Yu-Dong Cai

List of Publications by Year
in descending order

348 papers	14,188 citations	18887 64 h-index	38517 99 g-index
353 all docs	353 docs citations	353 times ranked	8766 citing authors

#	Article	IF	Citations
1	Predicting RNA 5-Methylcytosine Sites by Using Essential Sequence Features and Distributions. BioMed Research International, 2022, 2022, 1-11.	0.9	32
2	Identification of Novel Lung Cancer Driver Genes Connecting Different Omics Levels With a Heat Diffusion Algorithm. Frontiers in Cell and Developmental Biology, 2022, 10, 825272.	1.8	3
3	Predicting Heart Cell Types by Using Transcriptome Profiles and a Machine Learning Method. Life, 2022, 12, 228.	1.1	38
4	Exploring the Genomic Patterns in Human and Mouse Cerebellums Via Single-Cell Sequencing and Machine Learning Method. Frontiers in Genetics, 2022, 13, 857851.	1.1	9
5	Identification of Cell Markers and Their Expression Patterns in Skin Based on Single-Cell RNA-Sequencing Profiles. Life, 2022, 12, 550.	1.1	24
6	Detecting Blood Methylation Signatures in Response to Childhood Cancer Radiotherapy via Machine Learning Methods. Biology, 2022, 11, 607.	1.3	0
7	Identifying Key MicroRNA Signatures for Neurodegenerative Diseases With Machine Learning Methods. Frontiers in Genetics, 2022, 13, 880997.	1.1	7
8	Identifying luminal and basal mammary cell specific genes and their expression patterns during pregnancy. PLoS ONE, 2022, 17, e0267211.	1.1	0
9	Detecting Brain Structure-Specific Methylation Signatures and Rules for Alzheimer's Disease. Frontiers in Neuroscience, 2022, 16, 895181.	1.4	1
10	Identifying Methylation Signatures and Rules for COVID-19 With Machine Learning Methods. Frontiers in Molecular Biosciences, 2022, 9, .	1.6	5
11	Recognition of Immune Cell Markers of COVID-19 Severity with Machine Learning Methods. BioMed Research International, 2022, 2022, 1-12.	0.9	3
12	Protein–protein interaction networks as miners of biological discovery. Proteomics, 2022, 22, e2100190.	1.3	16
13	Identifying Functions of Proteins in Mice With Functional Embedding Features. Frontiers in Genetics, 2022, 13, .	1.1	6
14	Identifying COVID-19 Severity-Related SARS-CoV-2 Mutation Using a Machine Learning Method. Life, 2022, 12, 806.	1.1	11
15	Identifying In Vitro Cultured Human Hepatocytes Markers with Machine Learning Methods Based on Single-Cell RNA-Seq Data. Frontiers in Bioengineering and Biotechnology, 2022, 10, .	2.0	2
16	Identification of Type 2 Diabetes Biomarkers From Mixed Single-Cell Sequencing Data With Feature Selection Methods. Frontiers in Bioengineering and Biotechnology, 2022, 10, .	2.0	3
17	Analysis of Lymphoma-Related Genes with Gene Ontology and Kyoto Encyclopedia of Genes and Genomes Enrichment. BioMed Research International, 2022, 2022, 1-8.	0.9	0
18	Screening gene signatures for clinical response subtypes of lung transplantation. Molecular Genetics and Genomics, 2022, 297, 1301-1313.	1.0	2

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19	Identifying protein subcellular locations with embeddings-based node2loc. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	1.9	26
20	Identifying the Immunological Gene Signatures of Immune Cell Subtypes. BioMed Research International, 2021, 2021, 1-10.	0.9	1
21	Identifying the Signatures and Rules of Circulating Extracellular MicroRNA for Distinguishing Cancer Subtypes. Frontiers in Genetics, 2021, 12, 651610.	1.1	14
22	Investigating gene methylation signatures for fetal intolerance prediction. PLoS ONE, 2021, 16, e0250032.	1.1	1
23	Predicting gene phenotype by multi-label multi-class model based on essential functional features. Molecular Genetics and Genomics, 2021, 296, 905-918.	1.0	11
24	Editorial: Computational Methods in Predicting Complex Disease Associated Genes and Environmental Factors. Frontiers in Genetics, 2021, 12, 679651.	1.1	2
25	Identifying Infliximab- (IFX-) Responsive Blood Signatures for the Treatment of Rheumatoid Arthritis. BioMed Research International, 2021, 2021, 1-10.	0.9	1
26	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.	1.1	58
27	Analysis of the Sequence Characteristics of Antifreeze Protein. Life, 2021, 11, 520.	1.1	4
28	Identifying COVID-19-Specific Transcriptomic Biomarkers with Machine Learning Methods. BioMed Research International, 2021, 2021, 1-11.	0.9	17
29	Identification of Microbiota Biomarkers With Orthologous Gene Annotation for Type 2 Diabetes. Frontiers in Microbiology, 2021, 12, 711244.	1.5	7
30	Recognizing Pattern and Rule of Mutation Signatures Corresponding to Cancer Types. Frontiers in Cell and Developmental Biology, 2021, 9, 712931.	1.8	0
31	Identifying Lung Cancer Cell Markers with Machine Learning Methods and Single-Cell RNA-Seq Data. Life, 2021, 11, 940.	1.1	8
32	Predicting Human Protein Subcellular Locations by Using a Combination of Network and Function Features. Frontiers in Genetics, 2021, 12, 783128.	1.1	8
33	Identification of Pan-Cancer Biomarkers Based on the Gene Expression Profiles of Cancer Cell Lines. Frontiers in Cell and Developmental Biology, 2021, 9, 781285.	1.8	13
34	Identification of leukemia stem cell expression signatures through Monte Carlo feature selection strategy and support vector machine. Cancer Gene Therapy, 2020, 27, 56-69.	2.2	62
35	Screening Dys-Methylation Genes and Rules for Cancer Diagnosis by Using the Pan-Cancer Study. IEEE Access, 2020, 8, 489-501.	2.6	8
36	Identifying Robust Microbiota Signatures and Interpretable Rules to Distinguish Cancer Subtypes. Frontiers in Molecular Biosciences, 2020, 7, 604794.	1.6	13

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37	Identifying the RNA signatures of coronary artery disease from combined lncRNA and mRNA expression profiles. Genomics, 2020, 112, 4945-4958.	1.3	11
38	Investigation and Prediction of Human Interactome Based on Quantitative Features. Frontiers in Bioengineering and Biotechnology, 2020, 8, 730.	2.0	11
39	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.	0.9	16
40	Distinguishing Glioblastoma Subtypes by Methylation Signatures. Frontiers in Genetics, 2020, 11, 604336.	1.1	29
41	Editorial: Advanced Interpretable Machine Learning Methods for Clinical NGS Big Data of Complex Hereditary Diseases. Frontiers in Genetics, 2020, 11, 600902.	1.1	2
42	Disease Cluster Detection and Functional Characterization. IEEE Access, 2020, 8, 141958-141966.	2.6	5
43	Identifying Cell-Type Specific Genes and Expression Rules Based on Single-Cell Transcriptomic Atlas Data. Frontiers in Bioengineering and Biotechnology, 2020, 8, 350.	2.0	13
44	Discriminating Origin Tissues of Tumor Cell Lines by Methylation Signatures and Dys-Methylated Rules. Frontiers in Bioengineering and Biotechnology, 2020, 8, 507.	2.0	11
45	Alternative Polyadenylation Modification Patterns Reveal Essential Posttranscription Regulatory Mechanisms of Tumorigenesis in Multiple Tumor Types. BioMed Research International, 2020, 2020, 1-9.	0.9	5
46	Predicting protein subcellular location with network embedding and enrichment features. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2020, 1868, 140477.	1.1	11
47	Investigating the gene expression profiles of cells in seven embryonic stages with machine learning algorithms. Genomics, 2020, 112, 2524-2534.	1.3	28
48	Detecting the Multiomics Signatures of Factor-Specific Inflammatory Effects on Airway Smooth Muscles. Frontiers in Genetics, 2020, 11, 599970.	1.1	31
49	Identification of Gene Signatures and Expression Patterns During Epithelial-to-Mesenchymal Transition From Single-Cell Expression Atlas. Frontiers in Genetics, 2020, 11, 605012.	1.1	5
50	Identifying Transcriptomic Signatures and Rules for SARS-CoV-2 Infection. Frontiers in Cell and Developmental Biology, 2020, 8, 627302.	1.8	57
51	Identification of Protein Subcellular Localization With Network and Functional Embeddings. Frontiers in Genetics, 2020, 11, 626500.	1.1	44
52	Computational Method for Identifying Malonylation Sites by Using Random Forest Algorithm. Combinatorial Chemistry and High Throughput Screening, 2020, 23, 304-312.	0.6	1
53	Analysis of Four Types of Leukemia Using Gene Ontology Term and Kyoto Encyclopedia of Genes and Genomes Pathway Enrichment Scores. Combinatorial Chemistry and High Throughput Screening, 2020, 23, 295-303.	0.6	2
54	New Computational Tool Based on Machine-learning Algorithms for the Identification of Rhinovirus Infection-Related Genes. Combinatorial Chemistry and High Throughput Screening, 2020, 22, 665-674.	0.6	11

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55	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
56	Analysis of Protein–Protein Functional Associations by Using Gene Ontology and KEGG Pathway. BioMed Research International, 2019, 2019, 1-10.	0.9	18
57	Identifying Methylation Pattern and Genes Associated with Breast Cancer Subtypes. International Journal of Molecular Sciences, 2019, 20, 4269.	1.8	37
58	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
59	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
60	Primary Tumor Site Specificity is Preserved in Patient-Derived Tumor Xenograft Models. Frontiers in Genetics, 2019, 10, 738.	1.1	23
61	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
62	Analysis of Gene Expression Differences between Different Pancreatic Cells. ACS Omega, 2019, 4, 6421-6435.	1.6	11
63	Copy Number Variation Pattern for Discriminating MACROD2 States of Colorectal Cancer Subtypes. Frontiers in Bioengineering and Biotechnology, 2019, 7, 407.	2.0	18
64	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
65	Immunosignature Screening for Multiple Cancer Subtypes Based on Expression Rule. Frontiers in Bioengineering and Biotechnology, 2019, 7, 370.	2.0	9
66	Identification of the copy number variant biomarkers for breast cancer subtypes. Molecular Genetics and Genomics, 2019, 294, 95-110.	1.0	81
67	Classification of Widely and Rarely Expressed Genes with Recurrent Neural Network. Computational and Structural Biotechnology Journal, 2019, 17, 49-60.	1.9	49
68	HIV infection alters the human epigenetic landscape. Gene Therapy, 2019, 26, 29-39.	2.3	39
69	Tissue differences revealed by gene expression profiles of various cell lines. Journal of Cellular Biochemistry, 2019, 120, 7068-7081.	1.2	59
70	Identification of the functional alteration signatures across different cancer types with support vector machine and feature analysis. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 2218-2227.	1.8	20
71	Identification and analysis of the cleavage site in a signal peptide using SMOTE, dagging, and feature selection methods. Molecular Omics, 2018, 14, 64-73.	1.4	28
72	Gene expression differences among different MSI statuses in colorectal cancer. International Journal of Cancer, 2018, 143, 1731-1740.	2.3	137

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73	Accelerating precision medicine through genetic and genomic big data analysis. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 2215-2217.	1.8	1
74	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.	1.0	65
75	Identification of gene expression signatures across different types of neural stem cells with the Monteâ€Carlo feature selection method. Journal of Cellular Biochemistry, 2018, 119, 3394-3403.	1.2	78
76	A computational method using the random walk with restart algorithm for identifying novel epigenetic factors. Molecular Genetics and Genomics, 2018, 293, 293-301.	1.0	32
77	A Computational Method for Classifying Different Human Tissues with Quantitatively Tissue-Specific Expressed Genes. Genes, 2018, 9, 449.	1.0	23
78	Applications of Bioinformatics and Systems Biology in Precision Medicine and Immunooncology. BioMed Research International, 2018, 2018, 1-2.	0.9	7
79	Tissue Expression Difference between mRNAs and lncRNAs. International Journal of Molecular Sciences, 2018, 19, 3416.	1.8	64
80	Identification of the Gene Expression Rules That Define the Subtypes in Glioma. Journal of Clinical Medicine, 2018, 7, 350.	1.0	74
81	Novel Bioinformatics and Systems Biology approaches and techniques in Pharmaceutical and Biochemical Sciences. Combinatorial Chemistry and High Throughput Screening, 2018, 21, 391-392.	0.6	0
82	Analysis and Prediction of Nitrated Tyrosine Sites with the mRMR Method and Support Vector Machine Algorithm. Current Bioinformatics, 2018, 13, 3-13.	0.7	51
83	Identification of Differentially Expressed Genes between Original Breast Cancer and Xenograft Using Machine Learning Algorithms. Genes, 2018, 9, 155.	1.0	83
84	Identifying Patients with Atrioventricular Septal Defect in Down Syndrome Populations by Using Self-Normalizing Neural Networks and Feature Selection. Genes, 2018, 9, 208.	1.0	65
85	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.	1.8	41
86	Prediction of Protein-Peptide Interactions with a Nearest Neighbor Algorithm. Current Bioinformatics, 2018, 13, 14-24.	0.7	20
87	Data mining of the cancer-related lncRNAs GO terms and KEGG pathways by using mRMR method. Mathematical Biosciences, 2018, 304, 1-8.	0.9	29
88	Predicting Hepatotoxicity of Drug Metabolites Via an Ensemble Approach Based on Support Vector Machine. Combinatorial Chemistry and High Throughput Screening, 2018, 20, 839-849.	0.6	4
89	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.	0.6	29
90	Analysis and prediction of drugâ€"drug interaction by minimum redundancy maximum relevance and incremental feature selection. Journal of Biomolecular Structure and Dynamics, 2017, 35, 312-329.	2.0	81

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91	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.	1.8	34
92	Identification of the core regulators of the HLA I-peptide binding process. Scientific Reports, 2017, 7, 42768.	1.6	15
93	Analysis of cancer-related lncRNAs using gene ontology and KEGG pathways. Artificial Intelligence in Medicine, 2017, 76, 27-36.	3.8	136
94	Adaptive and freeze-tolerant heteronetwork organohydrogels with enhanced mechanical stability over a wide temperature range. Nature Communications, 2017, 8, 15911.	5.8	266
95	Identification of transcription factors that may reprogram lung adenocarcinoma. Artificial Intelligence in Medicine, 2017, 83, 52-57.	3.8	25
96	Identify Key Sequence Features to Improve CRISPR sgRNA Efficacy. IEEE Access, 2017, 5, 26582-26590.	2.6	153
97	Network-Based Method for Identifying Co-Regeneration Genes in Bone, Dentin, Nerve and Vessel Tissues. Genes, 2017, 8, 252.	1.0	11
98	Deciphering the Relationship between Obesity and Various Diseases from a Network Perspective. Genes, 2017, 8, 392.	1.0	5
99	Network-Based Method for Identifying Co-Regeneration Genes in Bone, Dentin, Nerve and Vessel Tissues. Genes, 2017, 8, 252.	1.0	1
100	Identification of Candidate Genes Related to Inflammatory Bowel Disease Using Minimum Redundancy Maximum Relevance, Incremental Feature Selection, and the Shortest-Path Approach. BioMed Research International, 2017, 2017, 1-15.	0.9	21
101	Cancer-Related Triplets of mRNA-lncRNA-miRNA Revealed by Integrative Network in Uterine Corpus Endometrial Carcinoma. BioMed Research International, 2017, 2017, 1-7.	0.9	30
102	An integrated method for the identification of novel genes related to oral cancer. PLoS ONE, 2017, 12, e0175185.	1.1	23
103	Prediction and analysis of essential genes using the enrichments of gene ontology and KEGG pathways. PLoS ONE, 2017, 12, e0184129.	1.1	202
104	Editorial: Investigate the Genetic and Environmental Interactions in Complex Systems with High Throughput Screening. Combinatorial Chemistry and High Throughput Screening, 2017, 20, 580-581.	0.6	0
105	Identifying and analyzing different cancer subtypes using RNA-seq data of blood platelets. Oncotarget, 2017, 8, 87494-87511.	0.8	47
106	A computational method for the identification of candidate drugs for non-small cell lung cancer. PLoS ONE, 2017, 12, e0183411.	1.1	1
107	Analysis and Prediction of Myristoylation Sites Using the mRMR Method, the IFS Method and an Extreme Learning Machine Algorithm. Combinatorial Chemistry and High Throughput Screening, 2017, 20, 96-106.	0.6	12
108	Predicting Citrullination Sites in Protein Sequences Using mRMR Method and Random Forest Algorithm. Combinatorial Chemistry and High Throughput Screening, 2017, 20, 164-173.	0.6	29

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109	Recognizing and Predicting Thioether Bridges Formed by Lanthionine and Î²-Methyllanthionine in Lantibiotics Using a Random Forest Approach with Feature Selection. Combinatorial Chemistry and High Throughput Screening, 2017, 20, 582-593.	0.6	7
110	Editorial (Thematic Issue: Investigate the Functions of Chemicals Through Heterogeneous Network of) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.6	0
111	The Use of Protein-Protein Interactions for the Analysis of the Associations between PM2.5 and Some Diseases. BioMed Research International, 2016, 2016, 1-7.	0.9	11
112	Analysis of Important Gene Ontology Terms and Biological Pathways Related to Pancreatic Cancer. BioMed Research International, 2016, 2016, 1-10.	0.9	12
113	Analysis and Identification of Aptamer-Compound Interactions with a Maximum Relevance Minimum Redundancy and Nearest Neighbor Algorithm. BioMed Research International, 2016, 2016, 1-9.	0.9	15
114	The Integrative Network of Gene Expression, MicroRNA, Methylation and Copy Number Variation in Colon and Rectal Cancer. Current Bioinformatics, 2016, 11, 59-65.	0.7	17
115	The Use of Gene Ontology Term and KEGG Pathway Enrichment for Analysis of Drug Half-Life. PLoS ONE, 2016, 11, e0165496.	1.1	9
116	Gene expression profiling gut microbiota in different races of humans. Scientific Reports, 2016, 6, 23075.	1.6	86
117	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.	1.6	28
118	Investigation of the roles of trace elements during hepatitis C virus infection using protein-protein interactions and a shortest path algorithm. Biochimica Et Biophysica Acta - General Subjects, 2016, 1860, 2756-2768.	1.1	8
119	Systems genetics - deciphering the complex disease with a systems approach. Biochimica Et Biophysica Acta - General Subjects, 2016, 1860, 2611-2612.	1.1	0
120	Identification of compoundâ€"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.	1.0	62
121	Prediction of protein N-formylation and comparison with N-acetylation based on a feature selection method. Neurocomputing, 2016, 217, 53-62.	3.5	20
122	Identification of new candidate drugs for lung cancer using chemicalâ€"chemical interactions, chemicalâ€"protein interactions and a K-means clustering algorithm. Journal of Biomolecular Structure and Dynamics, 2016, 34, 906-917.	2.0	30
123	Identifying novel protein phenotype annotations by hybridizing proteinâ€"protein interactions and protein sequence similarities. Molecular Genetics and Genomics, 2016, 291, 913-934.	1.0	23
124	Mining for novel tumor suppressor genes using a shortest path approach. Journal of Biomolecular Structure and Dynamics, 2016, 34, 664-675.	2.0	24
125	Analysis of Gene Expression Profiles in the Human Brain Stem, Cerebellum and Cerebral Cortex. PLoS ONE, 2016, 11, e0159395.	1.1	13
126	A Shortest-Path-Based Method for the Analysis and Prediction of Fruit-Related Genes in Arabidopsis thaliana. PLoS ONE, 2016, 11, e0159519.	1.1	7

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127	Exploring Mouse Protein Function via Multiple Approaches. PLoS ONE, 2016, 11, e0166580.	1.1	22
128	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.	0.4	12
129	Genetic differences among ethnic groups. BMC Genomics, 2015, 16, 1093.	1.2	109
130	Analysis of the preferences for splice codes across tissues. Protein and Cell, 2015, 6, 904-907.	4.8	11
131	Identifying New Candidate Genes and Chemicals Related to Prostate Cancer Using a Hybrid Network and Shortest Path Approach. Computational and Mathematical Methods in Medicine, 2015, 2015, 1-12.	0.7	9
132	Classifying Ten Types of Major Cancers Based on Reverse Phase Protein Array Profiles. PLoS ONE, 2015, 10, e0123147.	1.1	58
133	Gene Ontology and KEGG Pathway Enrichment Analysis of a Drug Target-Based Classification System. PLoS ONE, 2015, 10, e0126492.	1.1	50
134	Prediction of Drug Indications Based on Chemical Interactions and Chemical Similarities. BioMed Research International, 2015, 2015, 1-14.	0.9	3
135	Application of Systems Biology and Bioinformatics Methods in Biochemistry and Biomedicine 2014. BioMed Research International, 2015, 2015, 1-2.	0.9	2
136	Identifying Novel Candidate Genes Related to Apoptosis from a Protein-Protein Interaction Network. Computational and Mathematical Methods in Medicine, 2015, 2015, 1-11.	0.7	8
137	Prediction of Colorectal Cancer Related Genes Based on Gene Ontology. Current Bioinformatics, 2015, 10, 22-30.	0.7	0
138	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.	2.0	33
139	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.	0.9	31
140	A computational method for the identification of new candidate carcinogenic and non-carcinogenic chemicals. Molecular BioSystems, 2015, 11, 2541-2550.	2.9	23
141	Prediction and analysis of cell-penetrating peptides using pseudo-amino acid composition and random forest models. Amino Acids, 2015, 47, 1485-1493.	1.2	77
142	Discriminating between deleterious and neutral non-frameshifting indels based on protein interaction networks and hybrid properties. Molecular Genetics and Genomics, 2015, 290, 343-352.	1.0	28
143	A Hybrid Computational Method for the Discovery of Novel Reproduction-Related Genes. PLoS ONE, 2015, 10, e0117090.	1.1	13
144	Discovery of New Candidate Genes Related to Brain Development Using Protein Interaction Information. PLoS ONE, 2015, 10, e0118003.	1.1	12

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145	The Use of Chemical-Chemical Interaction and Chemical Structure to Identify New Candidate Chemicals Related to Lung Cancer. PLoS ONE, 2015, 10, e0128696.	1.1	9
146	Identification of New Candidate Genes and Chemicals Related to Esophageal Cancer Using a Hybrid Interaction Network of Chemicals and Proteins. PLoS ONE, 2015, 10, e0129474.	1.1	4
147	Prediction of Cancer Drugs by Chemical-Chemical Interactions. PLoS ONE, 2014, 9, e87791.	1.1	14
148	Predicting A-to-I RNA Editing by Feature Selection and Random Forest. PLoS ONE, 2014, 9, e110607.	1.1	37
149	Computational Systems Biology Methods in Molecular Biology, Chemistry Biology, Molecular Biomedicine, and Biopharmacy. BioMed Research International, 2014, 2014, 1-2.	0.9	17
150	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.	0.9	14
151	Prediction of S-Nitrosylation Modification Sites Based on Kernel Sparse Representation Classification and mRMR Algorithm. BioMed Research International, 2014, 2014, 1-10.	0.9	14
152	Gene Ontology and KEGG Enrichment Analyses of Genes Related to Age-Related Macular Degeneration. BioMed Research International, 2014, 2014, 1-10.	0.9	24
153	Novel Computational Methods and Tools in Biomedicine and Biopharmacy. Computational and Mathematical Methods in Medicine, 2014, 2014, 1-2.	0.7	1
154	Predicting DNA-binding sites of proteins based on sequential and 3D structural information. Molecular Genetics and Genomics, 2014, 289, 489-499.	1.0	19
155	A hybrid method for prediction and repositioning of drug Anatomical Therapeutic Chemical classes. Molecular BioSystems, 2014, 10, 868.	2.9	70
156	Computational proteomics, systems biology and clinical implications. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 163-164.	1.1	0
157	Prediction of Aptamer-Target Interacting Pairs with Pseudo-Amino Acid Composition. PLoS ONE, 2014, 9, e86729.	1.1	41
158	Classification of Non-Small Cell Lung Cancer Based on Copy Number Alterations. PLoS ONE, 2014, 9, e88300.	1.1	35
159	Prediction of Multi-Type Membrane Proteins in Human by an Integrated Approach. PLoS ONE, 2014, 9, e93553.	1.1	15
160	Analysis of Tumor Suppressor Genes Based on Gene Ontology and the KEGG Pathway. PLoS ONE, 2014, 9, e107202.	1.1	44
161	Discriminating between Lysine Sumoylation and Lysine Acetylation Using mRMR Feature Selection and Analysis. PLoS ONE, 2014, 9, e107464.	1.1	12
162	Finding Candidate Drugs for Hepatitis C Based on Chemical-Chemical and Chemical-Protein Interactions. PLoS ONE, 2014, 9, e107767.	1.1	31

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163	Prediction of protein amidation sites by feature selection and analysis. Molecular Genetics and Genomics, 2013, 288, 391-400.	1.0	10
164	Synthesis and X-ray characterization of novel palladium(ii) complexes with tunable chiral anionic counterions. Dalton Transactions, 2013, 42, 5232.	1.6	3
165	Computationally identifying virulence factors based on KEGG pathways. Molecular BioSystems, 2013, 9, 1447.	2.9	23
166	Prediction of carbamylated lysine sites based on the one-class k-nearest neighbor method. Molecular BioSystems, 2013, 9, 2729.	2.9	16
167	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
168	Prediction of active sites of enzymes by maximum relevance minimum redundancy (mRMR) feature selection. Molecular BioSystems, 2013, 9, 61-69.	2.9	31
169	Enantioselective Bromoaminocyclization of Allyl N-Tosylcarbamates Catalyzed by a Chiral Phosphine–Sc(OTf)3 Complex. Journal of the American Chemical Society, 2013, 135, 8101-8104.	6.6	117
170	Signal Propagation in Protein Interaction Network during Colorectal Cancer Progression. BioMed Research International, 2013, 2013, 1-9.	0.9	53
171	Identification of Age-Related Macular Degeneration Related Genes by Applying Shortest Path Algorithm in Protein-Protein Interaction Network. BioMed Research International, 2013, 2013, 1-8.	0.9	19
172	Prediction of Metabolic Pathway Using Graph Property, Chemical Functional Group and Chemical Structural Set. Current Bioinformatics, 2013, 8, 200-207.	0.7	30
173	Predicting Drugs Side Effects Based on Chemical-Chemical Interactions and Protein-Chemical Interactions. BioMed Research International, 2013, 2013, 1-8.	0.9	23
174	Identification of Lung-Cancer-Related Genes with the Shortest Path Approach in a Protein-Protein Interaction Network. BioMed Research International, 2013, 2013, 1-8.	0.9	26
175	A Novel Method of Predicting Protein Disordered Regions Based on Sequence Features. BioMed Research International, 2013, 2013, 1-8.	0.9	17
176	Prediction of Gene Phenotypes Based on GO and KEGG Pathway Enrichment Scores. BioMed Research International, 2013, 2013, 1-7.	0.9	38
177	Prediction of Effective Drug Combinations by Chemical Interaction, Protein Interaction and Target Enrichment of KEGG Pathways. BioMed Research International, 2013, 2013, 1-10.	0.9	29
178	A Sequence-based Approach for Predicting Protein Disordered Regions. Protein and Peptide Letters, 2013, 20, 243-248.	0.4	0
179	Prediction of Protein-protein Interactions Based on Feature Selection and Data Balancing. Protein and Peptide Letters, 2013, 20, 336-345.	0.4	2
180	Inter- and Intra-Chain Disulfide Bond Prediction Based on Optimal Feature Selection. Protein and Peptide Letters, 2013, 20, 324-335.	0.4	3

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