity is Preserved in Patient-Derived Tumor Xenograft Models. Frontiers in Genetics, 2019, 10, 738.	1.1	23
101	The Identification and Analysis of mRNA-lncRNA-miRNA Cliques From the Integrative Network of Ovarian Cancer. Frontiers in Genetics, 2019, 10, 751.	1.1	26
102	BMAL1 knockout macaque monkeys display reduced sleep and psychiatric disorders. National Science Review, 2019, 6, 87-100.	4.6	98
103	Analysis of Expression Pattern of snoRNAs in Different Cancer Types with Machine Learning Algorithms. International Journal of Molecular Sciences, 2019, 20, 2185.	1.8	44
104	Genome-wide identification of mRNA 5-methylcytosine in mammals. Nature Structural and Molecular Biology, 2019, 26, 380-388.	3.6	176
105	Analysis of Gene Expression Differences between Different Pancreatic Cells. ACS Omega, 2019, 4, 6421-6435.	1.6	11
106	Copy Number Variation Pattern for Discriminating MACROD2 States of Colorectal Cancer Subtypes. Frontiers in Bioengineering and Biotechnology, 2019, 7, 407.	2.0	18
107	The transcriptome difference between colorectal tumor and normal tissues revealed by single-cell sequencing. Journal of Cancer, 2019, 10, 5883-5890.	1.2	32
108	Screening of Methylation Signature and Gene Functions Associated With the Subtypes of Isocitrate Dehydrogenase-Mutation Gliomas. Frontiers in Bioengineering and Biotechnology, 2019, 7, 339.	2.0	20

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109	Immunosignature Screening for Multiple Cancer Subtypes Based on Expression Rule. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 370.	2.0	9
110	Identification of the copy number variant biomarkers for breast cancer subtypes. <i>Molecular Genetics and Genomics</i> , 2019, 294, 95-110.	1.0	81
111	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
112	HIV infection alters the human epigenetic landscape. <i>Gene Therapy</i> , 2019, 26, 29-39.	2.3	39
113	Tissue differences revealed by gene expression profiles of various cell lines. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 7068-7081.	1.2	59
114	The early detection of asthma based on blood gene expression. <i>Molecular Biology Reports</i> , 2019, 46, 217-223.	1.0	29
115	Editorial: Machine Learning Advanced Dynamic Omics Data Analysis for Precision Medicine. <i>Frontiers in Genetics</i> , 2019, 10, 1343.	1.1	5
116	Identification and analysis of the cleavage site in a signal peptide using SMOTE, dagging, and feature selection methods. <i>Molecular Omics</i> , 2018, 14, 64-73.	1.4	28
117	<scp>G</scp>ene expression differences among different <scp>MSI</scp> statuses in colorectal cancer. <i>International Journal of Cancer</i> , 2018, 143, 1731-1740.	2.3	137
118	The Reconstruction and Analysis of Gene Regulatory Networks. <i>Methods in Molecular Biology</i> , 2018, 1754, 137-154.	0.4	17
119	Accelerating precision medicine through genetic and genomic big data analysis. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018, 1864, 2215-2217.	1.8	1
120	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
121	Predicting and analyzing early wake-up associated gene expressions by integrating GWAS and eQTL studies. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018, 1864, 2241-2246.	1.8	46
122	Identification of gene expression signatures across different types of neural stem cells with the Monteâ€C Carlo feature selection method. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 3394-3403.	1.2	78
123	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
124	A Computational Method for Classifying Different Human Tissues with Quantitatively Tissue-Specific Expressed Genes. <i>Genes</i> , 2018, 9, 449.	1.0	23
125	Copy Number Variations in Tumors. , 2018, , .		0
126	Next-generation sequencing identifies novel genes with rare variants in total anomalous pulmonary venous connection. <i>EBioMedicine</i> , 2018, 38, 217-227.	2.7	67

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127	Proteogenomic characterization and comprehensive integrative genomic analysis of human colorectal cancer liver metastasis. <i>Molecular Cancer</i> , 2018, 17, 139.	7.9	62
128	Genetic Modulation of RNA Splicing with a CRISPR-Guided Cytidine Deaminase. <i>Molecular Cell</i> , 2018, 72, 380-394.e7.	4.5	107
129	Discovery of (E)-N-(4-((4-methylpiperazin-1-yl)methyl)-3-(trifluoromethyl)phenyl)-3-((3-(2-(pyridin-2-yl)vinyl)-1H-indazol-6-yl)thio)propanamide (CHMFL-ABL-121) as a highly potent ABL kinase inhibitor capable of overcoming a variety of ABL mutants including T315I for chronic myeloid leukemia. <i>European Journal of Medicinal Chemistry</i> , 2018, 160, 61-81.	2.6	32
130	Tissue Expression Difference between mRNAs and lncRNAs. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3416.	1.8	64
131	Identification of the Gene Expression Rules That Define the Subtypes in Glioma. <i>Journal of Clinical Medicine</i> , 2018, 7, 350.	1.0	74
132	Identification and Analysis of Blood Gene Expression Signature for Osteoarthritis With Advanced Feature Selection Methods. <i>Frontiers in Genetics</i> , 2018, 9, 246.	1.1	21
133	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-yl)methyl)pyridin-2-yl)amino)propanamide (JSH-150) as a novel highly selective and potent CDK9 kinase inhibitor. <i>European Journal of Medicinal Chemistry</i> , 2018, 158, 896-916.	2.6	32
134	Cross talk of chromosome instability, CpG island methylator phenotype and mismatch repair in colorectal cancer. <i>Oncology Letters</i> , 2018, 16, 1736-1746.	0.8	31
135	Identification of Differentially Expressed Genes between Original Breast Cancer and Xenograft Using Machine Learning Algorithms. <i>Genes</i> , 2018, 9, 155.	1.0	83
136	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
137	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
138	Prediction of Protein-Peptide Interactions with a Nearest Neighbor Algorithm. <i>Current Bioinformatics</i> , 2018, 13, 14-24.	0.7	20
139	Implications of Newly Identified Brain eQTL Genes and Their Interactors in Schizophrenia. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 12, 433-442.	2.3	63
140	Computational Method for Distinguishing Lysine Acetylation, Sumoylation, and Ubiquitination using the Random Forest Algorithm with a Feature Selection Procedure. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2018, 20, 886-895.	0.6	2
141	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
142	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
143	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
144	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

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145	Identification of the core regulators of the HLA I-peptide binding process. <i>Scientific Reports</i> , 2017, 7, 42768.	1.6	15
146	Analysis of cancer-related lncRNAs using gene ontology and KEGG pathways. <i>Artificial Intelligence in Medicine</i> , 2017, 76, 27-36.	3.8	136
147	Identification of transcription factors that may reprogram lung adenocarcinoma. <i>Artificial Intelligence in Medicine</i> , 2017, 83, 52-57.	3.8	25
148	Aneuploid Cell Survival Relies upon Sphingolipid Homeostasis. <i>Cancer Research</i> , 2017, 77, 5272-5286.	0.4	37
149	Identify Key Sequence Features to Improve CRISPR sgRNA Efficacy. <i>IEEE Access</i> , 2017, 5, 26582-26590.	2.6	153
150	Network-Based Method for Identifying Co-Regeneration Genes in Bone, Dentin, Nerve and Vessel Tissues. <i>Genes</i> , 2017, 8, 252.	1.0	11
151	Deciphering the Relationship between Obesity and Various Diseases from a Network Perspective. <i>Genes</i> , 2017, 8, 392.	1.0	5
152	Network-Based Method for Identifying Co-Regeneration Genes in Bone, Dentin, Nerve and Vessel Tissues. <i>Genes</i> , 2017, 8, 252.	1.0	1
153	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
154	An integrated method for the identification of novel genes related to oral cancer. <i>PLoS ONE</i> , 2017, 12, e0175185.	1.1	23
155	A network-based method using a random walk with restart algorithm and screening tests to identify novel genes associated with Meniere's disease. <i>PLoS ONE</i> , 2017, 12, e0182592.	1.1	41
156	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
157	Identifying and analyzing different cancer subtypes using RNA-seq data of blood platelets. <i>Oncotarget</i> , 2017, 8, 87494-87511.	0.8	47
158	Prediction of synergistic anti-cancer drug combinations based on drug target network and drug induced gene expression profiles. <i>Artificial Intelligence in Medicine</i> , 2017, 83, 35-43.	3.8	71
159	A computational method for the identification of candidate drugs for non-small cell lung cancer. <i>PLoS ONE</i> , 2017, 12, e0183411.	1.1	1
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