

Yi-Ping Phoebe Chen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4369599/publications.pdf>

Version: 2024-02-01

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	Generative and Contrastive Self-Supervised Learning for Graph Anomaly Detection. IEEE Transactions on Knowledge and Data Engineering, 2023, 35, 12220-12233.	4.0	28
2	LDICDL: LncRNA-Disease Association Identification Based on Collaborative Deep Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1715-1723.	1.9	47
3	Multi-Classifiers and Motion Properties for Concurrent Visual SLAM in Dynamic Environments. IEEE Transactions on Multimedia, 2022, 24, 3947-3960.	5.2	9
4	Ransomware Mitigation in the Modern Era: A Comprehensive Review, Research Challenges, and Future Directions. ACM Computing Surveys, 2022, 54, 1-36.	16.1	32
5	KGANCD: predicting circRNA-disease associations based on knowledge graph attention network. Briefings in Bioinformatics, 2022, 23, .	3.2	33
6	Classification of Diabetic Retinopathy Severity Based on GCA Attention Mechanism. IEEE Access, 2022, 10, 2729-2739.	2.6	13
7	Fuzzy joint mutual information feature selection based on ideal vector. Expert Systems With Applications, 2022, 193, 116453.	4.4	12
8	A Fast and More Accurate Seed-and-Extension Density-based Clustering Algorithm. IEEE Transactions on Knowledge and Data Engineering, 2022, , 1-1.	4.0	1
9	A comprehensive review of federated learning for COVID-19 detection. International Journal of Intelligent Systems, 2022, 37, 2371-2392.	3.3	24
10	Using machine learning to predict health-related quality of life outcomes in patients with low grade glioma, meningioma, and acoustic neuroma. PLoS ONE, 2022, 17, e0267931.	1.1	7
11	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. Sustainability, 2022, 14, 7843.	1.6	7
12	A novel explainable neural network for Alzheimer's disease diagnosis. Pattern Recognition, 2022, 131, 108876.	5.1	12
13	Prediction of drug adverse events using deep learning in pharmaceutical discovery. Briefings in Bioinformatics, 2021, 22, 1884-1901.	3.2	42
14	Reply to: LncADeep performance on full-length transcripts. Nature Machine Intelligence, 2021, 3, 196-196.	8.3	1
15	A template-free machine vision-based crop row detection algorithm. Precision Agriculture, 2021, 22, 124-153.	3.1	20
16	Genetic source completeness of HIV-1 circulating recombinant forms (CRFs) predicted by multi-label learning. Bioinformatics, 2021, 37, 750-758.	1.8	3
17	Optimization of day-ahead and real-time prices for smart home community. International Journal of Electrical Power and Energy Systems, 2021, 124, 106403.	3.3	23
18	Perceptual image hashing using transform domain noise resistant local binary pattern. Multimedia Tools and Applications, 2021, 80, 9849-9875.	2.6	12

#	ARTICLE	IF	CITATIONS
19	Enforcing situation-aware access control to build malware-resilient file systems. <i>Future Generation Computer Systems</i> , 2021, 115, 568-582.	4.9	11
20	Tracking Neutrophil Migration in Zebrafish Model Using Multi-Channel Feature Learning. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021, 25, 1197-1205.	3.9	5
21	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
22	FexRNA: Exploratory Data Analysis and Feature Selection of Non-Coding RNA. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2795-2801.	1.9	5
23	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
24	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
25	A New Method for Extracting Individual Plant Bio-Characteristics from High-Resolution Digital Images. <i>Remote Sensing</i> , 2021, 13, 1212.	1.8	5
26	Network-based methods for gene function prediction. <i>Briefings in Functional Genomics</i> , 2021, 20, 249-257.	1.3	13
27	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
28	Mortality Prediction of Patients With Cardiovascular Disease Using Medical Claims Data Under Artificial Intelligence Architectures: Validation Study. <i>JMIR Medical Informatics</i> , 2021, 9, e25000.	1.3	2
29	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
30	Survey of Network Embedding for Drug Analysis and Prediction. <i>Current Protein and Peptide Science</i> , 2021, 22, 237-250.	0.7	4
31	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
32	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
33	Multi-Directional Convolution Networks with Spatial-Temporal Feature Pyramid Module for Action Recognition. , 2021, , .		0
34	Concept-based Topic Attention for a Convolutional Sequence Document Summarization Model. , 2021, , .		0
35	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
36	Distractor-Aware Tracker with a Domain-Special Optimized Benchmark for Soccer Player Tracking. , 2021, , .		2

#	ARTICLE	IF	CITATIONS
37	Editorial: Graph Embedding Methods for Multiple-Omics Data Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 762274.	1.1	0
38	Joint knowledge-powered topic level attention for a convolutional text summarization model. <i>Knowledge-Based Systems</i> , 2021, 228, 107273.	4.0	2
39	Dynamic user-centric access control for detection of ransomware attacks. <i>Computers and Security</i> , 2021, 111, 102461.	4.0	12
40	Shot Boundary Detection Through Multi-stage Deep Convolution Neural Network. <i>Lecture Notes in Computer Science</i> , 2021, , 456-468.	1.0	3
41	Guest Editorial for the 17th Asia Pacific Bioinformatics Conference. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2123-2124.	1.9	0
42	Ensuring privacy and security of genomic data and functionalities. <i>Briefings in Bioinformatics</i> , 2020, 21, 511-526.	3.2	27
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	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
45	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
46	Ensemble Fuzzy Feature Selection Based on Relevancy, Redundancy, and Dependency Criteria. <i>Entropy</i> , 2020, 22, 757.	1.1	10
47	SSET: a dataset for shot segmentation, event detection, player tracking in soccer videos. <i>Multimedia Tools and Applications</i> , 2020, 79, 28971-28992.	2.6	12
48	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
49	Fine-Grain Level Sports Video Search Engine. <i>Lecture Notes in Computer Science</i> , 2020, , 519-531.	1.0	0
50	A Human-Machine Language Dictionary. <i>International Journal of Computational Intelligence Systems</i> , 2020, 13, 904.	1.6	1
51	Guest Editorial for the 16th Asia Pacific Bioinformatics Conference. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1-2.	1.9	0
52	A novel decision strategy for a bilateral energy contract. <i>Applied Energy</i> , 2019, 253, 113571.	5.1	22
53	TC-GAN. , 2019, , .		5
54	Comprehensive structured knowledge base system construction with natural language presentation. <i>Human-centric Computing and Information Sciences</i> , 2019, 9, .	6.1	7

#	ARTICLE	IF	CITATIONS
55	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
56	A novel multimodal clustering framework for images with diverse associated text. <i>Multimedia Tools and Applications</i> , 2019, 78, 17623-17652.	2.6	5
57	Evaluation of deep learning in non-coding RNA classification. <i>Nature Machine Intelligence</i> , 2019, 1, 246-256.	8.3	105
58	Machine learning on adverse drug reactions for pharmacovigilance. <i>Drug Discovery Today</i> , 2019, 24, 1332-1343.	3.2	44
59	Structural Network Embedding using Multi-modal Deep Auto-encoders for Predicting Drug-drug Interactions. , 2019, , .		21
60	Detection of Cell Types from Single-cell RNA-seq Data using Similarity via Kernel Preserving Learning Embedding. , 2019, , .		4
61	Hybrid deep learning and empirical mode decomposition model for time series applications. <i>Expert Systems With Applications</i> , 2019, 120, 128-138.	4.4	79
62	Optimized Configuration of Exponential Smoothing and Extreme Learning Machine for Traffic Flow Forecasting. <i>IEEE Transactions on Industrial Informatics</i> , 2019, 15, 23-34.	7.2	58
63	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
64	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
65	Guest Editorial for the 14 th Asia Pacific Bioinformatics Conference. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 396-397.	1.9	0
66	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
67	Discriminative binary feature learning and quantization in biometric key generation. <i>Pattern Recognition</i> , 2018, 77, 289-305.	5.1	33
68	Guest Editorial for the 15th Asia Pacific Bioinformatics Conference. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1513-1514.	1.9	0
69	Smooth point matching based on SIFT. , 2018, , .		1
70	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
71	Linguistic Patterns and Cross Modality-based Image Retrieval for Complex Queries. , 2018, , .		3
72	GCOTraj: A storage approach for historical trajectory data sets using grid cells ordering. <i>Information Sciences</i> , 2018, 459, 1-19.	4.0	8

#	ARTICLE	IF	CITATIONS
73	Research on folding diversity in statistical learning methods for RNA secondary structure prediction. International Journal of Biological Sciences, 2018, 14, 872-882.	2.6	7
74	Large-scale frequent stem pattern mining in RNA families. Journal of Theoretical Biology, 2018, 455, 131-139.	0.8	0
75	A comprehensive study of RNA secondary structure alignment algorithms. Briefings in Bioinformatics, 2017, 18, bbw009.	3.2	8
76	TACD: a transportable ant colony discrimination model for corporate bankruptcy prediction. Enterprise Information Systems, 2017, 11, 758-785.	3.3	2
77	Exploring Consensus RNA Substructural Patterns Using Subgraph Mining. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1134-1146.	1.9	10
78	Identification of protein complexes by integrating multiple alignment of protein interaction networks. Bioinformatics, 2017, 33, 1681-1688.	1.8	72
79	Recent advances in sequence assembly: principles and applications. Briefings in Functional Genomics, 2017, 16, 361-378.	1.3	14
80	Using propensity scores to predict the kinases of unannotated phosphopeptides. Knowledge-Based Systems, 2017, 135, 60-76.	4.0	7
81	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
82	Exploiting visual and textual neighborhood information to improve image-tag relevance. , 2017, , .		2
83	Application of a Bayesian non-linear model hybrid scheme to sequence data for genomic prediction and QTL mapping. BMC Genomics, 2017, 18, 618.	1.2	17
84	A hybrid expectation maximisation and MCMC sampling algorithm to implement Bayesian mixture model based genomic prediction and QTL mapping. BMC Genomics, 2016, 17, 744.	1.2	18
85	Changes in snoRNA and snRNA abundance in the human, chimpanzee, macaque and mouse brain. Genome Biology and Evolution, 2016, 8, evw038.	1.1	10
86	Interval-Based Similarity for Classifying Conserved RNA Secondary Structures. IEEE Intelligent Systems, 2016, 31, 78-85.	4.0	6
87	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
88	Workload-Based Ordering of Multi-Dimensional Data. IEEE Transactions on Knowledge and Data Engineering, 2016, 28, 831-844.	4.0	5
89	PaMeCo join: A parallel main memory compact hash join. Information Systems, 2016, 58, 105-125.	2.4	3
90	Systematic review of virtual speech therapists for speech disorders. Computer Speech and Language, 2016, 37, 98-128.	2.9	42

#	ARTICLE	IF	CITATIONS
91	A computationally efficient algorithm for genomic prediction using a Bayesian model. <i>Genetics Selection Evolution</i> , 2015, 47, 34.	1.2	23
92	A catalogue of novel bovine long noncoding RNA across 18 tissues. <i>PLoS ONE</i> , 2015, 10, e0141225.	1.1	130
93	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
94	Bioinformatics in protein kinases regulatory network and drug discovery. <i>Mathematical Biosciences</i> , 2015, 262, 147-156.	0.9	17
95	Image based computer aided diagnosis system for cancer detection. <i>Expert Systems With Applications</i> , 2015, 42, 5356-5365.	4.4	115
96	Editorial. <i>Computational Biology and Chemistry</i> , 2015, 57, 1-2.	1.1	0
97	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
98	Potential therapeutic targets and the role of technology in developing novel antileishmanial drugs. <i>Drug Discovery Today</i> , 2015, 20, 958-968.	3.2	59
99	Pairwise RNA secondary structure alignment with conserved stem pattern. <i>Bioinformatics</i> , 2015, 31, 3914-3921.	1.8	11
100	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
101	Evaluation of Recent Computational Approaches in Short-Term Traffic Forecasting. <i>IFIP Advances in Information and Communication Technology</i> , 2015, , 108-116.	0.5	2
102	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
103	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
104	Subdividing globally important zones based on data distribution across multiple genome fragments. <i>Computers in Biology and Medicine</i> , 2014, 48, 109-118.	3.9	0
105	Cell cycle phase detection with cell deformation analysis. <i>Expert Systems With Applications</i> , 2014, 41, 2644-2651.	4.4	11
106	Computational developments in microRNA-regulated protein-protein interactions. <i>BMC Systems Biology</i> , 2014, 8, 14.	3.0	10
107	Skin cancer extraction with optimum fuzzy thresholding technique. <i>Applied Intelligence</i> , 2014, 40, 415-426.	3.3	22
108	A steered molecular dynamics mediated hit discovery for histone deacetylases. <i>Physical Chemistry Chemical Physics</i> , 2014, 16, 3777.	1.3	28

#	ARTICLE	IF	CITATIONS
109	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
110	Cell morphology based classification for red cells in blood smear images. <i>Pattern Recognition Letters</i> , 2014, 49, 155-161.	2.6	48
111	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
112	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
113	Determining common insertion sites based on retroviral insertion distribution across tumors. <i>Computational Biology and Chemistry</i> , 2014, 51, 83-92.	1.1	0
114	Advances in bioinformatics: Selected papers from APBC 2014. <i>Computational Biology and Chemistry</i> , 2014, 50, 1-2.	1.1	0
115	Guest editorial for the 12th Asia Pacific Bioinformatics Conference. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 614-615.	1.9	0
116	Conjoint Mining of Data and Content with Applications in Business, Bio-medicine, Transport Logistics and Electrical Power Systems. <i>Lecture Notes in Computer Science</i> , 2014, , 1-19.	1.0	2
117	Identification of Important Positions within miRNAs by Integrating Sequential and Structural Features. <i>Current Protein and Peptide Science</i> , 2014, 15, 591-597.	0.7	12
118	Dynamically predicting protein functions from semantic associations of proteins. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2013, 2, 175-183.	1.2	4
119	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
120	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
121	Semantically predicting protein functions based on protein functional connectivity. <i>Computational Biology and Chemistry</i> , 2013, 44, 9-14.	1.1	4
122	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
123	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
124	Association rule mining to detect factors which contribute to heart disease in males and females. <i>Expert Systems With Applications</i> , 2013, 40, 1086-1093.	4.4	352
125	Computational intelligence for heart disease diagnosis: A medical knowledge driven approach. <i>Expert Systems With Applications</i> , 2013, 40, 96-104.	4.4	195
126	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

#	ARTICLE	IF	CITATIONS
127	Evolutionary and ontogenetic changes in RNA editing in human, chimpanzee, and macaque brains. <i>Rna</i> , 2013, 19, 1693-1702.	1.6	41
128	Identification of well-differentiated gene expressions between Han Chinese and Japanese using genome-wide microarray data analysis. <i>Journal of Medical Genetics</i> , 2013, 50, 534-542.	1.5	4
129	SeTPR*-tree: Efficient Buffering for Spatiotemporal Indexes Via Shared Execution. <i>Computer Journal</i> , 2013, 56, 115-137.	1.5	4
130	Ligand release mechanisms and channels in histone deacetylases. <i>Journal of Computational Chemistry</i> , 2013, 34, 2270-2283.	1.5	16
131	Widespread splicing changes in human brain development and aging. <i>Molecular Systems Biology</i> , 2013, 9, 633.	3.2	183
132	Guest Editorial: Advanced Algorithms of Bioinformatics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 273-273.	1.9	1
133	Select Cluster Features for Better Layered Protein Function Prediction. <i>Current Bioinformatics</i> , 2013, 9, 306-314.	0.7	1
134	MCJoin. , 2012, , .		10
135	A Scheduling Method for Node Relay-based Webcast Considering Reconnection. , 2012, , .		2
136	Reordering video shots for event classification using bag-of-words models and string kernels. , 2012, , .		1
137	Guest Editorial: Application and Development of Bioinformatics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1265-1265.	1.9	0
138	Accelerated aging-related transcriptome changes in the female prefrontal cortex. <i>Aging Cell</i> , 2012, 11, 894-901.	3.0	31
139	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
140	Discovering Inhibition Pathways for Protein Kinases. <i>IEEE Intelligent Systems</i> , 2012, 27, 19-26.	4.0	4
141	Exploiting multi-layered information to iteratively predict protein functions. <i>Mathematical Biosciences</i> , 2012, 236, 108-116.	0.9	4
142	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
143	Predicting miRNA-mediated gene silencing mode based on miRNA-target duplex features. <i>Computers in Biology and Medicine</i> , 2012, 42, 1-7.	3.9	10
144	Metabolic classification of microbial genomes using functional probes. <i>BMC Genomics</i> , 2012, 13, 157.	1.2	6

#	ARTICLE	IF	CITATIONS
145	Computational methods for protein interaction and structural prediction. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 1416-1417.	1.1	0
146	A Scheduling Method to Reduce Waiting Time for Close-Range Broadcasting. <i>Mobile Information Systems</i> , 2012, 8, 303-314.	0.4	3
147	The Tenth Asia Pacific Bioinformatics Conference (APBC 2012). <i>BMC Genomics</i> , 2012, 13, 11.	1.2	10
148	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
149	Conformational Features of Topologically Classified RNA Secondary Structures. <i>PLoS ONE</i> , 2012, 7, e39907.	1.1	8
150	A Scheduling Method for Selective Contents Broadcasting with Fast-Forwarding. , 2011, , .		1
151	Identifying multiple stem-loops pre-miRNA using support vector machine. , 2011, , .		0
152	Function Annotation for Pseudoknot Using Structure Similarity. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 1535-1544.	1.9	3
153	Mining Protein Kinases Regulation Using Graphical Models. <i>IEEE Transactions on Nanobioscience</i> , 2011, 10, 1-8.	2.2	3
154	Modeling Conserved Structure Patterns for Functional Noncoding RNA. <i>IEEE Transactions on Biomedical Engineering</i> , 2011, 58, 1528-1533.	2.5	5
155	Structure-based drug design to augment hit discovery. <i>Drug Discovery Today</i> , 2011, 16, 831-839.	3.2	223
156	Significant Cancer Prevention Factor Extraction: An Association Rule Discovery Approach. <i>Journal of Medical Systems</i> , 2011, 35, 353-367.	2.2	38
157	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
158	The Ninth Asia Pacific Bioinformatics Conference (APBC2011). <i>BMC Bioinformatics</i> , 2011, 12, .	1.2	1
159	Genetic variation of the hemagglutinin of avian influenza virus H9N2. <i>Journal of Medical Virology</i> , 2011, 83, 838-846.	2.5	17
160	Interval-based distance function for identifying RNA structure candidates. <i>Journal of Theoretical Biology</i> , 2011, 269, 280-286.	0.8	10
161	External Sorting on Flash Memory Via Natural Page Run Generation. <i>Computer Journal</i> , 2011, 54, 1882-1990.	1.5	11
162	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

#	ARTICLE	IF	CITATIONS
163	A method to reduce waiting time for close-range broadcasting. , 2011, , .		1
164	Ranking inter-relationships between clusters. International Journal of Systems Science, 2011, 42, 2071-2083.	3.7	3
165	Impact of Complex Formation on Predicting Conformational Epitopes. , 2011, , .		0
166	Semantic and layered protein function prediction from PPI networks. Journal of Theoretical Biology, 2010, 267, 129-136.	0.8	17
167	Inferring Minimal Feasible Metabolic Networks of Escherichia coli. Applied Biochemistry and Biotechnology, 2010, 160, 222-231.	1.4	1
168	Exploring Cross-Species-Related miRNAs Based on Sequence and Secondary Structure. IEEE Transactions on Biomedical Engineering, 2010, 57, 1547-1553.	2.5	6
169	Mining Characteristic Relations Bind to RNA Secondary Structures. IEEE Transactions on Information Technology in Biomedicine, 2010, 14, 10-15.	3.6	2
170	Exploring the ncRNAâ€™ncRNA patterns based on bridging rules. Journal of Biomedical Informatics, 2010, 43, 569-577.	2.5	1
171	Spectral shape descriptor using spherical harmonics. Integrated Computer-Aided Engineering, 2010, 17, 167-173.	2.5	4
172	Bacterial genomic G+C composition-eliciting environmental adaptation. Genomics, 2010, 95, 7-15.	1.3	143
173	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
174	IDENTIFYING CO-REGULATING MICRORNA GROUPS. Journal of Bioinformatics and Computational Biology, 2010, 08, 99-115.	0.3	20
175	microDoR for HUMAN: A web server to predict mode of miRNA-mediated gene silencing. , 2010, , .		0
176	Insights into Bacterial Genome Composition through Variable Target GC Content Profiling. Journal of Computational Biology, 2010, 17, 79-96.	0.8	3
177	High Functional Coherence in k-Partite Protein Cliques of Protein Interaction Networks. , 2009, , .		4
178	Data Pre-processing for More Effective Gene Clustering. , 2009, , .		1
179	Discovery of Structural and Functional Features in RNA Pseudoknots. IEEE Transactions on Knowledge and Data Engineering, 2009, 21, 974-984.	4.0	14
180	Analysis on relationship between extreme pathways and correlated reaction sets. BMC Bioinformatics, 2009, 10, S58.	1.2	7

#	ARTICLE	IF	CITATIONS
181	Acoustic feature selection for automatic emotion recognition from speech. Information Processing and Management, 2009, 45, 315-328.	5.4	153
182	Candidate working set strategy based SMO algorithm in support vector machine. Information Processing and Management, 2009, 45, 584-592.	5.4	13
183	Compensatory ability to null mutation in metabolic networks. Biotechnology and Bioengineering, 2009, 103, 361-369.	1.7	14
184	Finding rule groups to classify high dimensional gene expression datasets. Computational Biology and Chemistry, 2009, 33, 108-113.	1.1	9
185	Spherical Harmonics and Distance Transform for Image Representation and Retrieval. Lecture Notes in Computer Science, 2009, , 309-316.	1.0	5
186	Early Breast Cancer Identification: Which Way to Go? Microarray or Image Based Computer Aided Diagnosis!. , 2009, , .		3
187	Feasible Strategy for Allocating Cost of Primary Frequency Regulation. IEEE Transactions on Power Systems, 2009, 24, 508-515.	4.6	5
188	Identifying targets for drug discovery using bioinformatics. Expert Opinion on Therapeutic Targets, 2008, 12, 383-389.	1.5	70
189	POEM, A 3-Dimensional exon taxonomy and patterns in untranslated exons. BMC Genomics, 2008, 9, 428.	1.2	1
190	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
191	Finding edging genes from microarray data. Journal of Biotechnology, 2008, 135, 233-240.	1.9	6
192	Image retrieval based on semantics of intra-region color properties. , 2008, , .		1
193	A scalable and extensible segment-event-object-based sports video retrieval system. ACM Transactions on Multimedia Computing, Communications and Applications, 2008, 4, 1-40.	3.0	8
194	Rule-based dependency models for security protocol analysis. Integrated Computer-Aided Engineering, 2008, 15, 369-380.	2.5	7
195	Using Bioinformatics Techniques for Gene Identification in Drug Discovery and Development. Current Drug Metabolism, 2008, 9, 567-573.	0.7	14
196	Preface to CMLSA 2008. Lecture Notes in Computer Science, 2008, , 1-1.	1.0	0
197	Medical Knowledge Discovery from a Regional Asthma Dataset. Lecture Notes in Computer Science, 2008, , 888-895.	1.0	0
198	KERNEL-BASED NAIVE BAYES CLASSIFIER FOR BREAST CANCER PREDICTION. Journal of Biological Systems, 2007, 15, 17-25.	0.5	26

#	ARTICLE	IF	CITATIONS
199	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
200	An evaluation of contemporary hidden Markov model genefinders with a predicted exon taxonomy. <i>Nucleic Acids Research</i> , 2007, 35, 317-324.	6.5	37
201	Learning Dependency Model for AMP-Activated Protein Kinase Regulation. , 2007, , 221-229.		1
202	Acoustic Features Extraction for Emotion Recognition. , 2007, , .		40
203	Microarray Classification and Rule Based Cancer Identification. , 2007, , .		2
204	Non-quantized minimum free energy in untranslated region exons. , 2007, , .		0
205	Finding Motifs in miRNA Sequences. , 2007, , .		0
206	Microarray Data Classification Using Automatic SVM Kernel Selection. <i>DNA and Cell Biology</i> , 2007, 26, 707-712.	0.9	21
207	CIDB: Chlamydia Interactive Database for cross-querying genomics, transcriptomics and proteomics data. <i>New Biotechnology</i> , 2007, 24, 603-608.	2.7	4
208	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
209	Detecting inconsistency in biological molecular databases using ontologies. <i>Data Mining and Knowledge Discovery</i> , 2007, 15, 275-296.	2.4	15
210	INTERACTING AMINO ACID PREFERENCES OF 3D PATTERN PAIRS AT THE BINDING SITES OF TRANSIENT AND OBLIGATE PROTEIN COMPLEXES. , 2007, , .		4
211	Probabilistic Reasoning of Inconsistent Belief in Protocol Analysis. , 2007, , .		0
212	Identifying Dependency Between Secure Messages for Protocol Analysis. , 2007, , 30-38.		1
213	Preface to CMLSA 2007. , 2007, , 1-2.		0
214	Finding Short Patterns to Classify Text Documents. , 2006, , .		1
215	MDSM: Microarray database schema matching using the Hungarian method. <i>Information Sciences</i> , 2006, 176, 2771-2790.	4.0	15
216	Using object and trajectory analysis to facilitate indexing and retrieval of video. <i>Knowledge-Based Systems</i> , 2006, 19, 639-646.	4.0	5

#	ARTICLE	IF	CITATIONS
217	Guest editorsâ€™ introduction: multimedia modelling. <i>Visual Computer</i> , 2006, 22, 300-301.	2.5	0
218	Mining frequent patterns for AMP-activated protein kinase regulation on skeletal muscle. <i>BMC Bioinformatics</i> , 2006, 7, 394.	1.2	37
219	An evolutionary learning approach for adaptive negotiation agents. <i>International Journal of Intelligent Systems</i> , 2006, 21, 41-72.	3.3	56
220	Statistical Analysis of TATA Box and Its Extensions in the Promoters of Human Genes. <i>Current Bioinformatics</i> , 2006, 1, 337-345.	0.7	0
221	Using Decision-Tree to Automatically Construct Learned-Heuristics for Events Classification in Sports Video. , 2006, , .		3
222	A Similarity Search Algorithm to Predict Protein Structures. <i>Lecture Notes in Computer Science</i> , 2006, , 1305-1312.	1.0	0
223	Biological Sequence Assembly and Alignment. , 2005, , 243-261.		0
224	Pattern Matching for Motifs. , 2005, , 299-312.		0
225	Introduction to Bioinformatics. , 2005, , 1-13.		0
226	Machine Learning in Bioinformatics. , 2005, , 117-153.		7
227	Microarray Data Analysis. , 2005, , 353-388.		4
228	Modeling for Bioinformatics. , 2005, , 263-298.		0
229	DDR: an index method for large time-series datasets. <i>Information Systems</i> , 2005, 30, 333-348.	2.4	22
230	Visualization and Fractal Analysis of Biological Sequences. , 2005, , 313-351.		1
231	Content-based video indexing for sports applications using integrated multi-modal approach. , 2005, , .		12
232	ANNODA: Tool for integrating Molecular-biological Annotation Data. , 2005, , .		2
233	GUEST EDITOR'S INTRODUCTION: ADVANCED TECHNIQUES FOR BIOINFORMATICS. <i>Journal of Bioinformatics and Computational Biology</i> , 2005, 03, 99-102.	0.3	0
234	A framework for merging inconsistent beliefs in security protocol analysis. , 2005, , .		0

#	ARTICLE	IF	CITATIONS
235	A New Indexing Method for High Dimensional Dataset. Lecture Notes in Computer Science, 2005, , 385-397.	1.0	5
236	Analyzing Security Protocols Using Association Rule Mining. Lecture Notes in Computer Science, 2005, , 245-253.	1.0	1
237	Yet Another Induction Algorithm. Lecture Notes in Computer Science, 2005, , 37-44.	1.0	1
238	TRENDS IN CODON AND AMINO ACID USAGE IN HUMAN PATHOGEN <i>TROPHERYMA WHIPPLEI</i> , THE ONLY KNOWN ACTINOBACTERIA WITH REDUCED GENOME. , 2005, , .		0
239	ANALYZING INCONSISTENCY TOWARD ENHANCING INTEGRATION OF BIOLOGICAL MOLECULAR DATABASES. , 2005, , .		2
240	Highlights for more complete sports video summarization. IEEE MultiMedia, 2004, 11, 22-37.	1.5	68
241	Knowledge Creation in Export Trading. Journal of Information and Knowledge Management, 2004, 03, 297-316.	0.8	1
242	A Grid-Based Index Method for Time Warping Distance. Lecture Notes in Computer Science, 2004, , 65-75.	1.0	0
243	The power of play-break for automatic detection and browsing of self-consumable sport video highlights. , 2004, , .		20
244	Surface Spatial Index Structure of High-Dimensional Space. Lecture Notes in Computer Science, 2004, , 272-278.	1.0	0
245	Database Technologies for L-System Simulations in Virtual Plant Applications on Bioinformatics. Knowledge and Information Systems, 2003, 5, 288-314.	2.1	4
246	Biomedical visualization. Journal of Visual Languages and Computing, 2003, 14, 295-297.	1.8	1
247	Performance Assessment of Kernel Density Clustering for Gene Expression Profile Data. Comparative and Functional Genomics, 2003, 4, 287-299.	2.0	35
248	Sports video summarization using highlights and play-breaks. , 2003, , .		29
249	Information management for microarray experimental data. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2003, 36, 377-382.	0.4	1
250	A Hybrid Framework Using SOM and Fuzzy Theory for Textual Classification in Data Mining. Lecture Notes in Computer Science, 2003, , 153-167.	1.0	9
251	A Framework for Customizable Sports Video Management and Retrieval. Lecture Notes in Computer Science, 2003, , 248-265.	1.0	0
252	Partial automation of database processing of simulation outputs from L-systems models of plant morphogenesis. BioSystems, 2002, 65, 187-197.	0.9	0

#	ARTICLE	IF	CITATIONS
253	Content-Based Indexing and Retrieval Using MPEG-7 and X-Query in Video Data Management Systems. World Wide Web, 2002, 5, 207-227.	2.7	18
254	DML: a bridge between database systems and L-systems for biological research. , 0, , .		0
255	Classification of self-consumable highlights for soccer video summaries. , 0, , .		6
256	Concept Learning of Text Documents. , 0, , .		0
257	A computational framework for nucleic acid sub-sequence identification. , 0, , .		0
258	Content exploration for e-learning using XML web services. , 0, , .		0
259	Keyword extraction for text categorization. , 0, , .		4
260	Towards Universal and Statistical-Driven Heuristics for Automatic Classification of Sports Video Events. , 0, , .		0
261	Mining Frequent Itemsets for Protein Kinase Regulation. , 0, , 222-230.		0