

Pietro Lio'

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2653344/publications.pdf>

Version: 2024-02-01

371
papers

12,358
citations

53660

45
h-index

35952

97
g-index

421
all docs

421
docs citations

421
times ranked

18286
citing authors

#	ARTICLE	IF	CITATIONS
1	Heterogeneous Model Fusion Federated Learning Mechanism Based on Model Mapping. IEEE Internet of Things Journal, 2022, 9, 6058-6068.	5.5	10
2	Adversarial generation of gene expression data. Bioinformatics, 2022, 38, 730-737.	1.8	23
3	Modeling Brain-Heart Crosstalk Information in Patients with Traumatic Brain Injury. Neurocritical Care, 2022, 36, 738-750.	1.2	7
4	SCMTHP: A New Approach for Identifying and Characterizing of Tumor-Homing Peptides Using Estimated Propensity Scores of Amino Acids. Pharmaceutics, 2022, 14, 122.	2.0	10
5	Guest Editorial: Non-Euclidean Machine Learning. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2022, 44, 723-726.	9.7	7
6	Transcriptional biomarkers of response to pharmacological treatments in severe mental disorders: A systematic review. European Neuropsychopharmacology, 2022, 55, 112-157.	0.3	7
7	Early downregulation of hsa-miR-144-3p in serum from drug-naïve Parkinson's disease patients. Scientific Reports, 2022, 12, 1330.	1.6	14
8	System Neural Network: Evolution and Change Based Structure Learning. IEEE Transactions on Artificial Intelligence, 2022, 3, 426-435.	3.4	4
9	Metabolite and lipoprotein profiles reveal sex-related oxidative stress imbalance in de novo drug-naive Parkinson's disease patients. Npj Parkinson's Disease, 2022, 8, 14.	2.5	11
10	Metabolically Driven Latent Space Learning for Gene Expression Data. , 2022, , 131-155.		0
11	AI-Based Reconstruction for Fast MRI—A Systematic Review and Meta-Analysis. Proceedings of the IEEE, 2022, 110, 224-245.	16.4	57
12	SCORPION is a stacking-based ensemble learning framework for accurate prediction of phage virion proteins. Scientific Reports, 2022, 12, 4106.	1.6	21
13	Unsupervised construction of computational graphs for gene expression data with explicit structural inductive biases. Bioinformatics, 2022, 38, 1320-1327.	1.8	1
14	CellVGAE: an unsupervised scRNA-seq analysis workflow with graph attention networks. Bioinformatics, 2022, 38, 1277-1286.	1.8	16
15	StackDPPIV: A novel computational approach for accurate prediction of dipeptidyl peptidase IV (DPP-IV) inhibitory peptides. Methods, 2022, 204, 189-198.	1.9	34
16	Molecular Markers and Genomics for Food and Beverages Characterization. , 2022, , 889-909.		0
17	End-to-End Deep Learning of Non-rigid Groupwise Registration and Reconstruction of Dynamic MRI. Frontiers in Cardiovascular Medicine, 2022, 9, 880186.	1.1	6
18	AMYPred-FRL is a novel approach for accurate prediction of amyloid proteins by using feature representation learning. Scientific Reports, 2022, 12, 7697.	1.6	27

#	ARTICLE	IF	CITATIONS
19	A deep graph neural network architecture for modelling spatio-temporal dynamics in resting-state functional MRI data. <i>Medical Image Analysis</i> , 2022, 79, 102471.	7.0	20
20	NEPTUNE: A novel computational approach for accurate and large-scale identification of tumor homing peptides. <i>Computers in Biology and Medicine</i> , 2022, 148, 105700.	3.9	9
21	Cell graph neural networks enable the precise prediction of patient survival in gastric cancer. <i>Npj Precision Oncology</i> , 2022, 6, .	2.3	22
22	Signal metrics analysis of oscillatory patterns in bacterial multi-omic networks. <i>Bioinformatics</i> , 2021, 37, 1411-1419.	1.8	1
23	Pathogenetic profiling of COVID-19 and SARS-like viruses. <i>Briefings in Bioinformatics</i> , 2021, 22, 1175-1196.	3.2	42
24	A Multiplex Social Contagion Dynamics Model to Shape and Discriminate D2D Content Dissemination. <i>IEEE Transactions on Cognitive Communications and Networking</i> , 2021, 7, 581-593.	4.9	3
25	How artificial intelligence and machine learning can help healthcare systems respond to COVID-19. <i>Machine Learning</i> , 2021, 110, 1-14.	3.4	102
26	An Effective Loss Function for Generating 3D Models from Single 2D Image Without Rendering. <i>IFIP Advances in Information and Communication Technology</i> , 2021, , 309-322.	0.5	4
27	Emotion Recognition From EEG Signal Focusing on Deep Learning and Shallow Learning Techniques. <i>IEEE Access</i> , 2021, 9, 94601-94624.	2.6	77
28	Deep Learning for Protein-Protein Interaction Site Prediction. <i>Methods in Molecular Biology</i> , 2021, 2361, 263-288.	0.4	10
29	Deep convolutional neural networks based ECG beats classification to diagnose cardiovascular conditions. <i>Biomedical Engineering Letters</i> , 2021, 11, 147-162.	2.1	24
30	Teaching sustainability as complex systems approach: a sustainable development goals workshop. <i>International Journal of Sustainability in Higher Education</i> , 2021, 22, 25-41.	1.6	19
31	A geroscience approach for Parkinson's disease: Conceptual framework and design of PROPAG-AGEING project. <i>Mechanisms of Ageing and Development</i> , 2021, 194, 111426.	2.2	14
32	Advantages of using graph databases to explore chromatin conformation capture experiments. <i>BMC Bioinformatics</i> , 2021, 22, 43.	1.2	1
33	ML-SIM: universal reconstruction of structured illumination microscopy images using transfer learning. <i>Biomedical Optics Express</i> , 2021, 12, 2720.	1.5	42
34	Temporal pointwise convolutional networks for length of stay prediction in the intensive care unit. , 2021, , .		24
35	Deep Learning Enables Fast and Accurate Imputation of Gene Expression. <i>Frontiers in Genetics</i> , 2021, 12, 624128.	1.1	14
36	Multilayer modelling of the human transcriptome and biological mechanisms of complex diseases and traits. <i>Npj Systems Biology and Applications</i> , 2021, 7, 24.	1.4	7

#	ARTICLE	IF	CITATIONS
37	Integration and interplay of machine learning and bioinformatics approach to identify genetic interaction related to ovarian cancer chemoresistance. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	5
38	Analysis of single-cell RNA sequencing data based on autoencoders. <i>BMC Bioinformatics</i> , 2021, 22, 309.	1.2	15
39	Deep Graph Mapper: Seeing Graphs Through the Neural Lens. <i>Frontiers in Big Data</i> , 2021, 4, 680535.	1.8	11
40	Resilience learning through self adaptation in digital twins of human-cyber-physical systems. , 2021, , .		7
41	Arbitrary Scale Super-Resolution for Medical Images. <i>International Journal of Neural Systems</i> , 2021, 31, 2150037.	3.2	24
42	iBitter-Fuse: A Novel Sequence-Based Bitter Peptide Predictor by Fusing Multi-View Features. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8958.	1.8	27
43	A Fine-Grained IoT Data Access Control Scheme Combining Attribute-Based Encryption and Blockchain. <i>Security and Communication Networks</i> , 2021, 2021, 1-13.	1.0	11
44	From Infection to Immunity: Understanding the Response to SARS-CoV2 Through In-Silico Modeling. <i>Frontiers in Immunology</i> , 2021, 12, 646972.	2.2	35
45	Graph Representation Forecasting of Patient's Medical Conditions: Toward a Digital Twin. <i>Frontiers in Genetics</i> , 2021, 12, 652907.	1.1	20
46	Heterogeneity of prodromal Parkinson symptoms in siblings of Parkinson disease patients. <i>Npj Parkinson's Disease</i> , 2021, 7, 78.	2.5	2
47	Analysis of Cardio-Cerebral Crosstalk Events in an Adult Cohort from the CENTER-TBI Study. <i>Acta Neurochirurgica Supplementum</i> , 2021, 131, 39-42.	0.5	2
48	Evolution toward beta common chain receptor usage links the matrix proteins of HIV-1 and its ancestors to human erythropoietin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2021366118.	3.3	4
49	A class-contrastive human-interpretable machine learning approach to predict mortality in severe mental illness. <i>NPJ Schizophrenia</i> , 2021, 7, 60.	2.0	2
50	A Universal Malicious Documents Static Detection Framework Based on Feature Generalization. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 12134.	1.3	5
51	COSMONET: An R Package for Survival Analysis Using Screening-Network Methods. <i>Mathematics</i> , 2021, 9, 3262.	1.1	4
52	XFlow: Cross-Modal Deep Neural Networks for Audiovisual Classification. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2020, 31, 3711-3720.	7.2	17
53	A Novel Methodology for designing Policies in Mobile Crowdsensing Systems. <i>Pervasive and Mobile Computing</i> , 2020, 67, 101230.	2.1	6
54	Unsupervised stratification in neuroimaging through deep latent embeddings. , 2020, 2020, 1568-1571.		7

#	ARTICLE	IF	CITATIONS
55	DADIM: A distance adjustment dynamic influence map model. <i>Future Generation Computer Systems</i> , 2020, 112, 1122-1130.	4.9	2
56	Introducing brain-heart crosstalks information in clinical decision support systems for TBI patients, through ICM+. , 2020, , .		0
57	MARLeME: A Multi-Agent Reinforcement Learning Model Extraction Library. , 2020, , .		3
58	A deep spatiotemporal graph learning architecture for brain connectivity analysis. , 2020, 2020, 1120-1123.		4
59	A novel Graph Attention Network Architecture for modeling multimodal brain connectivity. , 2020, 2020, 1071-1074.		3
60	Evidence in cortical folding patterns for prenatal predispositions to hallucinations in schizophrenia. <i>Translational Psychiatry</i> , 2020, 10, 387.	2.4	17
61	PECLIDES Neuro: A Personalisable Clinical Decision Support System for Neurological Diseases. <i>Frontiers in Artificial Intelligence</i> , 2020, 3, 23.	2.0	11
62	A machine learning model to identify early stage symptoms of SARS-Cov-2 infected patients. <i>Expert Systems With Applications</i> , 2020, 160, 113661.	4.4	120
63	Domain-Oriented Topic Discovery Based on Features Extraction and Topic Clustering. <i>IEEE Access</i> , 2020, 8, 93648-93662.	2.6	5
64	Privacy-Preserving Asynchronous Federated Learning Mechanism for Edge Network Computing. <i>IEEE Access</i> , 2020, 8, 48970-48981.	2.6	88
65	Horizontal gene transfer and silver nanoparticles production in a new <i>Marinomonas</i> strain isolated from the Antarctic psychrophilic ciliate <i>Euplotes focardii</i> . <i>Scientific Reports</i> , 2020, 10, 10218.	1.6	22
66	Unsupervised generative and graph representation learning for modelling cell differentiation. <i>Scientific Reports</i> , 2020, 10, 9790.	1.6	11
67	Proximal Distilled Evolutionary Reinforcement Learning. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2020, 34, 3283-3290.	3.6	25
68	ChronoMIDâ€™Cross-modal neural networks for 3-D temporal medical imaging data. <i>PLoS ONE</i> , 2020, 15, e0228962.	1.1	0
69	Machine Learning and Bioinformatics Models to Identify Pathways that Mediate Influences of Welding Fumes on Cancer Progression. <i>Scientific Reports</i> , 2020, 10, 2795.	1.6	23
70	Latest advances in parallel, distributed, and networkâ€™based processing. <i>Concurrency Computation Practice and Experience</i> , 2020, 32, e5683.	1.4	2
71	Arbitrary Scale Super-Resolution forâ€™Brain MRI Images. <i>IFIP Advances in Information and Communication Technology</i> , 2020, , 165-176.	0.5	10
72	NeoHiC: A Web Application for the Analysis of Hi-C Data. <i>Lecture Notes in Computer Science</i> , 2020, , 98-107.	1.0	1

#	ARTICLE	IF	CITATIONS
73	Continuous authentication by free-text keystroke based on CNN and RNN. Computers and Security, 2020, 96, 101861.	4.0	35
74	Dynamic survival prediction in intensive care units from heterogeneous time series without the need for variable selection or curation. Scientific Reports, 2020, 10, 22129.	1.6	16
75	Neural Models for Brain Networks Connectivity Analysis. Lecture Notes in Computer Science, 2020, , 212-226.	1.0	1
76	Resolution of Blockchain Conflicts through Heuristics-based Game Theory and Multilayer Network Modeling. , 2020, , .		1
77	Learning Mobility Flows from Urban Features with Spatial Interaction Models and Neural Networks. , 2020, , .		6
78	Identification of strategic molecules for future circular supply chains using large reaction networks. Reaction Chemistry and Engineering, 2019, 4, 1969-1981.	1.9	16
79	Modeling breast cancer progression to bone: how driver mutation order and metabolism matter. BMC Medical Genomics, 2019, 12, 106.	0.7	7
80	Variational Autoencoders for Cancer Data Integration: Design Principles and Computational Practice. Frontiers in Genetics, 2019, 10, 1205.	1.1	76
81	How Can We Make Gan Perform Better in Single Medical Image Super-Resolution? A Lesion Focused Multi-Scale Approach. , 2019, , .		43
82	Improving QoE in Multi-layer Social Sensing. , 2019, , .		2
83	Integration of Machine Learning Methods to Dissect Genetically Imputed Transcriptomic Profiles in Alzheimer's Disease. Frontiers in Genetics, 2019, 10, 726.	1.1	18
84	Social dynamics modeling of chrono-nutrition. PLoS Computational Biology, 2019, 15, e1006714.	1.5	9
85	A Logical Framework for Modelling Breast Cancer Progression. Lecture Notes in Computer Science, 2019, , 121-141.	1.0	4
86	GenHap: a novel computational method based on genetic algorithms for haplotype assembly. BMC Bioinformatics, 2019, 20, 172.	1.2	26
87	A Machine Learning Tool for Interpreting Differences in Cognition Using Brain Features. IFIP Advances in Information and Communication Technology, 2019, , 475-486.	0.5	1
88	ASSCA: API sequence and statistics features combined architecture for malware detection. Computer Networks, 2019, 157, 99-111.	3.2	30
89	Predicting factors for survival of breast cancer patients using machine learning techniques. BMC Medical Informatics and Decision Making, 2019, 19, 48.	1.5	166
90	Systems based analysis of human embryos and gene networks involved in cell lineage allocation. BMC Genomics, 2019, 20, 171.	1.2	16

#	ARTICLE	IF	CITATIONS
91	Genetic effects of welding fumes on the development of respiratory system diseases. <i>Computers in Biology and Medicine</i> , 2019, 108, 142-149.	3.9	30
92	How to integrate wet lab and bioinformatics procedures for wine DNA admixture analysis and compositional profiling: Case studies and perspectives. <i>PLoS ONE</i> , 2019, 14, e0211962.	1.1	14
93	High Performance Computing for Haplotyping: Models and Platforms. <i>Lecture Notes in Computer Science</i> , 2019, , 650-661.	1.0	1
94	Comorbidity Effects of Mitochondrial Dysfunction to the Progression of Neurological Disorders: Insights from a Systems Biomedicine Perspective. , 2019, , .		0
95	Machine Learning-Based Models for Early Stage Detection of Autism Spectrum Disorders. <i>IEEE Access</i> , 2019, 7, 166509-166527.	2.6	101
96	Integrating Petri Nets and Flux Balance Methods in Computational Biology Models: a Methodological and Computational Practice. <i>Fundamenta Informaticae</i> , 2019, 171, 367-392.	0.3	7
97	Genetic effects of welding fumes on the progression of neurodegenerative diseases. <i>NeuroToxicology</i> , 2019, 71, 93-101.	1.4	37
98	A parameter-efficient deep learning approach to predict conversion from mild cognitive impairment to Alzheimer's disease. <i>NeuroImage</i> , 2019, 189, 276-287.	2.1	260
99	Multi-omic Network Regression: Methodology, Tool and Case Study. <i>Studies in Computational Intelligence</i> , 2019, , 611-624.	0.7	0
100	Lesion focused super-resolution. , 2019, , .		11
101	Modelling Trait-dependent Speciation with Approximate Bayesian Computation. <i>Acta Physica Polonica B, Proceedings Supplement</i> , 2019, 12, 25.	0.0	4
102	Parapred: antibody paratope prediction using convolutional and recurrent neural networks. <i>Bioinformatics</i> , 2018, 34, 2944-2950.	1.8	124
103	Parallel swarm intelligence strategies for large-scale clustering based on MapReduce with application to epigenetics of aging. <i>Applied Soft Computing Journal</i> , 2018, 69, 771-783.	4.1	3
104	Quantifying the propagation of distress and mental disorders in social networks. <i>Scientific Reports</i> , 2018, 8, 5005.	1.6	25
105	Optimization of Multi-Omic Genome-Scale Models: Methodologies, Hands-on Tutorial, and Perspectives. <i>Methods in Molecular Biology</i> , 2018, 1716, 389-408.	0.4	14
106	Bioinformatics methodologies for coeliac disease and its comorbidities. <i>Briefings in Bioinformatics</i> , 2018, , .	3.2	6
107	Guest Editorsâ€™ Introduction to the Special Section on the 14th International Conference on Computational Methods in Systems Biology (CMSB 2016). <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1122-1123.	1.9	0
108	A Multi-modal Convolutional Neural Network Framework for the Prediction of Alzheimerâ€™s Disease. , 2018, 2018, 1271-1274.		34

#	ARTICLE	IF	CITATIONS
109	Pathway-based subnetworks enable cross-disease biomarker discovery. Nature Communications, 2018, 9, 4746.	5.8	30
110	Terminal Sensitive Data Protection by Adjusting Access Time Bidirectionally and Automatically. , 2018, , .		0
111	Neural network fusion: a novel CT-MR aortic aneurysm image segmentation method. , 2018, 10574, .		11
112	Multi-omic analysis of signalling factors in inflammatory comorbidities. BMC Bioinformatics, 2018, 19, 439.	1.2	11
113	CiliateGEM: an open-project and a tool for predictions of ciliate metabolic variations and experimental condition design. BMC Bioinformatics, 2018, 19, 442.	1.2	1
114	Using Deep Data Augmentation Training to Address Software and Hardware Heterogeneities in Wearable and Smartphone Sensing Devices. , 2018, , .		47
115	Cross-modal Recurrent Models for Weight Objective Prediction from Multimodal Time-series Data. , 2018, , .		17
116	STable: a novel approach to de novo assembly of RNA-seq data and its application in a metabolic model network based metatranscriptomic workflow. BMC Bioinformatics, 2018, 19, 184.	1.2	3
117	Computational Models for Trapping Ebola Virus Using Engineered Bacteria. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 2017-2027.	1.9	8
118	Stochastic Channel Switching of Frequency-Encoded Signals in Molecular Communication Networks. IEEE Communications Letters, 2018, 22, 332-335.	2.5	11
119	Message from Organizing Chairs. , 2018, , .		0
120	A study on multi-omic oscillations in Escherichia coli metabolic networks. BMC Bioinformatics, 2018, 19, 194.	1.2	6
121	Combining Pathway Identification and Breast Cancer Survival Prediction via Screening-Network Methods. Frontiers in Genetics, 2018, 9, 206.	1.1	10
122	Simultaneous Transients of Intracranial Pressure and Heart Rate in Traumatic Brain Injury: Methods of Analysis. Acta Neurochirurgica Supplementum, 2018, 126, 147-151.	0.5	7
123	Automatic Inference of Cross-Modal Connection Topologies for X-CNNs. Lecture Notes in Computer Science, 2018, , 54-63.	1.0	1
124	Making life difficult for Clostridium difficile: augmenting the pathogen's metabolic model with transcriptomic and codon usage data for better therapeutic target characterization. BMC Systems Biology, 2017, 11, 25.	3.0	22
125	Seeing the wood for the trees: a forest of methods for optimization and omic-network integration in metabolic modelling. Briefings in Bioinformatics, 2017, 19, 1218-1235.	3.2	32
126	DrugClust: A machine learning approach for drugs side effects prediction. Computational Biology and Chemistry, 2017, 68, 204-210.	1.1	51

#	ARTICLE	IF	CITATIONS
127	A big-data layered architecture for analyzing molecular communications systems in blood vessels. , 2017, , .		1
128	Genetic Profiling and Comorbidities of Zika Infection. Journal of Infectious Diseases, 2017, 216, 703-712.	1.9	48
129	Single-cell RNA-sequencing uncovers transcriptional states and fate decisions in haematopoiesis. Nature Communications, 2017, 8, 2045.	5.8	147
130	NuChart-II: The road to a fast and scalable tool for Hi-C data analysis. International Journal of High Performance Computing Applications, 2017, 31, 196-211.	2.4	4
131	A multiplex network approach for the analysis of intracranial pressure and heart rate data in traumatic brain injured patients. Applied Network Science, 2017, 2, 29.	0.8	13
132	Global gene expression profiling and senescence biomarker analysis of hESC exposed to H2O2 induced non-cytotoxic oxidative stress. Stem Cell Research and Therapy, 2017, 8, 160.	2.4	7
133	Comparative Study of Inference Methods for Bayesian Nonnegative Matrix Factorisation. Lecture Notes in Computer Science, 2017, , 513-529.	1.0	8
134	Transcriptome and proteome analysis of Salmonella enterica serovar Typhimurium systemic infection of wild type and immune-deficient mice. PLoS ONE, 2017, 12, e0181365.	1.1	6
135	Effect of Aging, Disease Versus Health Conditions in the Design of Nano-communications in Blood Vessels. Modeling and Optimization in Science and Technologies, 2017, , 447-471.	0.7	1
136	Iterative Multi Level Calibration of Metabolic Networks. Current Bioinformatics, 2016, 11, 93-105.	0.7	4
137	The Genome Conformation As an Integrator of Multi-Omic Data: The Example of Damage Spreading in Cancer. Frontiers in Genetics, 2016, 7, 194.	1.1	22
138	Distance-Based Opportunistic Mobile Data Offloading. Sensors, 2016, 16, 878.	2.1	6
139	Computational Modeling, Formal Analysis, and Tools for Systems Biology. PLoS Computational Biology, 2016, 12, e1004591.	1.5	162
140	Cancer Markers Selection Using Network-Based Cox Regression: A Methodological and Computational Practice. Frontiers in Physiology, 2016, 7, 208.	1.3	27
141	X-CNN: Cross-modal convolutional neural networks for sparse datasets. , 2016, , .		11
142	Parameter estimation of tuberculosis transmission model using Ensemble Kalman filter across Indian states and union territories. Infection, Disease and Health, 2016, 21, 184-191.	0.5	9
143	Animal inference on human mitochondrial diseases. Computational Biology and Chemistry, 2016, 62, 17-28.	1.1	0
144	Combining evolutionary game theory and network theory to analyze human cooperation patterns. Chaos, Solitons and Fractals, 2016, 91, 17-24.	2.5	31

#	ARTICLE	IF	CITATIONS
145	Protein Interaction Networks Link Schizophrenia Risk Loci to Synaptic Function. Schizophrenia Bulletin, 2016, 42, 1334-1342.	2.3	16
146	Warped Matrix Factorisation for Multi-view Data Integration. Lecture Notes in Computer Science, 2016, , 789-804.	1.0	1
147	Opportunities for community awareness platforms in personal genomics and bioinformatics education. Briefings in Bioinformatics, 2016, 18, bbw078.	3.2	2
148	NuchaRt: Embedding High-Level Parallel Computing in R for Augmented Hi-C Data Analysis. Lecture Notes in Computer Science, 2016, , 259-272.	1.0	2
149	Channel modelling of molecular communications across blood vessels and nerves. , 2016, , .		9
150	The Impact of Heterogeneity and Awareness in Modeling Epidemic Spreading on Multiplex Networks. Scientific Reports, 2016, 6, 37105.	1.6	45
151	Bioinformatics Challenges and Potentialities in Studying Extreme Environments. Lecture Notes in Computer Science, 2016, , 205-219.	1.0	0
152	MolComML. , 2016, , .		4
153	Muxstep: an open-source C++ multiplex HMM library for making inferences on multiple data types. Bioinformatics, 2016, 32, 2562-2564.	1.8	2
154	Multiplex methods provide effective integration of multi-omic data in genome-scale models. BMC Bioinformatics, 2016, 17, 83.	1.2	37
155	Metabolic disorders: how can systems modelling help?. Lancet Diabetes and Endocrinology, the, 2016, 4, 306.	5.5	2
156	Systems medicine of inflammaging. Briefings in Bioinformatics, 2016, 17, 527-540.	3.2	35
157	Hierarchical block matrices as efficient representations of chromosome topologies and their application for 3C data integration. Bioinformatics, 2016, 32, 1121-1129.	1.8	5
158	How computer science can help in understanding the 3D genome architecture. Briefings in Bioinformatics, 2016, 17, 733-744.	3.2	10
159	Bio-Inspired ICT for Big Data Management in Healthcare. Studies in Big Data, 2016, , 1-26.	0.8	3
160	Applications of molecular communications to medicine: A survey. Nano Communication Networks, 2016, 7, 27-45.	1.6	128
161	Predictive analytics of environmental adaptability in multi-omic network models. Scientific Reports, 2015, 5, 15147.	1.6	43
162	DAPPER: a data-mining resource for protein-protein interactions. BioData Mining, 2015, 8, 30.	2.2	5

#	ARTICLE	IF	CITATIONS
163	How to build personalized multi-omics comorbidity profiles. <i>Frontiers in Cell and Developmental Biology</i> , 2015, 3, 28.	1.8	53
164	Multi-Target Analysis and Design of Mitochondrial Metabolism. <i>PLoS ONE</i> , 2015, 10, e0133825.	1.1	8
165	Quantifying the Role of Homophily in Human Cooperation Using Multiplex Evolutionary Game Theory. <i>PLoS ONE</i> , 2015, 10, e0140646.	1.1	29
166	Parallel Exploration of the Nuclear Chromosome Conformation with NuChart-II. , 2015, , .		3
167	Privacy Information Security Classification and Comparison between the Westerner and Chinese. , 2015, , .		0
168	CytoCom: a Cytoscape app to visualize, query and analyse disease comorbidity networks. <i>Bioinformatics</i> , 2015, 31, 969-971.	1.8	42
169	The BioMart community portal: an innovative alternative to large, centralized data repositories. <i>Nucleic Acids Research</i> , 2015, 43, W589-W598.	6.5	682
170	Multi omic oscillations in bacterial pathways. , 2015, , .		0
171	Molecular multiplex network inference using Gaussian mixture hidden Markov models. <i>Journal of Complex Networks</i> , 2015, , cnv029.	1.1	3
172	Advances in Artificial Life: Synthesis and Simulation of Living Systems: Editorial. <i>Artificial Life</i> , 2015, 21, 395-397.	1.0	3
173	Multi -omics and metabolic modelling pipelines: Challenges and tools for systems microbiology. <i>Microbiological Research</i> , 2015, 171, 52-64.	2.5	125
174	Comorbidity networks: beyond disease correlations. <i>Journal of Complex Networks</i> , 2015, 3, 319-332.	1.1	18
175	Analysis and design of molecular machines. <i>Theoretical Computer Science</i> , 2015, 599, 102-117.	0.5	3
176	Modelling Circulating Tumour Cells for Personalised Survival Prediction in Metastatic Breast Cancer. <i>PLoS Computational Biology</i> , 2015, 11, e1004199.	1.5	12
177	Integrating multi-omic features exploiting Chromosome Conformation Capture data. <i>Frontiers in Genetics</i> , 2015, 6, 40.	1.1	11
178	Analyzing seasonality of tuberculosis across Indian states and union territories. <i>Journal of Epidemiology and Global Health</i> , 2015, 5, 337.	1.1	31
179	Bioaccumulation modelling and sensitivity analysis for discovering key players in contaminated food webs: The case study of PCBs in the Adriatic Sea. <i>Ecological Modelling</i> , 2015, 306, 205-215.	1.2	15
180	M<sc>e</sc>D<sc>u</sc>S<sc>a</sc>: a multi-draft based scaffold. <i>Bioinformatics</i> , 2015, 31, 2443-2451.	1.8	359

#	ARTICLE	IF	CITATIONS
181	Improving Literature-Based Discovery with Advanced Text Mining. Lecture Notes in Computer Science, 2015, , 89-98.	1.0	4
182	Automated Detection of Fluorescent Probes in Molecular Imaging. Lecture Notes in Computer Science, 2015, , 68-75.	1.0	1
183	Network regularised Cox regression and multiplex network models to predict disease comorbidities and survival of cancer. Computational Biology and Chemistry, 2015, 59, 15-31.	1.1	37
184	A Hybrid of Metabolic Flux Analysis and Bayesian Factor Modeling for Multiomic Temporal Pathway Activation. ACS Synthetic Biology, 2015, 4, 880-889.	1.9	18
185	Bayesian Melding Approach to Estimate the Reproduction Number for Tuberculosis Transmission in Indian States and Union Territories. Asia-Pacific Journal of Public Health, 2015, 27, 723-732.	0.4	3
186	Genome-scale metabolic reconstruction and constraint-based modelling of the Antarctic bacterium <i>Pseudoalteromonas haloplanktis</i> TAC125. Environmental Microbiology, 2015, 17, 751-766.	1.8	53
187	Genome-Scale Metabolic Network Reconstruction. Methods in Molecular Biology, 2015, 1231, 233-256.	0.4	24
188	Applications of Network-based Survival Analysis Methods for Pathways Detection in Cancer. Lecture Notes in Computer Science, 2015, , 76-88.	1.0	2
189	NuChart-II: A Graph-Based Approach for Analysis and Interpretation of Hi-C Data. Lecture Notes in Computer Science, 2015, , 298-311.	1.0	1
190	A content dissemination model for mobile internet to minimize load on cellular network. , 2015, , 289-294.		0
191	A Molecular Communication System in Blood Vessels for Tumor Detection. , 2014, , .		24
192	Modeling TGF- β 2 in Early Stages of Cancer Tissue Dynamics. PLoS ONE, 2014, 9, e88533.	1.1	7
193	Bioremediation in marine ecosystems: a computational study combining ecological modeling and flux balance analysis. Frontiers in Genetics, 2014, 5, 319.	1.1	11
194	Who Wrote This? Textual Modeling with Authorship Attribution in Big Data. , 2014, , .		11
195	Nodes Density Adaptive Opportunistic Forwarding Protocol for Intermittently Connected Networks. , 2014, , .		2
196	Network-based analysis of comorbidities risk during an infection: SARS and HIV case studies. BMC Bioinformatics, 2014, 15, 333.	1.2	93
197	MtPAN3: Site-class specific amino acid replacement matrices for mitochondrial proteins of Pancrustacea and Collembola. Molecular Phylogenetics and Evolution, 2014, 75, 239-244.	1.2	1
198	Exploring the complexity of pathway-drug relationships using latent Dirichlet allocation. Computational Biology and Chemistry, 2014, 53, 144-152.	1.1	16

#	ARTICLE	IF	CITATIONS
199	Combining a wavelet change point and the Bayes factor for analysing chromosomal interaction data. <i>Molecular BioSystems</i> , 2014, 10, 1576-1585.	2.9	46
200	FisHiCal: an R package for iterative FISH-based calibration of Hi-C data. <i>Bioinformatics</i> , 2014, 30, 3120-3122.	1.8	35
201	Directional communication with movement prediction in mobile wireless sensor networks. <i>Personal and Ubiquitous Computing</i> , 2014, 18, 1941-1953.	1.9	4
202	comoR: a software for disease comorbidity risk assessment. <i>Journal of Clinical Bioinformatics</i> , 2014, 4, 8.	1.2	81
203	Pathway-based Bayesian inference of drug-disease interactions. <i>Molecular BioSystems</i> , 2014, 10, 1538-1548.	2.9	17
204	Forward and Reverse coding for chromosome transfer in bacterial nanonetworks. <i>Nano Communication Networks</i> , 2014, 5, 15-24.	1.6	19
205	Draft genomes of three Antarctic <i>Psychrobacter</i> strains producing antimicrobial compounds against <i>Burkholderia cepacia</i> complex, opportunistic human pathogens. <i>Marine Genomics</i> , 2014, 13, 37-38.	0.4	17
206	Advances in translational biomedicine from systems approaches. <i>Frontiers in Genetics</i> , 2014, 5, 273.	1.1	4
207	The Bio-Inspired and Social Evolution of Node and Data in a Multilayer Network. , 2014, , .		6
208	Endovascular Mobile Sensor Network for Detecting Circulating Tumoral Cells. , 2014, , .		1
209	Short and long-term genome stability analysis of prokaryotic genomes. <i>BMC Genomics</i> , 2013, 14, 309.	1.2	9
210	Comorbidity: a multidimensional approach. <i>Trends in Molecular Medicine</i> , 2013, 19, 515-521.	3.5	54
211	Offloading mobile data from cellular networks through peer-to-peer WiFi communication: A subscribe-and-send architecture. <i>China Communications</i> , 2013, 10, 35-46.	2.0	36
212	It measures like me: An IoTs algorithm in WSNs based on heuristics behavior and clustering methods. <i>Ad Hoc Networks</i> , 2013, 11, 2637-2647.	3.4	13
213	CytoHiC: a cytoscape plugin for visual comparison of Hi-C networks. <i>Bioinformatics</i> , 2013, 29, 1206-1207.	1.8	17
214	Design and strain selection criteria for bacterial communication networks. <i>Nano Communication Networks</i> , 2013, 4, 155-163.	1.6	1
215	Differential impacts of R5 vs. X4 HIV-1 on the transcriptome of primary CD4+ T cells. <i>Retrovirology</i> , 2013, 10, .	0.9	1
216	Multi objective design for bacterial communication networks. , 2013, , .		1

#	ARTICLE	IF	CITATIONS
217	Speeding up the transition to collective awareness. , 2013, , .		3
218	A design automation framework for computational bioenergetics in biological networks. Molecular BioSystems, 2013, 9, 2554.	2.9	8
219	Pareto Optimality in Organelle Energy Metabolism Analysis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1032-1044.	1.9	22
220	A review of experimental opportunities for molecular communication. Nano Communication Networks, 2013, 4, 43-52.	1.6	67
221	Efficient Behavior of Photosynthetic Organelles via Pareto Optimality, Identifiability, and Sensitivity Analysis. ACS Synthetic Biology, 2013, 2, 274-288.	1.9	10
222	Multi-Hop Conjugation Based Bacteria Nanonetworks. IEEE Transactions on Nanobioscience, 2013, 12, 47-59.	2.2	89
223	Pareto epsilon-dominance and identifiable solutions for BioCAD modeling. , 2013, , .		3
224	A Location Prediction Algorithm for Mobile Communications Using Directional Antennas. International Journal of Distributed Sensor Networks, 2013, 9, 418606.	1.3	5
225	The Puzzling Role of CXCR4 in Human Immunodeficiency Virus Infection. Theranostics, 2013, 3, 18-25.	4.6	23
226	NuChart: An R Package to Study Gene Spatial Neighbourhoods with Multi-Omics Annotations. PLoS ONE, 2013, 8, e75146.	1.1	42
227	Physio-Environmental Sensing and Live Modeling. Interactive Journal of Medical Research, 2013, 2, e3.	0.6	7
228	The Onset of Type 2 Diabetes: Proposal for a Multi-Scale Model. JMIR Research Protocols, 2013, 2, e44.	0.5	13
229	The Role of the Genome in the Evolution of the Complexity of Metabolic Machines. Springer Proceedings in Complexity, 2013, , 1063-1069.	0.2	0
230	Identification of Sensitive Enzymes in the Photosynthetic Carbon Metabolism. Advances in Experimental Medicine and Biology, 2012, 736, 441-459.	0.8	5
231	Wavelet Kernel Principal Component Analysis in Noisy Multiscale Data Classification. , 2012, 2012, 1-13.		7
232	Modeling TGF- β signaling pathway in epithelial-mesenchymal transition. AIP Advances, 2012, 2, 011201.	0.6	2
233	Disease processes as hybrid dynamical systems. Electronic Proceedings in Theoretical Computer Science, EPTCS, 2012, 92, 152-166.	0.8	0
234	Multilevel Computational Modeling and Quantitative Analysis of Bone Remodeling. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1366-1378.	1.9	16

#	ARTICLE	IF	CITATIONS
235	The landscape of DNA repeat elements in human heart failure. <i>Genome Biology</i> , 2012, 13, R90.	13.9	33
236	Robust design of microbial strains. <i>Bioinformatics</i> , 2012, 28, 3097-3104.	1.8	53
237	Information dynamics algorithm for detecting communities in networks. <i>Communications in Nonlinear Science and Numerical Simulation</i> , 2012, 17, 4294-4303.	1.7	20
238	Modelling osteomyelitis. <i>BMC Bioinformatics</i> , 2012, 13, S12.	1.2	31
239	Statistical Approaches to Use a Model Organism for Regulatory Sequences Annotation of Newly Sequenced Species. <i>PLoS ONE</i> , 2012, 7, e42489.	1.1	1
240	An adaptive directional MAC protocol for ad hoc networks using directional antennas. <i>Science China Information Sciences</i> , 2012, 55, 1360-1371.	2.7	9
241	Opportunistic routing through conjugation in bacteria communication nanonetwork. <i>Nano Communication Networks</i> , 2012, 3, 36-45.	1.6	223
242	Multi-objective Optimisation, Sensitivity and Robustness Analysis in FBA Modelling. <i>Lecture Notes in Computer Science</i> , 2012, , 127-147.	1.0	7
243	Multiple Verification in Complex Biological Systems: The Bone Remodelling Case Study. <i>Lecture Notes in Computer Science</i> , 2012, , 53-76.	1.0	7
244	Investigating Meta-Approaches for Reconstructing Gene Networks in a Mammalian Cellular Context. <i>PLoS ONE</i> , 2012, 7, e28713.	1.1	11
245	Collective Human Mobility Pattern from Taxi Trips in Urban Area. <i>PLoS ONE</i> , 2012, 7, e34487.	1.1	150
246	Rational design of organelle compartments in cells. <i>EMBnet Journal</i> , 2012, 18, 20.	0.2	3
247	Unity in Diversity: Phylogenetic-inspired Techniques for Reverse Engineering and Detection of Malware Families. , 2011, , .		5
248	How the Mutational-Selection Interplay Organizes the Fitness Landscape. <i>Journal of Nonlinear Mathematical Physics</i> , 2011, 18, 265.	0.8	0
249	Evolving Model of Opportunistic Routing in Delay Tolerant Networks. , 2011, , .		3
250	ADMAC: An adaptive directional MAC protocol for mobile ad hoc networks. , 2011, , .		1
251	Parallel Hematopoietic Stem Cell Division Rate Estimation Using an Agent-Based Model on the Grid. , 2011, , .		0
252	Stochastic analysis of a miRNA-protein toggle switch. <i>Molecular BioSystems</i> , 2011, 7, 2796.	2.9	16

#	ARTICLE	IF	CITATIONS
253	Alterations of primary fatty acid amides in serum of patients with severe mental illness. <i>Frontiers in Bioscience - Elite</i> , 2011, E3, 308-314.	0.9	12
254	Message from the workshop on the future of social networking. <i>Computer Communication Review</i> , 2011, 41, 14-18.	1.5	0
255	Methodological Bridges for Multi-Level Systems. <i>Procedia Computer Science</i> , 2011, 7, 180-182.	1.2	0
256	Biological principles for future internet architecture design. , 2011, 49, 44-52.		31
257	A Combined Process Algebraic and Stochastic Approach to Bone Remodeling. <i>Electronic Notes in Theoretical Computer Science</i> , 2011, 277, 41-52.	0.9	5
258	Assessing ventilation system performance in isolation rooms. <i>Energy and Buildings</i> , 2011, 43, 246-252.	3.1	21
259	Design of robust metabolic pathways. , 2011, , .		12
260	Epileptic EEG Detection via a Novel Pattern Recognition Framework. , 2011, , .		5
261	EpiChIP: gene-by-gene quantification of epigenetic modification levels. <i>Nucleic Acids Research</i> , 2011, 39, e27-e27.	6.5	36
262	Distinct Epigenomic Features in End-Stage Failing Human Hearts. <i>Circulation</i> , 2011, 124, 2411-2422.	1.6	245
263	A Variance-Components Model for Distance-Matrix Phylogenetic Reconstruction. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, .	0.2	0
264	StochKit-FF: Efficient Systems Biology on Multicore Architectures. <i>Lecture Notes in Computer Science</i> , 2011, , 167-175.	1.0	5
265	Community Structure in Social Networks: Applications for Epidemiological Modelling. <i>PLoS ONE</i> , 2011, 6, e22220.	1.1	31
266	Biologically inspired networking [Guest Editorial. <i>IEEE Network</i> , 2010, 24, 4-4.	4.9	5
267	Intra- and inter-chromosomal interactions correlate with CTCF binding genome wide. <i>Molecular Systems Biology</i> , 2010, 6, 426.	3.2	92
268	An integrated modelling approach for R524X mutation and HAART therapy assessment. <i>Swarm Intelligence</i> , 2010, 4, 319-340.	1.3	0
269	Detection Probability Estimation of Directional Antennas and Omni-Directional Antennas. <i>Wireless Personal Communications</i> , 2010, 55, 51-63.	1.8	8
270	Formal reasoning on qualitative models of coinfection of HIV and Tuberculosis and HAART therapy. <i>BMC Bioinformatics</i> , 2010, 11, S67.	1.2	6

#	ARTICLE	IF	CITATIONS
271	Statistical mechanics of rumour spreading in network communities. <i>Procedia Computer Science</i> , 2010, 1, 2331-2339.	1.2	28
272	Risk perception and disease spread on social networks. <i>Procedia Computer Science</i> , 2010, 1, 2345-2354.	1.2	30
273	Cognitive network dynamics in chatlines. <i>Procedia Computer Science</i> , 2010, 1, 2355-2362.	1.2	7
274	Identification of Targeted Analyte Clusters for Studies of Schizophrenia. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 510-522.	2.5	28
275	Features extraction via wavelet kernel PCA for data classification. , 2010, , .		3
276	Morphogenesis in computer networks. , 2010, , .		2
277	Generic spaced DNA motif discovery using Genetic Algorithm. , 2010, , .		5
278	Feature extraction via dynamic PCA for epilepsy diagnosis and epileptic seizure detection. , 2010, , .		2
279	Analysis and Optimization of C3 Photosynthetic Carbon Metabolism. , 2010, , .		11
280	Evolution of Metabolic Pathways and Evolution of Genomes. , 2010, , 37-68.		1
281	Combining Replicates and Nearby Species Data: A Bayesian Approach. <i>Lecture Notes in Computer Science</i> , 2010, , 191-205.	1.0	1
282	Noise and non-linearities in high-throughput data. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2009, 2009, P01014.	0.9	1
283	Estimating Dormant and Active Hematopoietic Stem Cell Kinetics through Extensive Modeling of Bromodeoxyuridine Label-Retaining Cell Dynamics. <i>PLoS ONE</i> , 2009, 4, e6972.	1.1	71
284	Towards real-time community detection in large networks. <i>Physical Review E</i> , 2009, 79, 066107.	0.8	223
285	Using Mutual Information and Models of Evolution for Improved Pattern Detection. , 2009, , .		0
286	A comparative study of noise effect on wavelet based de-noising methods. , 2009, , .		1
287	Trends in modeling Biomedical Complex Systems. <i>BMC Bioinformatics</i> , 2009, 10, I1.	1.2	25
288	Clinical bioinformatics for complex disorders: a schizophrenia case study. <i>BMC Bioinformatics</i> , 2009, 10, S6.	1.2	12

#	ARTICLE	IF	CITATIONS
289	Measuring similarity between gene expression profiles: a Bayesian approach. BMC Genomics, 2009, 10, S14.	1.2	11
290	The Evolution of Histidine Biosynthesis in Archaea: Insights into the his Genes Structure and Organization in LUCA. Journal of Molecular Evolution, 2009, 69, 512-526.	0.8	19
291	Bio-inspired multi-agent data harvesting in a proactive urban monitoring environment. Ad Hoc Networks, 2009, 7, 725-741.	3.4	41
292	Hematopoietic Stem Cells Reversibly Switch from Dormancy to Self-Renewal during Homeostasis and Repair. Cell, 2009, 138, 209.	13.5	2
293	Size Matters: Variation in Personal Network Size, Personality and Effect on Information Transmission. , 2009, , .		13
294	Impact of altruism on opportunistic communications. , 2009, , .		23
295	Selfishness, Altruism and Message Spreading in Mobile Social Networks. , 2009, , .		69
296	Minimizing Detection Probability Routing in Ad Hoc Networks Using Directional Antennas. Eurasip Journal on Wireless Communications and Networking, 2009, 2009, .	1.5	11
297	Information Processing and Timing Mechanisms in Vision. Lecture Notes in Computer Science, 2009, , 325-334.	1.0	1
298	Mathematical Model of HIV Superinfection and Comparative Drug Therapy. Lecture Notes in Computer Science, 2009, , 41-53.	1.0	0
299	Formal Analysis of the Genetic Toggle. Lecture Notes in Computer Science, 2009, , 96-110.	1.0	0
300	Searching for Glycomics Role in Stem Cell Development. Lecture Notes in Computer Science, 2009, , 198-209.	1.0	0
301	Substitution Matrices and Mutual Information Approaches to Modeling Evolution. Lecture Notes in Computer Science, 2009, , 259-272.	1.0	1
302	A Case Study of ICA with Multi-scale PCA of Simulated Traffic Data. Lecture Notes in Computer Science, 2009, , 358-367.	1.0	0
303	The Structural Network Properties of Biological Systems. World Scientific Lecture Notes in Complex Systems, 2009, , 9-31.	0.1	0
304	Modeling Sequence Evolution. Methods in Molecular Biology, 2008, 452, 255-285.	0.4	5
305	Analysis of plasmid genes by phylogenetic profiling and visualization of homology relationships using Blast2Network. BMC Bioinformatics, 2008, 9, 551.	1.2	57
306	Hematopoietic Stem Cells Reversibly Switch from Dormancy to Self-Renewal during Homeostasis and Repair. Cell, 2008, 135, 1118-1129.	13.5	1,627

#	ARTICLE	IF	CITATIONS
307	Security estimation model with directional antennas. , 2008, , .		10
308	Bio-Inspired Multi-agent Collaboration for Urban Monitoring Applications. Lecture Notes in Computer Science, 2008, , 204-216.	1.0	6
309	Combining Experimental Evidences from Replicates and Nearby Species Data for Annotating Novel Genomes. AIP Conference Proceedings, 2008, , .	0.3	2
310	Prediction by Graph Theoretic Measures of Structural Effects in Proteins Arising from Non-Synonymous Single Nucleotide Polymorphisms. PLoS Computational Biology, 2008, 4, e1000135.	1.5	53
311	Parametric & non-parametric analysis of mean treatment effects of number of packets in transit in data network model. Canadian Conference on Electrical and Computer Engineering, 2008, , .	0.0	2
312	A Location Prediction Algorithm for Directional Communication. , 2008, , .		5
313	Social Networking for Pervasive Adaptation. , 2008, , .		11
314	Identity Privacy Protection by Delayed Transmission in Pocket Switched Networks. , 2008, , .		0
315	A biologically inspired MANET architecture. Proceedings of SPIE, 2008, , .	0.8	0
316	Combining Molecular and Physiological Data of Complex Disorders. Communications in Computer and Information Science, 2008, , 362-376.	0.4	1
317	Bayesian Phylogeny on Grid. Communications in Computer and Information Science, 2008, , 404-416.	0.4	9
318	Inference on Missing Values in Genetic Networks Using High-Throughput Data. , 2008, , 106-116.		1
319	A Novel Mobility Model from a Heterogeneous Military MANET Trace. Lecture Notes in Computer Science, 2008, , 463-474.	1.0	13
320	Human Heuristics for Autonomous Agents. Lecture Notes in Computer Science, 2008, , 340-351.	1.0	2
321	Wavelet-Domain Statistics of Packet Switching Networks Near Traffic Congestion. Lecture Notes in Computer Science, 2008, , 268-279.	1.0	3
322	Topological Metrics in Blast Data Mining: Plasmid and Nitrogen-Fixing Proteins Case Studies. Communications in Computer and Information Science, 2008, , 207-220.	0.4	0
323	A Stochastic Multi-agent Model of Stem Cell Proliferation. Lecture Notes in Computer Science, 2008, , 500-505.	1.0	0
324	Bayesian Inference on Hidden Knowledge in High-Throughput Molecular Biology Data. Lecture Notes in Computer Science, 2008, , 829-838.	1.0	1

#	ARTICLE	IF	CITATIONS
325	Contact Network Modeling of Flu Epidemics. Lecture Notes in Computer Science, 2008, , 354-361.	1.0	0
326	Bottleneck Genes and Community Structure in the Cell Cycle Network of <i>S. pombe</i> . PLoS Computational Biology, 2007, 3, e103.	1.5	23
327	MotifScorer: using a compendium of microarrays to identify regulatory motifs. Bioinformatics, 2007, 23, 493-495.	1.8	8
328	Risk perception in epidemic modeling. Physical Review E, 2007, 76, 061904.	0.8	119
329	Current trends in the bioinformatic sequence analysis of metabolic pathways in prokaryotes. Briefings in Bioinformatics, 2007, 9, 34-45.	3.2	4
330	Wavelet Spectral Analysis of Packet Traffic Near Phase Transition Point from Free Flow to Congestion in Data Network Model. , 2007, , .		3
331	Grid Methodology for Identifying Co-Regulated Genes and Transcription Factor Binding Sites. IEEE Transactions on Nanobioscience, 2007, 6, 162-167.	2.2	4
332	Phylogenetics and Computational Biology of Multigene Families. Biological and Medical Physics Series, 2007, , 191-205.	0.3	1
333	Topological and dynamical properties of genetic and social networks. Proceedings in Applied Mathematics and Mechanics, 2007, 7, 2070007-2070008.	0.2	0
334	The role of gene fusions in the evolution of metabolic pathways: the histidine biosynthesis case. BMC Evolutionary Biology, 2007, 7, S4.	3.2	59
335	Modeling HIV quasispecies evolutionary dynamics. BMC Evolutionary Biology, 2007, 7, S5.	3.2	18
336	Phylogenetic analysis of mitochondrial protein coding genes confirms the reciprocal parphyly of Hexapoda and Crustacea. BMC Evolutionary Biology, 2007, 7, S8.	3.2	137
337	Multiple Protein Phosphatases Are Required for Mitosis in <i>Drosophila</i> . Current Biology, 2007, 17, 293-303.	1.8	119
338	Antarctic Fish Mitochondrial Genomes Lack ND6 Gene. Journal of Molecular Evolution, 2007, 65, 519-528.	0.8	38
339	Biometric Evidence that Sexual Selection Has Shaped the Hominin Face. PLoS ONE, 2007, 2, e710.	1.1	182
340	Keyword Searching in Structured Overlays Via Content Distance Addressing. Lecture Notes in Computer Science, 2007, , 259-272.	1.0	0
341	Beta Random Projection. , 2007, , .		0
342	Beta Random Projection. , 2007, , .		0

#	ARTICLE	IF	CITATIONS
343	A novel algorithm and web-based tool for comparing two alternative phylogenetic trees. <i>Bioinformatics</i> , 2006, 22, 117-119.	1.8	163
344	Computational framework for the prediction of transcription factor binding sites by multiple data integration. <i>BMC Neuroscience</i> , 2006, 7, S8.	0.8	3
345	Forensic DNA and bioinformatics. <i>Briefings in Bioinformatics</i> , 2006, 8, 117-128.	3.2	21
346	Modeling Evolutionary Dynamics of HIV Infection. <i>Lecture Notes in Computer Science</i> , 2006, , 196-211.	1.0	0
347	The Origin and Evolution of Operons: The Piecewise Building of the Proteobacterial Histidine Operon. <i>Journal of Molecular Evolution</i> , 2005, 60, 378-390.	0.8	52
348	Phylogenetic and structural analysis of mitochondrial complex I proteins. <i>Gene</i> , 2005, 345, 55-64.	1.0	9
349	Identification of DNA regulatory motifs using Bayesian variable selection. <i>Bioinformatics</i> , 2004, 20, 2553-2561.	1.8	33
350	Periodic gene expression program of the fission yeast cell cycle. <i>Nature Genetics</i> , 2004, 36, 809-817.	9.4	472
351	Phylogenomics and bioinformatics of SARS-CoV. <i>Trends in Microbiology</i> , 2004, 12, 106-111.	3.5	36
352	Statistical bioinformatic methods in microbial genome analysis. <i>BioEssays</i> , 2003, 25, 266-273.	1.2	6
353	Wavelets in bioinformatics and computational biology: state of art and perspectives. <i>Bioinformatics</i> , 2003, 19, 2-9.	1.8	265
354	Investigating the evolution and structure of chemokine receptors. <i>Gene</i> , 2003, 317, 29-37.	1.0	21
355	Dimensionality and dependence problems in statistical genomics. <i>Briefings in Bioinformatics</i> , 2003, 4, 168-177.	3.2	2
356	Investigating the Relationship Between Genome Structure, Composition, and Ecology in Prokaryotes. <i>Molecular Biology and Evolution</i> , 2002, 19, 789-800.	3.5	11
357	Modeling Mitochondrial Protein Evolution Using Structural Information. <i>Journal of Molecular Evolution</i> , 2002, 54, 519-529.	0.8	12
358	Modeling Mitochondrial Protein Evolution Using Structural Information. <i>Journal of Molecular Evolution</i> , 2002, 54, 519-529.	0.8	7
359	Molecular phylogenetics: state-of-the-art methods for looking into the past. <i>Trends in Genetics</i> , 2001, 17, 262-272.	2.9	376
360	Molecular Evolution of Nitrogen Fixation: The Evolutionary History of the nifD, nifK, nifE, and nifN Genes. <i>Journal of Molecular Evolution</i> , 2000, 51, 1-11.	0.8	141

#	ARTICLE	IF	CITATIONS
361	Models of Molecular Evolution and Phylogeny: Table 1.. Genome Research, 1998, 8, 1233-1244.	2.4	252
362	Association of the Gln 27 β 2-Adrenoceptor Polymorphism and IgE Variability in Asthmatic Families. Chest, 1997, 111, 78S-79S.	0.4	5
363	Genome flux in tomato cell clones cultured in vitro in different physiological equilibria. II. A RAPD analysis of variability. Genome, 1996, 39, 846-853.	0.9	36
364	High Statistics Block Entropy Measures of DNA Sequences. Journal of Theoretical Biology, 1996, 180, 151-160.	0.8	31
365	Analysis of Genomic Patchiness of Haemophilus influenzae and Saccharomyces cerevisiae Chromosomes. Journal of Theoretical Biology, 1996, 183, 455-469.	0.8	11
366	Selection, mutations and codon usage in a bacterial model. Journal of Theoretical Biology, 1995, 173, 271-281.	0.8	20
367	The evolution of the histidine biosynthetic genes in prokaryotes: A common ancestor for the hisA and hisF genes. Journal of Molecular Evolution, 1994, 38, 489-495.	0.8	69
368	Third Codon G + C Periodicity as a Possible Signal for an "Internal" Selective Constraint. Journal of Theoretical Biology, 1994, 171, 215-223.	0.8	20
369	Transcription factors and gene regulatory networks. , 0, , 36-52.		0
370	Multiple verification in computational modeling of bone pathologies. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 67, 82-96.	0.8	4
371	Unseen Word Representation by Aligning Heterogeneous Lexical Semantic Spaces. Proceedings of the AAAI Conference on Artificial Intelligence, 0, 33, 6900-6907.	3.6	6