

# Yi-Ping Phoebe Chen

## List of Publications by Year in descending order

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261  
papers

4,951  
citations

109137

35  
h-index

128067

60  
g-index

280  
all docs

280  
docs citations

280  
times ranked

6115  
citing authors

#	ARTICLE	IF	CITATIONS
1	Association rule mining to detect factors which contribute to heart disease in males and females. Expert Systems With Applications, 2013, 40, 1086-1093.	4.4	352
2	Structure-based drug design to augment hit discovery. Drug Discovery Today, 2011, 16, 831-839.	3.2	223
3	Computational intelligence for heart disease diagnosis: A medical knowledge driven approach. Expert Systems With Applications, 2013, 40, 96-104.	4.4	195
4	Optimized Structure of the Traffic Flow Forecasting Model With a Deep Learning Approach. IEEE Transactions on Neural Networks and Learning Systems, 2017, 28, 2371-2381.	7.2	192
5	Widespread splicing changes in human brain development and aging. Molecular Systems Biology, 2013, 9, 633.	3.2	183
6	Acoustic feature selection for automatic emotion recognition from speech. Information Processing and Management, 2009, 45, 315-328.	5.4	153
7	Bacterial genomic G+C composition-eliciting environmental adaptation. Genomics, 2010, 95, 7-15.	1.3	143
8	A catalogue of novel bovine long noncoding RNA across 18 tissues. PLoS ONE, 2015, 10, e0141225.	1.1	130
9	Image based computer aided diagnosis system for cancer detection. Expert Systems With Applications, 2015, 42, 5356-5365.	4.4	115
10	Evaluation of deep learning in non-coding RNA classification. Nature Machine Intelligence, 2019, 1, 246-256.	8.3	105
11	Hybrid deep learning and empirical mode decomposition model for time series applications. Expert Systems With Applications, 2019, 120, 128-138.	4.4	79
12	Knowledge-Discounted Event Detection in Sports Video. IEEE Transactions on Systems, Man and Cybernetics, Part A: Systems and Humans, 2010, 40, 1009-1024.	3.4	76
13	Identification of protein complexes by integrating multiple alignment of protein interaction networks. Bioinformatics, 2017, 33, 1681-1688.	1.8	72
14	Identifying targets for drug discovery using bioinformatics. Expert Opinion on Therapeutic Targets, 2008, 12, 383-389.	1.5	70
15	Highlights for more complete sports video summarization. IEEE MultiMedia, 2004, 11, 22-37.	1.5	68
16	True real time pricing and combined power scheduling of electric appliances in residential energy management system. Applied Energy, 2016, 165, 592-600.	5.1	63
17	Potential therapeutic targets and the role of technology in developing novel antileishmanial drugs. Drug Discovery Today, 2015, 20, 958-968.	3.2	59
18	Optimized Configuration of Exponential Smoothing and Extreme Learning Machine for Traffic Flow Forecasting. IEEE Transactions on Industrial Informatics, 2019, 15, 23-34.	7.2	58

#	ARTICLE	IF	CITATIONS
19	ILDMSF: Inferring Associations Between Long Non-Coding RNA and Disease Based on Multi-Similarity Fusion. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1106-1112.	1.9	57
20	An evolutionary learning approach for adaptive negotiation agents. <i>International Journal of Intelligent Systems</i> , 2006, 21, 41-72.	3.3	56
21	Cell morphology based classification for red cells in blood smear images. <i>Pattern Recognition Letters</i> , 2014, 49, 155-161.	2.6	48
22	Regulatory and coding genome regions are enriched for trait associated variants in dairy and beef cattle. <i>BMC Genomics</i> , 2014, 15, 436.	1.2	47
23	LDICDL: LncRNA-Disease Association Identification Based on Collaborative Deep Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 1715-1723.	1.9	47
24	Machine learning on adverse drug reactions for pharmacovigilance. <i>Drug Discovery Today</i> , 2019, 24, 1332-1343.	3.2	44
25	Computational intelligence for microarray data and biomedical image analysis for the early diagnosis of breast cancer. <i>Expert Systems With Applications</i> , 2012, 39, 12371-12377.	4.4	43
26	Systematic review of virtual speech therapists for speech disorders. <i>Computer Speech and Language</i> , 2016, 37, 98-128.	2.9	42
27	Representation learning with extreme learning machines and empirical mode decomposition for wind speed forecasting methods. <i>Artificial Intelligence</i> , 2019, 277, 103176.	3.9	42
28	Prediction of drug adverse events using deep learning in pharmaceutical discovery. <i>Briefings in Bioinformatics</i> , 2021, 22, 1884-1901.	3.2	42
29	Evolutionary and ontogenetic changes in RNA editing in human, chimpanzee, and macaque brains. <i>Rna</i> , 2013, 19, 1693-1702.	1.6	41
30	Acoustic Features Extraction for Emotion Recognition. , 2007, , .		40
31	Energy based pharmacophore mapping of HDAC inhibitors against class I HDAC enzymes. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 317-328.	1.1	40
32	Exploring Inhibitor Release Pathways in Histone Deacetylases Using Random Acceleration Molecular Dynamics Simulations. <i>Journal of Chemical Information and Modeling</i> , 2012, 52, 589-603.	2.5	39
33	Data mining in lung cancer pathologic staging diagnosis: Correlation between clinical and pathology information. <i>Expert Systems With Applications</i> , 2015, 42, 6168-6176.	4.4	39
34	Significant Cancer Prevention Factor Extraction: An Association Rule Discovery Approach. <i>Journal of Medical Systems</i> , 2011, 35, 353-367.	2.2	38
35	Mining frequent patterns for AMP-activated protein kinase regulation on skeletal muscle. <i>BMC Bioinformatics</i> , 2006, 7, 394.	1.2	37
36	An evaluation of contemporary hidden Markov model gene finders with a predicted exon taxonomy. <i>Nucleic Acids Research</i> , 2007, 35, 317-324.	6.5	37

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37	Modelling and enhanced molecular dynamics to steer structure-based drug discovery. <i>Progress in Biophysics and Molecular Biology</i> , 2014, 114, 123-136.	1.4	36
38	Performance Assessment of Kernel Density Clustering for Gene Expression Profile Data. <i>Comparative and Functional Genomics</i> , 2003, 4, 287-299.	2.0	35
39	Discriminative binary feature learning and quantization in biometric key generation. <i>Pattern Recognition</i> , 2018, 77, 289-305.	5.1	33
40	KGANCUDA: predicting circRNA-disease associations based on knowledge graph attention network. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	33
41	Ransomware Mitigation in the Modern Era: A Comprehensive Review, Research Challenges, and Future Directions. <i>ACM Computing Surveys</i> , 2022, 54, 1-36.	16.1	32
42	Accelerated aging-related transcriptome changes in the female prefrontal cortex. <i>Aging Cell</i> , 2012, 11, 894-901.	3.0	31
43	Designing secure substitution boxes based on permutation of symmetric group. <i>Neural Computing and Applications</i> , 2020, 32, 7045-7056.	3.2	31
44	Sports video summarization using highlights and play-breaks. , 2003, , .		29
45	A steered molecular dynamics mediated hit discovery for histone deacetylases. <i>Physical Chemistry Chemical Physics</i> , 2014, 16, 3777.	1.3	28
46	Generative and Contrastive Self-Supervised Learning for Graph Anomaly Detection. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2023, 35, 12220-12233.	4.0	28
47	Ensuring privacy and security of genomic data and functionalities. <i>Briefings in Bioinformatics</i> , 2020, 21, 511-526.	3.2	27
48	CircR2Cancer: a manually curated database of associations between circRNAs and cancers. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	27
49	A Similarity Searching System for Biological Phenotype Images Using Deep Convolutional Encoder-decoder Architecture. <i>Current Bioinformatics</i> , 2019, 14, 628-639.	0.7	27
50	KERNEL-BASED NAIVE BAYES CLASSIFIER FOR BREAST CANCER PREDICTION. <i>Journal of Biological Systems</i> , 2007, 15, 17-25.	0.5	26
51	Descriptive prediction of drug side-effects using a hybrid deep learning model. <i>International Journal of Intelligent Systems</i> , 2021, 36, 2491-2510.	3.3	26
52	A comprehensive review of federated learning for COVID-19 detection. <i>International Journal of Intelligent Systems</i> , 2022, 37, 2371-2392.	3.3	24
53	A computationally efficient algorithm for genomic prediction using a Bayesian model. <i>Genetics Selection Evolution</i> , 2015, 47, 34.	1.2	23
54	Optimization of day-ahead and real-time prices for smart home community. <i>International Journal of Electrical Power and Energy Systems</i> , 2021, 124, 106403.	3.3	23

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55	DDR: an index method for large time-series datasets. <i>Information Systems</i> , 2005, 30, 333-348.	2.4	22
56	Development and application of a modified dynamic time warping algorithm (DTW-S) to analyses of primate brain expression time series. <i>BMC Bioinformatics</i> , 2011, 12, 347.	1.2	22
57	Quantum polarized ligand docking investigation to understand the significance of protonation states in histone deacetylase inhibitors. <i>Journal of Molecular Graphics and Modelling</i> , 2013, 44, 44-53.	1.3	22
58	Skin cancer extraction with optimum fuzzy thresholding technique. <i>Applied Intelligence</i> , 2014, 40, 415-426.	3.3	22
59	A novel decision strategy for a bilateral energy contract. <i>Applied Energy</i> , 2019, 253, 113571.	5.1	22
60	Machine learning for medical imaging-based COVID-19 detection and diagnosis. <i>International Journal of Intelligent Systems</i> , 2021, 36, 5085-5115.	3.3	22
61	Microarray Data Classification Using Automatic SVM Kernel Selection. <i>DNA and Cell Biology</i> , 2007, 26, 707-712.	0.9	21
62	Effectively Identifying Compound-Protein Interactions by Learning from Positive and Unlabeled Examples. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1832-1843.	1.9	21
63	Structural Network Embedding using Multi-modal Deep Auto-encoders for Predicting Drug-drug Interactions. , 2019, , .		21
64	The power of play-break for automatic detection and browsing of self-consumable sport video highlights. , 2004, , .		20
65	IDENTIFYING CO-REGULATING MICRORNA GROUPS. <i>Journal of Bioinformatics and Computational Biology</i> , 2010, 08, 99-115.	0.3	20
66	A template-free machine vision-based crop row detection algorithm. <i>Precision Agriculture</i> , 2021, 22, 124-153.	3.1	20
67	Variance explained by whole genome sequence variants in coding and regulatory genome annotations for six dairy traits. <i>BMC Genomics</i> , 2018, 19, 237.	1.2	19
68	Content-Based Indexing and Retrieval Using MPEG-7 and X-Query in Video Data Management Systems. <i>World Wide Web</i> , 2002, 5, 207-227.	2.7	18
69	A pHMM-ANN based discriminative approach to promoter identification in prokaryote genomic contexts. <i>Nucleic Acids Research</i> , 2007, 35, e12-e12.	6.5	18
70	GI-POP: A combinational annotation and genomic island prediction pipeline for ongoing microbial genome projects. <i>Gene</i> , 2013, 518, 114-123.	1.0	18
71	A hybrid expectation maximisation and MCMC sampling algorithm to implement Bayesian mixture model based genomic prediction and QTL mapping. <i>BMC Genomics</i> , 2016, 17, 744.	1.2	18
72	Enhancing the Quality of Image Tagging Using a Visio-Textual Knowledge Base. <i>IEEE Transactions on Multimedia</i> , 2020, 22, 897-911.	5.2	18

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73	Semantic and layered protein function prediction from PPI networks. <i>Journal of Theoretical Biology</i> , 2010, 267, 129-136.	0.8	17
74	Genetic variation of the hemagglutinin of avian influenza virus H9N2. <i>Journal of Medical Virology</i> , 2011, 83, 838-846.	2.5	17
75	Bioinformatics in protein kinases regulatory network and drug discovery. <i>Mathematical Biosciences</i> , 2015, 262, 147-156.	0.9	17
76	Application of a Bayesian non-linear model hybrid scheme to sequence data for genomic prediction and QTL mapping. <i>BMC Genomics</i> , 2017, 18, 618.	1.2	17
77	Probing the structure of <i>Leishmania major</i> DHFR TS and structure based virtual screening of peptide library for the identification of anti-leishmanial leads. <i>Journal of Molecular Modeling</i> , 2012, 18, 4089-4100.	0.8	16
78	Ligand release mechanisms and channels in histone deacetylases. <i>Journal of Computational Chemistry</i> , 2013, 34, 2270-2283.	1.5	16
79	MDSM: Microarray database schema matching using the Hungarian method. <i>Information Sciences</i> , 2006, 176, 2771-2790.	4.0	15
80	Detecting inconsistency in biological molecular databases using ontologies. <i>Data Mining and Knowledge Discovery</i> , 2007, 15, 275-296.	2.4	15
81	Discovery of Structural and Functional Features in RNA Pseudoknots. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2009, 21, 974-984.	4.0	14
82	Compensatory ability to null mutation in metabolic networks. <i>Biotechnology and Bioengineering</i> , 2009, 103, 361-369.	1.7	14
83	Prediction of pre-miRNA with multiple stem-loops using pruning algorithm. <i>Computers in Biology and Medicine</i> , 2013, 43, 409-416.	3.9	14
84	Model-based approach to spatial-temporal sampling of video clips for video object detection by classification. <i>Journal of Visual Communication and Image Representation</i> , 2014, 25, 1018-1030.	1.7	14
85	Recent advances in sequence assembly: principles and applications. <i>Briefings in Functional Genomics</i> , 2017, 16, 361-378.	1.3	14
86	Feature selection and threshold method based on fuzzy joint mutual information. <i>International Journal of Approximate Reasoning</i> , 2021, 132, 107-126.	1.9	14
87	Using Bioinformatics Techniques for Gene Identification in Drug Discovery and Development. <i>Current Drug Metabolism</i> , 2008, 9, 567-573.	0.7	14
88	Candidate working set strategy based SMO algorithm in support vector machine. <i>Information Processing and Management</i> , 2009, 45, 584-592.	5.4	13
89	IGNSCDA: Predicting CircRNA-Disease Associations Based on Improved Graph Convolutional Network and Negative Sampling. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, PP, 1-1.	1.9	13
90	Network-based methods for gene function prediction. <i>Briefings in Functional Genomics</i> , 2021, 20, 249-257.	1.3	13

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91	Classification of Diabetic Retinopathy Severity Based on GCA Attention Mechanism. IEEE Access, 2022, 10, 2729-2739.	2.6	13
92	Content-based video indexing for sports applications using integrated multi-modal approach. , 2005, , .		12
93	The Competitive Model Based on the Demand Response in the Off-Peak Period for the Taipower System. IEEE Transactions on Industry Applications, 2008, 44, 1303-1307.	3.3	12
94	SSET: a dataset for shot segmentation, event detection, player tracking in soccer videos. Multimedia Tools and Applications, 2020, 79, 28971-28992.	2.6	12
95	Perceptual image hashing using transform domain noise resistant local binary pattern. Multimedia Tools and Applications, 2021, 80, 9849-9875.	2.6	12
96	Dynamic user-centric access control for detection of ransomware attacks. Computers and Security, 2021, 111, 102461.	4.0	12
97	Identification of Important Positions within miRNAs by Integrating Sequential and Structural Features. Current Protein and Peptide Science, 2014, 15, 591-597.	0.7	12
98	Fuzzy joint mutual information feature selection based on ideal vector. Expert Systems With Applications, 2022, 193, 116453.	4.4	12
99	A novel explainable neural network for Alzheimer's disease diagnosis. Pattern Recognition, 2022, 131, 108876.	5.1	12
100	External Sorting on Flash Memory Via Natural Page Run Generation. Computer Journal, 2011, 54, 1882-1990.	1.5	11
101	Cell cycle phase detection with cell deformation analysis. Expert Systems With Applications, 2014, 41, 2644-2651.	4.4	11
102	Pairwise RNA secondary structure alignment with conserved stem pattern. Bioinformatics, 2015, 31, 3914-3921.	1.8	11
103	Enforcing situation-aware access control to build malware-resilient file systems. Future Generation Computer Systems, 2021, 115, 568-582.	4.9	11
104	Interval-based distance function for identifying RNA structure candidates. Journal of Theoretical Biology, 2011, 269, 280-286.	0.8	10
105	MCJoin. , 2012, , .		10
106	Predicting miRNA-mediated gene silencing mode based on miRNA-target duplex features. Computers in Biology and Medicine, 2012, 42, 1-7.	3.9	10
107	The Tenth Asia Pacific Bioinformatics Conference (APBC 2012). BMC Genomics, 2012, 13, 11.	1.2	10
108	Computational developments in microRNA-regulated protein-protein interactions. BMC Systems Biology, 2014, 8, 14.	3.0	10

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109	Changes in snoRNA and snRNA abundance in the human, chimpanzee, macaque and mouse brain. <i>Genome Biology and Evolution</i> , 2016, 8, evw038.	1.1	10
110	Exploring Consensus RNA Substructural Patterns Using Subgraph Mining. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 1134-1146.	1.9	10
111	Ensemble Fuzzy Feature Selection Based on Relevancy, Redundancy, and Dependency Criteria. <i>Entropy</i> , 2020, 22, 757.	1.1	10
112	New Insights Into Drug Repurposing for COVID-19 Using Deep Learning. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2021, 32, 4770-4780.	7.2	10
113	Finding rule groups to classify high dimensional gene expression datasets. <i>Computational Biology and Chemistry</i> , 2009, 33, 108-113.	1.1	9
114	GHT-based associative memory learning and its application to Human action detection and classification. <i>Pattern Recognition</i> , 2013, 46, 3117-3128.	5.1	9
115	k-Partite cliques of protein interactions: A novel subgraph topology for functional coherence analysis on PPI networks. <i>Journal of Theoretical Biology</i> , 2014, 340, 146-154.	0.8	9
116	A database of simulated tumor genomes towards accurate detection of somatic small variants in cancer. <i>PLoS ONE</i> , 2018, 13, e0202982.	1.1	9
117	Multi-Classes and Motion Properties for Concurrent Visual SLAM in Dynamic Environments. <i>IEEE Transactions on Multimedia</i> , 2022, 24, 3947-3960.	5.2	9
118	A Hybrid Framework Using SOM and Fuzzy Theory for Textual Classification in Data Mining. <i>Lecture Notes in Computer Science</i> , 2003, , 153-167.	1.0	9
119	Image Retrieval for Complex Queries Using Knowledge Embedding. <i>ACM Transactions on Multimedia Computing, Communications and Applications</i> , 2020, 16, 1-23.	3.0	9
120	A dimensionality reduction algorithm and its application for interactive visualization. <i>Journal of Visual Languages and Computing</i> , 2007, 18, 48-70.	1.8	8
121	A scalable and extensible segment-event-object-based sports video retrieval system. <i>ACM Transactions on Multimedia Computing, Communications and Applications</i> , 2008, 4, 1-40.	3.0	8
122	Comparative study of computational methods to detect the correlated reaction sets in biochemical networks. <i>Briefings in Bioinformatics</i> , 2011, 12, 132-150.	3.2	8
123	A comprehensive study of RNA secondary structure alignment algorithms. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw009.	3.2	8
124	GCOTraj: A storage approach for historical trajectory data sets using grid cells ordering. <i>Information Sciences</i> , 2018, 459, 1-19.	4.0	8
125	Conformational Features of Topologically Classified RNA Secondary Structures. <i>PLoS ONE</i> , 2012, 7, e39907.	1.1	8
126	Machine Learning in Bioinformatics. , 2005, , 117-153.		7



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127	Rule-based dependency models for security protocol analysis. <i>Integrated Computer-Aided Engineering</i> , 2008, 15, 369-380.	2.5	7
128	Analysis on relationship between extreme pathways and correlated reaction sets. <i>BMC Bioinformatics</i> , 2009, 10, S58.	1.2	7
129	Using propensity scores to predict the kinases of unannotated phosphopeptides. <i>Knowledge-Based Systems</i> , 2017, 135, 60-76.	4.0	7
130	Research on folding diversity in statistical learning methods for RNA secondary structure prediction. <i>International Journal of Biological Sciences</i> , 2018, 14, 872-882.	2.6	7
131	Comprehensive structured knowledge base system construction with natural language presentation. <i>Human-centric Computing and Information Sciences</i> , 2019, 9, .	6.1	7
132	Using machine learning to predict health-related quality of life outcomes in patients with low grade glioma, meningioma, and acoustic neuroma. <i>PLoS ONE</i> , 2022, 17, e0267931.	1.1	7
133	A Proposed Strategy Based on Instructional Design Models through an LMS to Develop Online Learning in Higher Education Considering the Lockdown Period of the COVID-19 Pandemic. <i>Sustainability</i> , 2022, 14, 7843.	1.6	7
134	Classification of self-consumable highlights for soccer video summaries. , 0, , .		6
135	Finding edging genes from microarray data. <i>Journal of Biotechnology</i> , 2008, 135, 233-240.	1.9	6
136	Exploring Cross-Species-Related miRNAs Based on Sequence and Secondary Structure. <i>IEEE Transactions on Biomedical Engineering</i> , 2010, 57, 1547-1553.	2.5	6
137	Metabolic classification of microbial genomes using functional probes. <i>BMC Genomics</i> , 2012, 13, 157.	1.2	6
138	Efficient Conversion of RNA Pseudoknots to Knot-Free Structures Using a Graphical Model. <i>IEEE Transactions on Biomedical Engineering</i> , 2015, 62, 1265-1271.	2.5	6
139	Interval-Based Similarity for Classifying Conserved RNA Secondary Structures. <i>IEEE Intelligent Systems</i> , 2016, 31, 78-85.	4.0	6
140	Using object and trajectory analysis to facilitate indexing and retrieval of video. <i>Knowledge-Based Systems</i> , 2006, 19, 639-646.	4.0	5
141	Spherical Harmonics and Distance Transform for Image Representation and Retrieval. <i>Lecture Notes in Computer Science</i> , 2009, , 309-316.	1.0	5
142	Feasible Strategy for Allocating Cost of Primary Frequency Regulation. <i>IEEE Transactions on Power Systems</i> , 2009, 24, 508-515.	4.6	5
143	Modeling Conserved Structure Patterns for Functional Noncoding RNA. <i>IEEE Transactions on Biomedical Engineering</i> , 2011, 58, 1528-1533.	2.5	5
144	Workload-Based Ordering of Multi-Dimensional Data. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2016, 28, 831-844.	4.0	5

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145	TC-GAN. , 2019, , .		5
146	A novel multimodal clustering framework for images with diverse associated text. Multimedia Tools and Applications, 2019, 78, 17623-17652.	2.6	5
147	Tracking Neutrophil Migration in Zebrafish Model Using Multi-Channel Feature Learning. IEEE Journal of Biomedical and Health Informatics, 2021, 25, 1197-1205.	3.9	5
148	FexRNA: Exploratory Data Analysis and Feature Selection of Non-Coding RNA. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2795-2801.	1.9	5
149	A New Method for Extracting Individual Plant Bio-Characteristics from High-Resolution Digital Images. Remote Sensing, 2021, 13, 1212.	1.8	5
150	A New Indexing Method for High Dimensional Dataset. Lecture Notes in Computer Science, 2005, , 385-397.	1.0	5
151	Database Technologies for L-System Simulations in Virtual Plant Applications on Bioinformatics. Knowledge and Information Systems, 2003, 5, 288-314.	2.1	4
152	Microarray Data Analysis. , 2005, , 353-388.		4
153	Keyword extraction for text categorization. , 0, , .		4
154	CIDB: Chlamydia Interactive Database for cross-querying genomics, transcriptomics and proteomics data. New Biotechnology, 2007, 24, 603-608.	2.7	4
155	High Functional Coherence in k-Partite Protein Cliques of Protein Interaction Networks. , 2009, , .		4
156	Spectral shape descriptor using spherical harmonics. Integrated Computer-Aided Engineering, 2010, 17, 167-173.	2.5	4
157	Discovering Inhibition Pathways for Protein Kinases. IEEE Intelligent Systems, 2012, 27, 19-26.	4.0	4
158	Exploiting multi-layered information to iteratively predict protein functions. Mathematical Biosciences, 2012, 236, 108-116.	0.9	4
159	Dynamically predicting protein functions from semantic associations of proteins. Network Modeling Analysis in Health Informatics and Bioinformatics, 2013, 2, 175-183.	1.2	4
160	Semantically predicting protein functions based on protein functional connectivity. Computational Biology and Chemistry, 2013, 44, 9-14.	1.1	4
161	Identification of well-differentiated gene expressions between Han Chinese and Japanese using genome-wide microarray data analysis. Journal of Medical Genetics, 2013, 50, 534-542.	1.5	4
162	SeTPR*-tree: Efficient Buffering for Spatiotemporal Indexes Via Shared Execution. Computer Journal, 2013, 56, 115-137.	1.5	4

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163	Computer-Based Rehabilitation for Developing Speech and Language in Hearing-Impaired Children: A Systematic Review. <i>Deafness and Education International</i> , 2015, 17, 111-119.	0.8	4
164	Detection of Cell Types from Single-cell RNA-seq Data using Similarity via Kernel Preserving Learning Embedding. , 2019, , .		4
165	Survey of Network Embedding for Drug Analysis and Prediction. <i>Current Protein and Peptide Science</i> , 2021, 22, 237-250.	0.7	4
166	INTERACTING AMINO ACID PREFERENCES OF 3D PATTERN PAIRS AT THE BINDING SITES OF TRANSIENT AND OBLIGATE PROTEIN COMPLEXES. , 2007, , .		4
167	Using Decision-Tree to Automatically Construct Learned-Heuristics for Events Classification in Sports Video. , 2006, , .		3
168	Early Breast Cancer Identification: Which Way to Go? Microarray or Image Based Computer Aided Diagnosis!. , 2009, , .		3
169	Insights into Bacterial Genome Composition through Variable Target GC Content Profiling. <i>Journal of Computational Biology</i> , 2010, 17, 79-96.	0.8	3
170	Function Annotation for Pseudoknot Using Structure Similarity. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 1535-1544.	1.9	3
171	Mining Protein Kinases Regulation Using Graphical Models. <i>IEEE Transactions on Nanobioscience</i> , 2011, 10, 1-8.	2.2	3
172	Ranking inter-relationships between clusters. <i>International Journal of Systems Science</i> , 2011, 42, 2071-2083.	3.7	3
173	A Scheduling Method to Reduce Waiting Time for Close-Range Broadcasting. <i>Mobile Information Systems</i> , 2012, 8, 303-314.	0.4	3
174	Using Dead Ants to improve the robustness and adaptability of AntNet routing algorithm. <i>Journal of Network and Computer Applications</i> , 2014, 44, 196-211.	5.8	3
175	PaMeCo join: A parallel main memory compact hash join. <i>Information Systems</i> , 2016, 58, 105-125.	2.4	3
176	Linguistic Patterns and Cross Modality-based Image Retrieval for Complex Queries. , 2018, , .		3
177	Genetic source completeness of HIV-1 circulating recombinant forms (CRFs) predicted by multi-label learning. <i>Bioinformatics</i> , 2021, 37, 750-758.	1.8	3
178	MedFused: A framework to discover the relationships between drug chemical functional group impacts and side effects. <i>Computers in Biology and Medicine</i> , 2021, 133, 104361.	3.9	3
179	Tracking leukocytes in intravital time lapse images using 3D cell association learning network. <i>Artificial Intelligence in Medicine</i> , 2021, 118, 102129.	3.8	3
180	Shot Boundary Detection Through Multi-stage Deep Convolution Neural Network. <i>Lecture Notes in Computer Science</i> , 2021, , 456-468.	1.0	3

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181	ANNODA: Tool for integrating Molecular-biological Annotation Data. , 2005, , .		2
182	Microarray Classification and Rule Based Cancer Identification. , 2007, , .		2
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