Lei Chen

List of Publications by Citations

182 papers	3,879 citations	34 h-index	48 g-index
193 ext. papers	5,741 ext. citations	3.5 avg, IF	6.19 L-index

#	Paper	IF	Citations
182	Predicting Anatomical Therapeutic Chemical (ATC) classification of drugs by integrating chemical-chemical interactions and similarities. *PLoS ONE*, **2012**, 7, e35254	3.7	133
181	Identify Key Sequence Features to Improve CRISPR sgRNA Efficacy. *IEEE Access*, **2017**, 5, 26582-26590	3.5	91
180	A similarity-based method for prediction of drug side effects with heterogeneous information. *Mathematical Biosciences*, **2018**, 306, 136-144	3.9	89
179	Classification and analysis of regulatory pathways using graph property, biochemical and physicochemical property, and functional property. *PLoS ONE*, **2011**, 6, e25297	3.7	77
178	Analysis of cancer-related lncRNAs using gene ontology and KEGG pathways. *Artificial Intelligence in Medicine*, **2017**, 76, 27-36	7.4	74
177	Prediction and analysis of essential genes using the enrichments of gene ontology and KEGG pathways. *PLoS ONE*, **2017**, 12, e0184129	3.7	74
176	Prediction of protein domain with mRMR feature selection and analysis. *PLoS ONE*, **2012**, 7, e39308	3.7	74
175	Prediction of protein-protein interaction sites by random forest algorithm with mRMR and IFS. *PLoS ONE*, **2012**, 7, e43927	3.7	69
174	Gene expression differences among different MSI statuses in colorectal cancer. *International Journal of Cancer*, **2018**, 143, 1731-1740	7.5	68
173	Predicting Drug Side Effects with Compact Integration of Heterogeneous Networks. *Current Bioinformatics*, **2019**, 14, 709-720	4.7	64
172	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	3.6	61
171	Prediction and analysis of cell-penetrating peptides using pseudo-amino acid composition and random forest models. *Amino Acids*, **2015**, 47, 1485-93	3.5	59
170	A hybrid method for prediction and repositioning of drug Anatomical Therapeutic Chemical classes. *Molecular BioSystems*, **2014**, 10, 868-77		58
169	Gene expression profiling gut microbiota in different races of humans. *Scientific Reports*, **2016**, 6, 23075	4.9	55
168	Deciphering the effects of gene deletion on yeast longevity using network and machine learning approaches. *Biochimie*, **2012**, 94, 1017-25	4.6	54
167	Identification of Drug-Drug Interactions Using Chemical Interactions. *Current Bioinformatics*, **2017**, 12,	4.7	54
166	Predicting the network of substrate-enzyme-product triads by combining compound similarity and functional domain composition. *BMC Bioinformatics*, **2010**, 11, 293	3.6	50

165	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	3.1	48
164	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	3.1	45
163	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	4.7	45
162	iATC-NRAKEL: an efficient multi-label classifier for recognizing anatomical therapeutic chemical classes of drugs. *Bioinformatics*, **2020**, 36, 1391-1396	7.2	44
161	Identification of Differentially Expressed Genes between Original Breast Cancer and Xenograft Using Machine Learning Algorithms. *Genes*, **2018**, 9,	4.2	42
160	Identification of synthetic lethality based on a functional network by using machine learning algorithms. *Journal of Cellular Biochemistry*, **2019**, 120, 405-416	4.7	42
159	Signal propagation in protein interaction network during colorectal cancer progression. *BioMed Research International*, **2013**, 2013, 287019	3	41
158	Identification of the copy number variant biomarkers for breast cancer subtypes. *Molecular Genetics and Genomics*, **2019**, 294, 95-110	3.1	41
157	iATC-FRAKEL: a simple multi-label web server for recognizing anatomical therapeutic chemical classes of drugs with their fingerprints only. *Bioinformatics*, **2020**, 36, 3568-3569	7.2	40
156	Gene Ontology and KEGG Pathway Enrichment Analysis of a Drug Target-Based Classification System. *PLoS ONE*, **2015**, 10, e0126492	3.7	39
155	Prediction of Drug Side Effects with a Refined Negative Sample Selection Strategy. *Computational and Mathematical Methods in Medicine*, **2020**, 2020, 1573543	2.8	38
154	Identification of hepatocellular carcinoma related genes with k-th shortest paths in a protein-protein interaction network. *Molecular BioSystems*, **2013**, 9, 2720-8		37
153	Analysis of tumor suppressor genes based on gene ontology and the KEGG pathway. *PLoS ONE*, **2014**, 9, e107202	3.7	37
152	Application of the Shortest Path Algorithm for the Discovery of Breast Cancer-Related Genes. *Current Bioinformatics*, **2016**, 11, 51-58	4.7	37
151	Similarity-Based Machine Learning Model for Predicting the Metabolic Pathways of Compounds. *IEEE Access*, **2020**, 8, 130687-130696	3.5	36
150	The use of Gene Ontology terms and KEGG pathways for analysis and prediction of oncogenes. *Biochimica Et Biophysica Acta - General Subjects*, **2016**, 1860, 2725-34	4	35
149	Tissue Expression Difference between mRNAs and lncRNAs. *International Journal of Molecular Sciences*, **2018**, 19,	6.3	35
148	Classifying ten types of major cancers based on reverse phase protein array profiles. *PLoS ONE*, **2015**, 10, e0123147	3.7	33

147	Predicting metabolic pathways of small molecules and enzymes based on interaction information of chemicals and proteins. *PLoS ONE*, **2012**, 7, e45944	3.7	33
146	Predicting the types of metabolic pathway of compounds using molecular fragments and sequential minimal optimization. *Combinatorial Chemistry and High Throughput Screening*, **2016**, 19, 136-43	1.3	33
145	Identifying and analyzing different cancer subtypes using RNA-seq data of blood platelets. *Oncotarget*, **2017**, 8, 87494-87511	3.3	32
144	Identifying Patients with Atrioventricular Septal Defect in Down Syndrome Populations by Using Self-Normalizing Neural Networks and Feature Selection. *Genes*, **2018**, 9,	4.2	31
143	Multiple classifier integration for the prediction of protein structural classes. *Journal of Computational Chemistry*, **2009**, 30, 2248-54	3.5	31
142	Labelling algorithms for paired-domination problems in block and interval graphs. *Journal of Combinatorial Optimization*, **2010**, 19, 457-470	0.9	31
141	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	4	31
140	Identifying Transcriptomic Signatures and Rules for SARS-CoV-2 Infection. *Frontiers in Cell and Developmental Biology*, **2020**, 8, 627302	5.7	31
139	Identification of the Gene Expression Rules That Define the Subtypes in Glioma. *Journal of Clinical Medicine*, **2018**, 7,	5.1	30
138	Finding candidate drugs for hepatitis C based on chemical-chemical and chemical-protein interactions. *PLoS ONE*, **2014**, 9, e107767	3.7	29
137	Identification of Protein Subcellular Localization With Network and Functional Embeddings. *Frontiers in Genetics*, **2020**, 11, 626500	4.5	29
136	Identification of Human Membrane Protein Types by Incorporating Network Embedding Methods. *IEEE Access*, **2019**, 7, 140794-140805	3.5	28
135	Prediction of human genesTregulatory functions based on proteinprotein interaction network. *Protein and Peptide Letters*, **2012**, 19, 910-6	1.9	28
134	Prediction of Metabolic Pathway Using Graph Property, Chemical Functional Group and Chemical Structural Set. *Current Bioinformatics*, **2013**, 8, 200-207	4.7	27
133	A Binary Classifier for the Prediction of EC Numbers of Enzymes. *Current Proteomics*, **2019**, 16, 383-391	0.7	27
132	Identification of leukemia stem cell expression signatures through Monte Carlo feature selection strategy and support vector machine. *Cancer Gene Therapy*, **2020**, 27, 56-69	5.4	27
131	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	5.6	26
130	Identification of novel proliferative diabetic retinopathy related genes on protein□protein interaction network. *Neurocomputing*, **2016**, 217, 63-72	5.4	26

129	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	6.4	26
128	Prediction of gene phenotypes based on GO and KEGG pathway enrichment scores. *BioMed Research International*, **2013**, 2013, 870795	3	26
127	Classification of Widely and Rarely Expressed Genes with Recurrent Neural Network. *Computational and Structural Biotechnology Journal*, **2019**, 17, 49-60	6.8	26
126	Analysis of Expression Pattern of snoRNAs in Different Cancer Types with Machine Learning Algorithms. *International Journal of Molecular Sciences*, **2019**, 20,	6.3	25
125	Analysis of protein pathway networks using hybrid properties. *Molecules*, **2010**, 15, 8177-92	4.8	25
124	Computational analysis of HIV-1 resistance based on gene expression profiles and the virus-host interaction network. *PLoS ONE*, **2011**, 6, e17291	3.7	25
123	Mining for novel tumor suppressor genes using a shortest path approach. *Journal of Biomolecular Structure and Dynamics*, **2016**, 34, 664-75	3.6	24
122	SACICA: a sparse approximation coefficient-based ICA model for functional magnetic resonance imaging data analysis. *Journal of Neuroscience Methods*, **2013**, 216, 49-61	3	24
121	Prediction of effective drug combinations by chemical interaction, protein interaction and target enrichment of KEGG pathways. *BioMed Research International*, **2013**, 2013, 723780	3	24
120	Identifying Methylation Pattern and Genes Associated with Breast Cancer Subtypes. *International Journal of Molecular Sciences*, **2019**, 20,	6.3	23
119	A computational method using the random walk with restart algorithm for identifying novel epigenetic factors. *Molecular Genetics and Genomics*, **2018**, 293, 293-301	3.1	23
118	Inferring anatomical therapeutic chemical (ATC) class of drugs using shortest path and random walk with restart algorithms. *Biochimica Et Biophysica Acta - Molecular Basis of Disease*, **2018**, 1864, 2228-2240	6.9	22
117	Identifying novel protein phenotype annotations by hybridizing protein-protein interactions and protein sequence similarities. *Molecular Genetics and Genomics*, **2016**, 291, 913-34	3.1	22
116	A fast-FENICA method on resting state fMRI data. *Journal of Neuroscience Methods*, **2012**, 209, 1-12	3	22
115	Identifying protein complexes using hybrid properties. *Journal of Proteome Research*, **2009**, 8, 5212-8	5.6	22
114	Drug Target Group Prediction with Multiple Drug Networks. *Combinatorial Chemistry and High Throughput Screening*, **2020**, 23, 274-284	1.3	22
113	Tissue differences revealed by gene expression profiles of various cell lines. *Journal of Cellular Biochemistry*, **2018**, 120, 7068	4.7	22
112	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, 906-17	3.6	21

111	Predicting chemical toxicity effects based on chemical-chemical interactions. *PLoS ONE*, **2013**, 8, e56517	3.7	21
110	A Feature and Algorithm Selection Method for Improving the Prediction of Protein Structural Class. *Combinatorial Chemistry and High Throughput Screening*, **2017**, 20, 612-621	1.3	21
109	Detecting the Multiomics Signatures of Factor-Specific Inflammatory Effects on Airway Smooth Muscles. *Frontiers in Genetics*, **2020**, 11, 599970	4.5	21
108	A computational method for the identification of new candidate carcinogenic and non-carcinogenic chemicals. *Molecular BioSystems*, **2015**, 11, 2541-50		20
107	Predicting drugs side effects based on chemical-chemical interactions and protein-chemical interactions. *BioMed Research International*, **2013**, 2013, 485034	3	20
106	A linear-time algorithm for paired-domination problem in strongly chordal graphs. *Information Processing Letters*, **2009**, 110, 20-23	0.8	20
105	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	1.3	20
104	Identifying protein subcellular location with embedding features learned from networks. *Current Proteomics*, **2020**, 17,	0.7	20
103	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	4.9	20
102	iMPTCE-Hnetwork: A Multilabel Classifier for Identifying Metabolic Pathway Types of Chemicals and Enzymes with a Heterogeneous Network. *Computational and Mathematical Methods in Medicine* , **2021**, 2021, 6683051	2.8	20
101	Identification of drug□disease associations by using multiple drug and disease networks. *Current Bioinformatics*, **2021**, 16,	4.7	20
100	Computationally identifying virulence factors based on KEGG pathways. *Molecular BioSystems*, **2013** , 9, 1447-52		19
99	Gene ontology and KEGG enrichment analyses of genes related to age-related macular degeneration. *BioMed Research International*, **2014**, 2014, 450386	3	19
98	Identification of lung-cancer-related genes with the shortest path approach in a protein-protein interaction network. *BioMed Research International*, **2013**, 2013, 267375	3	19
97	HIV infection alters the human epigenetic landscape. *Gene Therapy*, **2019**, 26, 29-39	4	19
96	A Network Integration Method for Deciphering the Types of Metabolic Pathway of Chemicals with Heterogeneous Information. *Combinatorial Chemistry and High Throughput Screening*, **2018**, 21, 670-680	1.3	16
95	Identification of age-related macular degeneration related genes by applying shortest path algorithm in protein-protein interaction network. *BioMed Research International*, **2013**, 2013, 523415	3	16
94	Predicting subcellular location of proteins using integrated-algorithm method. *Molecular Diversity*, **2010**, 14, 551-8	3.1	16

93	Recognizing Novel Tumor Suppressor Genes Using a Network Machine Learning Strategy. *IEEE Access*, **2019**, 7, 155002-155013	3.5	16
92	An integrated method for the identification of novel genes related to oral cancer. *PLoS ONE*, **2017**, 12, e0175185	3.7	15
91	Prediction of drug target groups based on chemical-chemical similarities and chemical-chemical/protein connections. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2014**, 1844, 207-13	4	15
90	Joint Access Selection and Resource Allocation in Cache-Enabled HCNs with D2D Communications **2017**,		14
89	Determination of Genes Related to Uveitis by Utilization of the Random Walk with Restart Algorithm on a Protein-Protein Interaction Network. *International Journal of Molecular Sciences*, **2017**, 18,	6.3	14
88	A novel approach for fMRI data analysis based on the combination of sparse approximation and affinity propagation clustering. *Magnetic Resonance Imaging*, **2014**, 32, 736-46	3.3	14
87	Prediction of multi-type membrane proteins in human by an integrated approach. *PLoS ONE*, **2014**, 9, e93553	3.7	14
86	Prediction and analysis of retinoblastoma related genes through gene ontology and KEGG. *BioMed Research International*, **2013**, 2013, 304029	3	13
85	Identifying chemicals with potential therapy of HIV based on protein-protein and protein-chemical interaction network. *PLoS ONE*, **2013**, 8, e65207	3.7	13
84	Screening of Methylation Signature and Gene Functions Associated With the Subtypes of Isocitrate Dehydrogenase-Mutation Gliomas. *Frontiers in Bioengineering and Biotechnology*, **2019**, 7, 339	5.8	13
83	Investigating the gene expression profiles of cells in seven embryonic stages with machine learning algorithms. *Genomics*, **2020**, 112, 2524-2534	4.3	12
82	Hardness results and approximation algorithms for (weighted) paired-domination in graphs. *Theoretical Computer Science*, **2009**, 410, 5063-5071	1.1	12
81	Discriminating between lysine sumoylation and lysine acetylation using mRMR feature selection and analysis. *PLoS ONE*, **2014**, 9, e107464	3.7	12
80	A hybrid computational method for the discovery of novel reproduction-related genes. *PLoS ONE*, **2015**, 10, e0117090	3.7	12
79	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	1.9	12
78	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, 4256301	3	12
77	Prediction of cancer drugs by chemical-chemical interactions. *PLoS ONE*, **2014**, 9, e87791	3.7	11
76	Prediction of interactiveness between small molecules and enzymes by combining gene ontology and compound similarity. *Journal of Computational Chemistry*, **2010**, 31, 1766-76	3.5	11

75	Analysis of Gene Expression Profiles in the Human Brain Stem, Cerebellum and Cerebral Cortex. *PLoS ONE*, **2016**, 11, e0159395	3.7	11
74	A Binary Classifier for Prediction of the Types of Metabolic Pathway of Chemicals. *Combinatorial Chemistry and High Throughput Screening*, **2017**, 20, 140-146	1.3	11
73	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	1.3	11
72	Predicting Biological Functions of Protein Complexes Using Graphic and Functional Features.. *Current Bioinformatics*, **2013**, 8, 545-551	4.7	11
71	iMPT-FDNPL: Identification of Membrane Protein Types with Functional Domains and a Natural Language Processing Approach. *Computational and Mathematical Methods in Medicine*, **2021**, 2021, 7681497	2.8	11
70	Using compound similarity and functional domain composition for prediction of drug-target interaction networks. *Medicinal Chemistry*, **2010**, 6, 388-95	1.8	10
69	Predicting RNA 5-Methylcytosine Sites by Using Essential Sequence Features and Distributions.. *BioMed Research International*, **2022**, 2022, 4035462	3	10
68	Predicting Heart Cell Types by Using Transcriptome Profiles and a Machine Learning Method.. *Life*, **2022**, 12,	3	10
67	Prediction of Drug Combinations with a Network Embedding Method. *Combinatorial Chemistry and High Throughput Screening*, **2018**, 21, 789-797	1.3	10
66	Investigation and Prediction of Human Interactome Based on Quantitative Features. *Frontiers in Bioengineering and Biotechnology*, **2020**, 8, 730	5.8	10
65	Prediction of Linear B-Cell Epitopes with mRMR Feature Selection and Analysis. *Current Bioinformatics*, **2016**, 11, 22-31	4.7	10
64	Analysis of the chemical toxicity effects using the enrichment of Gene Ontology terms and KEGG pathways. *Biochimica Et Biophysica Acta - General Subjects*, **2016**, 1860, 2619-26	4	10
63	A Novel Brain Networks Enhancement Model (BNEM) for BOLD fMRI Data Analysis With Highly Spatial Reproducibility. *IEEE Journal of Biomedical and Health Informatics*, **2016**, 20, 1107-19	7.2	9
62	Identifying Essential Signature Genes and Expression Rules Associated With Distinctive Development Stages of Early Embryonic Cells. *IEEE Access*, **2019**, 7, 128570-128578	3.5	9
61	(k)-Power domination in block graphs. *Journal of Combinatorial Optimization*, **2016**, 31, 865-873	0.9	9
60	Validating the performance of one-time decomposition for fMRI analysis using ICA with automatic target generation process. *Magnetic Resonance Imaging*, **2013**, 31, 970-5	3.3	9
59	A Computational Method for Classifying Different Human Tissues with Quantitatively Tissue-Specific Expressed Genes. *Genes*, **2018**, 9,	4.2	9
58	Discovery of new candidate genes related to brain development using protein interaction information. *PLoS ONE*, **2015**, 10, e0118003	3.7	8

57	Distinguishing Glioblastoma Subtypes by Methylation Signatures. *Frontiers in Genetics*, **2020**, 11, 604336	4.5	8
56	Feature Classification and Analysis of Lung Cancer Related Genes through Gene Ontology and KEGG Pathways. *Current Bioinformatics*, **2016**, 11, 40-50	4.7	8
55	The Use of Gene Ontology Term and KEGG Pathway Enrichment for Analysis of Drug Half-Life. *PLoS ONE*, **2016**, 11, e0165496	3.7	8
54	Primary Tumor Site Specificity is Preserved in Patient-Derived Tumor Xenograft Models. *Frontiers in Genetics*, **2019**, 10, 738	4.5	7
53	Analysis of Protein-Protein Functional Associations by Using Gene Ontology and KEGG Pathway. *BioMed Research International*, **2019**, 2019, 4963289	3	7
52	Predicting triplet of transcription factor □mediating enzyme □target gene by functional profiles. *Neurocomputing*, **2011**, 74, 3677-3681	5.4	7
51	Identifying Robust Microbiota Signatures and Interpretable Rules to Distinguish Cancer Subtypes. *Frontiers in Molecular Biosciences*, **2020**, 7, 604794	5.6	7
50	Identifying the RNA signatures of coronary artery disease from combined lncRNA and mRNA expression profiles. *Genomics*, **2020**, 112, 4945-4958	4.3	7
49	Immunosignature Screening for Multiple Cancer Subtypes Based on Expression Rule. *Frontiers in Bioengineering and Biotechnology*, **2019**, 7, 370	5.8	7
48	Network-Based Method for Identifying Co- Regeneration Genes in Bone, Dentin, Nerve and Vessel Tissues. *Genes*, **2017**, 8,	4.2	6
47	Extremal problems on consecutive L(2,1)-labelling. *Discrete Applied Mathematics*, **2007**, 155, 1302-1313	1	6
46	The Use of Chemical-Chemical Interaction and Chemical Structure to Identify New Candidate Chemicals Related to Lung Cancer. *PLoS ONE*, **2015**, 10, e0128696	3.7	6
45	A Shortest-Path-Based Method for the Analysis and Prediction of Fruit-Related Genes in Arabidopsis thaliana. *PLoS ONE*, **2016**, 11, e0159519	3.7	6
44	Identifying the Signatures and Rules of Circulating Extracellular MicroRNA for Distinguishing Cancer Subtypes. *Frontiers in Genetics*, **2021**, 12, 651610	4.5	6
43	Analysis of Gene Expression Differences between Different Pancreatic Cells. *ACS Omega*, **2019**, 4, 6421-6435	3.7	5
42	Recognizing and Predicting Thioether Bridges Formed by Lanthionine and □Methyllanthionine in Lantibiotics Using a Random Forest Approach with Feature Selection. *Combinatorial Chemistry and High Throughput Screening*, **2017**, 20, 582-593	1.3	5
41	A path-based method for identification of protein phenotypic annotations. *Current Bioinformatics*, **2021**, 16,	4.7	5
40	iATC-NFMLP: Identifying classes of anatomical therapeutic chemicals based on drug networks, fingerprints and multilayer perceptron. *Current Bioinformatics*, **2022**, 17,	4.7	5

39	Inferring novel genes related to oral cancer with a network embedding method and one-class learning algorithms. *Gene Therapy*, **2019**, 26, 465-478	4	4
38	Alternative Polyadenylation Modification Patterns Reveal Essential Posttranscription Regulatory Mechanisms of Tumorigenesis in Multiple Tumor Types. *BioMed Research International*, **2020**, 2020, 6384120	3	4
37	Deciphering the Relationship between Obesity and Various Diseases from a Network Perspective. *Genes*, **2017**, 8,	4.2	4
36	Selection of reprogramming factors of induced pluripotent stem cells based on the protein interaction network and functional profiles. *Protein and Peptide Letters*, **2012**, 19, 113-9	1.9	4
35	Prediction of drugs target groups based on ChEBI ontology. *BioMed Research International*, **2013**, 2013, 132724	3	4
34	A two-step similarity-based method for prediction of drug's target group. *Protein and Peptide Letters*, **2013**, 20, 364-70	1.9	4
33	Predicting Protein Ligand Binding Sites with Structure Alignment Method on Hadoop. *Current Proteomics*, **2016**, 13, 113-121	0.7	4
32	A Fast Approximate Hypervolume Calculation Method by a Novel Decomposition Strategy. *Lecture Notes in Computer Science*, **2017**, 14-25	0.9	4
31	Predicting gene phenotype by multi-label multi-class model based on essential functional features. *Molecular Genetics and Genomics*, **2021**, 296, 905-918	3.1	4
30	Identification of Cell Markers and Their Expression Patterns in Skin Based on Single-Cell RNA-Sequencing Profiles.. *Life*, **2022**, 12,	3	4
29	Distance paired-domination problems on subclasses of chordal graphs. *Theoretical Computer Science*, **2009**, 410, 5072-5081	1.1	3
28	Analysis of metabolic pathway using hybrid properties. *Protein and Peptide Letters*, **2012**, 19, 99-107	1.9	3
27	Study of drug-drug combinations based on molecular descriptors and physicochemical properties. *Combinatorial Chemistry and High Throughput Screening*, **2016**, 19, 153-60	1.3	3
26	miR-29 mediates exercise-induced skeletal muscle angiogenesis by targeting VEGFA, COL4A1 and COL4A2 via the PI3K/Akt signaling pathway. *Molecular Medicine Reports*, **2020**, 22, 661-670	2.9	3
25	An Integrated Multi-Label Classifier with Chemical-Chemical Interactions for Prediction of Chemical Toxicity Effects. *Combinatorial Chemistry and High Throughput Screening*, **2018**, 21, 403-410	1.3	3
24	Prediction of membrane protein types by fusing protein-protein interaction and protein sequence information. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2020**, 1868, 140524	4	3
23	Recognizing novel chemicals/drugs for anatomical therapeutic chemical classes with a heat diffusion algorithm. *Biochimica Et Biophysica Acta - Molecular Basis of Disease*, **2020**, 1866, 165910	6.9	3
22	Drug-Drug Interactions Prediction Using Fingerprint Only.. *Computational and Mathematical Methods in Medicine*, **2022**, 2022, 7818480	2.8	3

21	NP-completeness and APX-completeness of restrained domination in graphs. *Theoretical Computer Science*, **2012**, 448, 1-8	1.1	2
20	Identification of Pan-Cancer Biomarkers Based on the Gene Expression Profiles of Cancer Cell Lines.. *Frontiers in Cell and Developmental Biology*, **2021**, 9, 781285	5.7	2
19	Computational method for distinguishing lysine acetylation, sumoylation, and ubiquitination using the random forest algorithm with a feature selection procedure. *Combinatorial Chemistry and High Throughput Screening*, **2017**,	1.3	2
18	iMPT-FRAKEL: A Simple Multi-label Web-server that Only Uses Fingerprints to Identify which Metabolic Pathway Types Compounds can Participate In. *Open Bioinformatics Journal*, **2020**, 13, 83-91	0.8	2
17	Identification of Latent Oncogenes with a Network Embedding Method and Random Forest. *BioMed Research International*, **2020**, 2020, 5160396	3	2
16	Identifying COVID-19-Specific Transcriptomic Biomarkers with Machine Learning Methods. *BioMed Research International*, **2021**, 2021, 9939134	3	2
15	Identification of Microbiota Biomarkers With Orthologous Gene Annotation for Type 2 Diabetes. *Frontiers in Microbiology*, **2021**, 12, 711244	5.7	2
14	Identification of Gene Signatures and Expression Patterns During Epithelial-to-Mesenchymal Transition From Single-Cell Expression Atlas. *Frontiers in Genetics*, **2020**, 11, 605012	4.5	2
13	Identification of Carcinogenic Chemicals with Network Embedding and Deep Learning Methods. *Current Bioinformatics*, **2021**, 15, 1017-1026	4.7	2
12	Similarity-Based Method with Multiple-Feature Sampling for Predicting Drug Side Effects.. *Computational and Mathematical Methods in Medicine*, **2022**, 2022, 9547317	2.8	2
11	Network-Based Method for Identifying Co-Regeneration Genes in Bone, Dentin, Nerve and Vessel Tissues. *Genes*, **2017**, 8, 252	4.2	1
10	Vertices in all minimum paired-dominating sets of block graphs. *Journal of Combinatorial Optimization*, **2012**, 24, 176-191	0.9	1
9	A computational method for the identification of candidate drugs for non-small cell lung cancer. *PLoS ONE*, **2017**, 12, e0183411	3.7	1
8	Analysis of the Sequence Characteristics of Antifreeze Protein. *Life*, **2021**, 11,	3	1
7	Identifying Lung Cancer Cell Markers with Machine Learning Methods and Single-Cell RNA-Seq Data. *Life*, **2021**, 11,	3	1
6	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	5.7	0
5	Recognition of Immune Cell Markers of COVID-19 Severity with Machine Learning Methods.. *BioMed Research International*, **2022**, 2022, 6089242	3	0
4	A Two-step Similarity-based Method for Prediction of Drug's Target Group. *Protein and Peptide Letters*, **2013**, 20, 364-370	1.9	

3	Constructive characterizations of (□p ,]1- and (□p , □pr)-trees. *Applied Mathematics*, **2008**, 23, 475-480	0.7
2	Novel Computational Methods in Current Biomedicine and Biopharmacy. *Current Bioinformatics*, **2021**, 15, 955-955	4.7
1	Recognizing Pattern and Rule of Mutation Signatures Corresponding to Cancer Types. *Frontiers in Cell and Developmental Biology*, **2021**, 9, 712931	5.7