Yu-Dong Cai

List of Publications by Year
in descending order

348 papers	14,188 citations	16451 64 h-index	33894 99 g-index
353 all docs	353 docs citations	353 times ranked	7868 citing authors

#	Article	IF	Citations
1	Using Functional Domain Composition and Support Vector Machines for Prediction of Protein Subcellular Location. Journal of Biological Chemistry, 2002, 277, 45765-45769.	3.4	449
2	Support Vector Machines for Predicting Membrane Protein Types by Using Functional Domain Composition. Biophysical Journal, 2003, 84, 3257-3263.	0.5	307
3	Adaptive and freeze-tolerant heteronetwork organohydrogels with enhanced mechanical stability over a wide temperature range. Nature Communications, 2017, 8, 15911.	12.8	266
4	Predicting Drug-Target Interaction Networks Based on Functional Groups and Biological Features. PLoS ONE, 2010, 5, e9603.	2.5	241
5	Prediction of protein structural classes by support vector machines. Computers & Chemistry, 2002, 26, 293-296.	1.2	218
6	Prediction and analysis of essential genes using the enrichments of gene ontology and KEGG pathways. PLoS ONE, 2017, 12, e0184129.	2.5	202
7	Using LogitBoost classifier to predict protein structural classes. Journal of Theoretical Biology, 2006, 238, 172-176.	1.7	182
8	Predicting protein structural class by functional domain composition. Biochemical and Biophysical Research Communications, 2004, 321, 1007-1009.	2.1	176
9	Prediction of Membrane Protein Types by Incorporating Amphipathic Effects. Journal of Chemical Information and Modeling, 2005, 45, 407-413.	5.4	171
10	Prediction of protein subcellular locations by GOâ€“FunDâ€“PseAA predictor. Biochemical and Biophysical Research Communications, 2004, 320, 1236-1239.	2.1	165
11	Application of SVM to predict membrane protein types. Journal of Theoretical Biology, 2004, 226, 373-376.	1.7	164
12	Prediction of Antimicrobial Peptides Based on Sequence Alignment and Feature Selection Methods. PLoS ONE, 2011, 6, e18476.	2.5	164
13	Predicting Anatomical Therapeutic Chemical (ATC) Classification of Drugs by Integrating Chemical-Chemical Interactions and Similarities. PLoS ONE, 2012, 7, e35254.	2.5	159
14	Predicting Proteinâˆ’Protein Interactions from Sequences in a Hybridization Space. Journal of Proteome Research, 2006, 5, 316-322.	3.7	158
15	Prediction and classification of protein subcellular location-sequence-order effect and pseudo amino acid composition. Journal of Cellular Biochemistry, 2003, 90, 1250-1260.	2.6	157
16	Identify Key Sequence Features to Improve CRISPR sgRNA Efficacy. IEEE Access, 2017, 5, 26582-26590.	4.2	153
17	Identification of Colorectal Cancer Related Genes with mRMR and Shortest Path in Protein-Protein Interaction Network. PLoS ONE, 2012, 7, e33393.	2.5	149
18	Support vector machines for predicting HIV protease cleavage sites in protein. Journal of Computational Chemistry, 2002, 23, 267-274.	3.3	145

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19	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
20	Predicting protein quaternary structure by pseudo amino acid composition. Proteins: Structure, Function and Bioinformatics, 2003, 53, 282-289.	2.6	138
21	Support vector machines for predicting protein structural class. BMC Bioinformatics, 2001, 2, 3.	2.6	137
22	<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
23	Analysis of cancer-related lncRNAs using gene ontology and KEGG pathways. Artificial Intelligence in Medicine, 2017, 76, 27-36.	6.5	136
24	A new hybrid approach to predict subcellular localization of proteins by incorporating gene ontology. Biochemical and Biophysical Research Communications, 2003, 311, 743-747.	2.1	133
25	Support vector machines for predicting rRNA-, RNA-, and DNA-binding proteins from amino acid sequence. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2003, 1648, 127-133.	2.3	131
26	Boosting classifier for predicting protein domain structural class. Biochemical and Biophysical Research Communications, 2005, 334, 213-217.	2.1	129
27	Prediction of lysine ubiquitination with mRMR feature selection and analysis. Amino Acids, 2012, 42, 1387-1395.	2.7	129
28	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
29	Enantioselective Bromoaminocyclization of Allyl N-Tosylcarbamates Catalyzed by a Chiral Phosphineâ€“Sc(OTf)3 Complex. Journal of the American Chemical Society, 2013, 135, 8101-8104.	13.7	117
30	Support vector machines for prediction of protein subcellular location by incorporating quasi-sequence-order effect. Journal of Cellular Biochemistry, 2002, 84, 343-348.	2.6	116
31	Predicting membrane protein type by functional domain composition and pseudo-amino acid composition. Journal of Theoretical Biology, 2006, 238, 395-400.	1.7	111
32	Predicting rRNA-, RNA-, and DNA-binding proteins from primary structure with support vector machines. Journal of Theoretical Biology, 2006, 240, 175-184.	1.7	111
33	Genetic differences among ethnic groups. BMC Genomics, 2015, 16, 1093.	2.8	109
34	Prediction of protein structural classes by neural network. Biochimie, 2000, 82, 783-785.	2.6	107
35	Nearest neighbour algorithm for predicting protein subcellular location by combining functional domain composition and pseudo-amino acid composition. Biochemical and Biophysical Research Communications, 2003, 305, 407-411.	2.1	107
36	Predicting protein localization in budding Yeast. Bioinformatics, 2005, 21, 944-950.	4.1	103

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37	Predicting Protein Structural Class with AdaBoost Learner. Protein and Peptide Letters, 2006, 13, 489-492.	0.9	103
38	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
39	Predicting Enzyme Subclass by Functional Domain Composition and Pseudo Amino Acid Composition. Journal of Proteome Research, 2005, 4, 967-971.	3.7	96
40	Prediction of Protein-Protein Interaction Sites by Random Forest Algorithm with mRMR and IFS. PLoS ONE, 2012, 7, e43927.	2.5	92
41	Predicting enzyme family classes by hybridizing gene product composition and pseudo-amino acid composition. Journal of Theoretical Biology, 2005, 234, 145-149.	1.7	90
42	Support vector machines for prediction of protein signal sequences and their cleavage sites. Peptides, 2003, 24, 159-161.	2.4	89
43	Predicting subcellular localization of proteins in a hybridization space. Bioinformatics, 2004, 20, 1151-1156.	4.1	88
44	Predicting subcellular localization of proteins by hybridizing functional domain composition and pseudo-amino acid composition. Journal of Cellular Biochemistry, 2004, 91, 1197-1203.	2.6	88
45	Prediction of Protein Domain with mRMR Feature Selection and Analysis. PLoS ONE, 2012, 7, e39308.	2.5	86
46	Gene expression profiling gut microbiota in different races of humans. Scientific Reports, 2016, 6, 23075.	3.3	86
47	Classification and Analysis of Regulatory Pathways Using Graph Property, Biochemical and Physicochemical Property, and Functional Property. PLoS ONE, 2011, 6, e25297.	2.5	84
48	Predicting O-glycosylation sites in mammalian proteins by using SVMs. Computational Biology and Chemistry, 2006, 30, 203-208.	2.3	83
49	Identification of Differentially Expressed Genes between Original Breast Cancer and Xenograft Using Machine Learning Algorithms. Genes, 2018, 9, 155.	2.4	83
50	Artificial neural network model for predicting HIV protease cleavage sites in protein. Advances in Engineering Software, 1998, 29, 119-128.	3.8	81
51	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.	3.5	81
52	Identification of the copy number variant biomarkers for breast cancer subtypes. Molecular Genetics and Genomics, 2019, 294, 95-110.	2.1	81
53	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.	2.6	78
54	Identify catalytic triads of serine hydrolases by support vector machines. Journal of Theoretical Biology, 2004, 228, 551-557.	1.7	77

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55	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
56	Predicting enzyme family class in a hybridization space. Protein Science, 2008, 13, 2857-2863.	7.6	75
57	Predict and analyze S-nitrosylation modification sites with the mRMR and IFS approaches. Journal of Proteomics, 2012, 75, 1654-1665.	2.4	74
58	Identification of the Gene Expression Rules That Define the Subtypes in Glioma. Journal of Clinical Medicine, 2018, 7, 350.	2.4	74
59	Prediction of Pharmacological and Xenobiotic Responses to Drugs Based on Time Course Gene Expression Profiles. PLoS ONE, 2009, 4, e8126.	2.5	74
60	Support Vector Machine for predicting Î±-turn types. Peptides, 2003, 24, 629-630.	2.4	73
61	Prediction of protease types in a hybridization space. Biochemical and Biophysical Research Communications, 2006, 339, 1015-1020.	2.1	73
62	A hybrid method for prediction and repositioning of drug Anatomical Therapeutic Chemical classes. Molecular BioSystems, 2014, 10, 868.	2.9	70
63	Prediction of Deleterious Non-Synonymous SNPs Based on Protein Interaction Network and Hybrid Properties. PLoS ONE, 2010, 5, e11900.	2.5	70
64	Support vector machines for predicting the specificity of GalNAc-transferase. Peptides, 2002, 23, 205-208.	2.4	68
65	Deciphering the effects of gene deletion on yeast longevity using network and machine learning approaches. Biochimie, 2012, 94, 1017-1025.	2.6	67
66	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
67	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
68	Support vector machines for the classification and prediction of ?-turn types. Journal of Peptide Science, 2002, 8, 297-301.	1.4	64
69	Predicting protease types by hybridizing gene ontology and pseudo amino acid composition. Proteins: Structure, Function and Bioinformatics, 2006, 63, 681-684.	2.6	64
70	Predicting Biological Functions of Compounds Based on Chemical-Chemical Interactions. PLoS ONE, 2011, 6, e29491.	2.5	64
71	Tissue Expression Difference between mRNAs and lncRNAs. International Journal of Molecular Sciences, 2018, 19, 3416.	4.1	64
72	Prediction of proteinâ€“protein interactions based on PseAA composition and hybrid feature selection. Biochemical and Biophysical Research Communications, 2009, 380, 318-322.	2.1	62

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73	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.	2.1	62
74	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
75	Predicting the network of substrate-enzyme-product triads by combining compound similarity and functional domain composition. BMC Bioinformatics, 2010, 11, 293.	2.6	61
76	Tissue differences revealed by gene expression profiles of various cell lines. Journal of Cellular Biochemistry, 2019, 120, 7068-7081.	2.6	59
77	Using AdaBoost for the prediction of subcellular location of prokaryotic and eukaryotic proteins. Molecular Diversity, 2008, 12, 41-45.	3.9	58
78	Classifying Ten Types of Major Cancers Based on Reverse Phase Protein Array Profiles. PLoS ONE, 2015, 10, e0123147.	2.5	58
79	Determining proteinâ€“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
80	Using Functional Domain Composition To Predict Enzyme Family Classes. Journal of Proteome Research, 2005, 4, 109-111.	3.7	57
81	Identifying Transcriptomic Signatures and Rules for SARS-CoV-2 Infection. Frontiers in Cell and Developmental Biology, 2020, 8, 627302.	3.7	57
82	Using GO-PseAA predictor to identify membrane proteins and their types. Biochemical and Biophysical Research Communications, 2005, 327, 845-847.	2.1	56
83	A novel computational method to predict transcription factor DNA binding preference. Biochemical and Biophysical Research Communications, 2006, 348, 1034-1037.	2.1	55
84	Using GO-PseAA predictor to predict enzyme sub-class. Biochemical and Biophysical Research Communications, 2004, 325, 506-509.	2.1	54
85	Predicting Subcellular Localization with AdaBoost Learner. Protein and Peptide Letters, 2008, 15, 286-289.	0.9	54
86	Signal Propagation in Protein Interaction Network during Colorectal Cancer Progression. BioMed Research International, 2013, 2013, 1-9.	1.9	53
87	Hepatitis C Virus Network Based Classification of Hepatocellular Cirrhosis and Carcinoma. PLoS ONE, 2012, 7, e34460.	2.5	52
88	Analysis and Prediction of Translation Rate Based on Sequence and Functional Features of the mRNA. PLoS ONE, 2011, 6, e16036.	2.5	51
89	Analysis and Prediction of Nitrated Tyrosine Sites with the mRMR Method and Support Vector Machine Algorithm. Current Bioinformatics, 2018, 13, 3-13.	1.5	51
90	Gene Ontology and KEGG Pathway Enrichment Analysis of a Drug Target-Based Classification System. PLoS ONE, 2015, 10, e0126492.	2.5	50

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91	Prediction of Saccharomyces cerevisiae protein functional class from functional domain composition. Bioinformatics, 2004, 20, 1292-1300.	4.1	49
92	Classification of Widely and Rarely Expressed Genes with Recurrent Neural Network. Computational and Structural Biotechnology Journal, 2019, 17, 49-60.	4.1	49
93	Predicting Metabolic Pathways of Small Molecules and Enzymes Based on Interaction Information of Chemicals and Proteins. PLoS ONE, 2012, 7, e45944.	2.5	49
94	Identification of hepatocellular carcinoma related genes with k-th shortest paths in a proteinâ€“protein interaction network. Molecular BioSystems, 2013, 9, 2720.	2.9	47
95	Identifying and analyzing different cancer subtypes using RNA-seq data of blood platelets. Oncotarget, 2017, 8, 87494-87511.	1.8	47
96	Predicting 22 protein localizations in budding yeast. Biochemical and Biophysical Research Communications, 2004, 323, 425-428.	2.1	46
97	ECS: An automatic enzyme classifier based on functional domain composition. Computational Biology and Chemistry, 2007, 31, 226-232.	2.3	46
98	Computational prediction and analysis of protein Î³-carboxylation sites based on a random forest method. Molecular BioSystems, 2012, 8, 2946.	2.9	46
99	Predicting Protein Phenotypes Based on Protein-Protein Interaction Network. PLoS ONE, 2011, 6, e17668.	2.5	44
100	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
101	Identification of Protein Subcellular Localization With Network and Functional Embeddings. Frontiers in Genetics, 2020, 11, 626500.	2.3	44
102	Analysis of Tumor Suppressor Genes Based on Gene Ontology and the KEGG Pathway. PLoS ONE, 2014, 9, e107202.	2.5	44
103	Support Vector Machines for Prediction of Protein Domain Structural Class. Journal of Theoretical Biology, 2003, 221, 115-120.	1.7	43
104	A Novel Computational Approach To Predict Transcription Factor DNA Binding Preference. Journal of Proteome Research, 2009, 8, 999-1003.	3.7	41
105	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
106	Prediction of Aptamer-Target Interacting Pairs with Pseudo-Amino Acid Composition. PLoS ONE, 2014, 9, e86729.	2.5	41
107	Prediction of Tyrosine Sulfation with mRMR Feature Selection and Analysis. Journal of Proteome Research, 2010, 9, 6490-6497.	3.7	40
108	Prediction of Body Fluids where Proteins are Secreted into Based on Protein Interaction Network. PLoS ONE, 2011, 6, e22989.	2.5	40

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109	Prediction of compoundsâ€™ biological function (metabolic pathways) based on functional group composition. Molecular Diversity, 2008, 12, 131-137.	3.9	39
110	HIV infection alters the human epigenetic landscape. Gene Therapy, 2019, 26, 29-39.	4.5	39
111	Multiple classifier integration for the prediction of protein structural classes. Journal of Computational Chemistry, 2009, 30, 2248-2254.	3.3	38
112	Prediction of Gene Phenotypes Based on GO and KEGG Pathway Enrichment Scores. BioMed Research International, 2013, 2013, 1-7.	1.9	38
113	Predicting Transcriptional Activity of Multiple Site p53 Mutants Based on Hybrid Properties. PLoS ONE, 2011, 6, e22940.	2.5	38
114	Predicting Heart Cell Types by Using Transcriptome Profiles and a Machine Learning Method. Life, 2022, 12, 228.	2.4	38
115	Is it a paradox or misinterpretation?. Proteins: Structure, Function and Bioinformatics, 2001, 43, 336-338.	2.6	37
116	Prediction and analysis of protein palmitoylation sites. Biochimie, 2011, 93, 489-496.	2.6	37
117	Prediction of Protein Cleavage Site with Feature Selection by Random Forest. PLoS ONE, 2012, 7, e45854.	2.5	37
118	Predicting A-to-I RNA Editing by Feature Selection and Random Forest. PLoS ONE, 2014, 9, e110607.	2.5	37
119	Identifying Methylation Pattern and Genes Associated with Breast Cancer Subtypes. International Journal of Molecular Sciences, 2019, 20, 4269.	4.1	37
120	Support Vector Machines for Prediction of Protein Subcellular Location. Molecular Cell Biology Research Communications: MCBRC: Part B of Biochemical and Biophysical Research Communications, 2000, 4, 230-233.	1.6	36
121	Classification of Non-Small Cell Lung Cancer Based on Copy Number Alterations. PLoS ONE, 2014, 9, e88300.	2.5	35
122	Prediction of subcellular protein localization based on functional domain composition. Biochemical and Biophysical Research Communications, 2007, 357, 366-370.	2.1	34
123	Identification of Genes Associated with Breast Cancer Metastasis to Bone on a Proteinâ€“Protein Interaction Network with a Shortest Path Algorithm. Journal of Proteome Research, 2017, 16, 1027-1038.	3.7	34
124	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
125	Demonstration of two novel methods for predicting functional siRNA efficiency. BMC Bioinformatics, 2006, 7, 271.	2.6	32
126	Prediction of Protein Subcellular Locations with Feature Selection and Analysis. Protein and Peptide Letters, 2010, 17, 464-472.	0.9	32

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127	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
128	Predicting RNA 5-Methylcytosine Sites by Using Essential Sequence Features and Distributions. BioMed Research International, 2022, 2022, 1-11.	1.9	32
129	Support vector machine for SAR/QSAR of phenethyl-amines. Acta Pharmacologica Sinica, 2007, 28, 1075-1086.	6.1	31
130	Prediction of active sites of enzymes by maximum relevance minimum redundancy (mRMR) feature selection. Molecular BioSystems, 2013, 9, 61-69.	2.9	31
131	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
132	Detecting the Multiomics Signatures of Factor-Specific Inflammatory Effects on Airway Smooth Muscles. Frontiers in Genetics, 2020, 11, 599970.	2.3	31
133	Finding Candidate Drugs for Hepatitis C Based on Chemical-Chemical and Chemical-Protein Interactions. PLoS ONE, 2014, 9, e107767.	2.5	31
134	Using Neural Networks for Prediction of Subcellular Location of Prokaryotic and Eukaryotic Proteins. Molecular Cell Biology Research Communications: MCBRC: Part B of Biochemical and Biophysical Research Communications, 2000, 4, 172-173.	1.6	30
135	Predicting N-terminal acetylation based on feature selection method. Biochemical and Biophysical Research Communications, 2008, 372, 862-865.	2.1	30
136	Prediction of Metabolic Pathway Using Graph Property, Chemical Functional Group and Chemical Structural Set. Current Bioinformatics, 2013, 8, 200-207.	1.5	30
137	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.	3.5	30
138	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
139	A novel approach to predict active sites of enzyme molecules. Proteins: Structure, Function and Bioinformatics, 2004, 55, 77-82.	2.6	29
140	Predicting the protein SUMO modification sites based on Properties Sequential Forward Selection (PSFS). Biochemical and Biophysical Research Communications, 2007, 358, 136-139.	2.1	29
141	A Comparison of Computational Methods for Identifying Virulence Factors. PLoS ONE, 2012, 7, e42517.	2.5	29
142	Prediction of Effective Drug Combinations by Chemical Interaction, Protein Interaction and Target Enrichment of KEGG Pathways. BioMed Research International, 2013, 2013, 1-10.	1.9	29
143	Data mining of the cancer-related lncRNAs GO terms and KEGG pathways by using mRMR method. Mathematical Biosciences, 2018, 304, 1-8.	1.9	29
144	Distinguishing Glioblastoma Subtypes by Methylation Signatures. Frontiers in Genetics, 2020, 11, 604336.	2.3	29

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145	Predicting Citrullination Sites in Protein Sequences Using mRMR Method and Random Forest Algorithm. Combinatorial Chemistry and High Throughput Screening, 2017, 20, 164-173.	1.1	29
146	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
147	Artificial Neural Network Model for Predicting Membrane Protein Types. Journal of Biomolecular Structure and Dynamics, 2001, 18, 607-610.	3.5	28
148	Protein sumoylation sites prediction based on two-stage feature selection. Molecular Diversity, 2010, 14, 81-86.	3.9	28
149	Analysis of Protein Pathway Networks Using Hybrid Properties. Molecules, 2010, 15, 8177-8192.	3.8	28
150	Identification of retinoblastoma related genes with shortest path in a proteinâ€“protein interaction network. Biochimie, 2012, 94, 1910-1917.	2.6	28
151	An Information-Theoretic Machine Learning Approach to Expression QTL Analysis. PLoS ONE, 2013, 8, e67899.	2.5	28
152	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
153	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
154	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
155	Investigating the gene expression profiles of cells in seven embryonic stages with machine learning algorithms. Genomics, 2020, 112, 2524-2534.	2.9	28
156	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
157	Artificial neural network model for predicting protein subcellular location. Computers & Chemistry, 2002, 26, 179-182.	1.2	27
158	Predicting Membrane Protein Types with Bagging Learner. Protein and Peptide Letters, 2008, 15, 590-594.	0.9	27
159	Identifying Protein Complexes Using Hybrid Properties. Journal of Proteome Research, 2009, 8, 5212-5218.	3.7	27
160	Prediction and analysis of protein methylarginine and methyllysine based on Multisequence features. Biopolymers, 2011, 95, 763-771.	2.4	27
161	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
162	Computational Methods for Protein-Protein Interaction and their Application. Current Protein and Peptide Science, 2005, 6, 443-449.	1.4	26

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163	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
164	Identifying protein subcellular locations with embeddings-based node2loc. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	26
165	Operon prediction based on SVM. Computational Biology and Chemistry, 2006, 30, 233-240.	2.3	25
166	Prediction of Small Molecules Metabolic Pathways Based on Functional Group Composition. Protein and Peptide Letters, 2009, 16, 969-976.	0.9	25
167	Predicting Chemical Toxicity Effects Based on Chemical-Chemical Interactions. PLoS ONE, 2013, 8, e56517.	2.5	25
168	Identification of transcription factors that may reprogram lung adenocarcinoma. Artificial Intelligence in Medicine, 2017, 83, 52-57.	6.5	25
169	Prediction of protein secondary structure content by artificial neural network. Journal of Computational Chemistry, 2003, 24, 727-731.	3.3	24
170	Prediction and Analysis of Protein Hydroxyproline and Hydroxylysine. PLoS ONE, 2010, 5, e15917.	2.5	24
171	Gene Ontology and KEGG Enrichment Analyses of Genes Related to Age-Related Macular Degeneration. BioMed Research International, 2014, 2014, 1-10.	1.9	24
172	Mining for novel tumor suppressor genes using a shortest path approach. Journal of Biomolecular Structure and Dynamics, 2016, 34, 664-675.	3.5	24
173	Identification of Cell Markers and Their Expression Patterns in Skin Based on Single-Cell RNA-Sequencing Profiles. Life, 2022, 12, 550.	2.4	24
174	Automatic transcription factor classifier based on functional domain composition. Biochemical and Biophysical Research Communications, 2006, 347, 141-144.	2.1	23
175	Prediction of interaction between small molecule and enzyme using AdaBoost. Molecular Diversity, 2009, 13, 313-320.	3.9	23
176	Computationally identifying virulence factors based on KEGG pathways. Molecular BioSystems, 2013, 9, 1447.	2.9	23
177	Predicting Drugs Side Effects Based on Chemical-Chemical Interactions and Protein-Chemical Interactions. BioMed Research International, 2013, 2013, 1-8.	1.9	23
178	A computational method for the identification of new candidate carcinogenic and non-carcinogenic chemicals. Molecular BioSystems, 2015, 11, 2541-2550.	2.9	23
179	Identifying novel protein phenotype annotations by hybridizing proteinâ€“protein interactions and protein sequence similarities. Molecular Genetics and Genomics, 2016, 291, 913-934.	2.1	23
180	An integrated method for the identification of novel genes related to oral cancer. PLoS ONE, 2017, 12, e0175185.	2.5	23

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181	A Computational Method for Classifying Different Human Tissues with Quantitatively Tissue-Specific Expressed Genes. Genes, 2018, 9, 449.	2.4	23
182	Primary Tumor Site Specificity is Preserved in Patient-Derived Tumor Xenograft Models. Frontiers in Genetics, 2019, 10, 738.	2.3	23
183	Using neural networks for prediction of domain structural classes. BBA - Proteins and Proteomics, 2000, 1476, 1-2.	2.1	22
184	HIVâ€1 protease cleavage site prediction based on amino acid property. Journal of Computational Chemistry, 2009, 30, 33-39.	3.3	22
185	GalNAc-transferase specificity prediction based on feature selection method. Peptides, 2009, 30, 359-364.	2.4	22
186	Exploring Mouse Protein Function via Multiple Approaches. PLoS ONE, 2016, 11, e0166580.	2.5	22
187	Classification of Transcription Factors Using Protein Primary Structure. Protein and Peptide Letters, 2010, 17, 899-908.	0.9	21
188	Prediction of RNA-Binding Proteins by Voting Systems. Journal of Biomedicine and Biotechnology, 2011, 2011, 1-8.	3.0	21
189	Predicting protein oxidation sites with feature selection and analysis approach. Journal of Biomolecular Structure and Dynamics, 2012, 29, 1154-1162.	3.5	21
190	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.	1.9	21
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