Pietro Lio'

List of Publications by Year
in descending order

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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	Hematopoietic Stem Cells Reversibly Switch from Dormancy to Self-Renewal during Homeostasis and Repair. Cell, 2008, 135, 1118-1129.	13.5	1,627
2	The BioMart community portal: an innovative alternative to large, centralized data repositories. Nucleic Acids Research, 2015, 43, W589-W598.	6.5	682
3	Periodic gene expression program of the fission yeast cell cycle. Nature Genetics, 2004, 36, 809-817.	9.4	472
4	Molecular phylogenetics: state-of-the-art methods for looking into the past. Trends in Genetics, 2001, 17, 262-272.	2.9	376
5	M<scp>e</scp>D<scp>u</scp>S<scp>a</scp>: a multi-draft based scaffolder. Bioinformatics, 2015, 31, 2443-2451.	1.8	359
6	Wavelets in bioinformatics and computational biology: state of art and perspectives. Bioinformatics, 2003, 19, 2-9.	1.8	265
7	A parameter-efficient deep learning approach to predict conversion from mild cognitive impairment to Alzheimer's disease. NeuroImage, 2019, 189, 276-287.	2.1	260
8	Models of Molecular Evolution and Phylogeny: Table 1.. Genome Research, 1998, 8, 1233-1244.	2.4	252
9	Distinct Epigenomic Features in End-Stage Failing Human Hearts. Circulation, 2011, 124, 2411-2422.	1.6	245
10	Towards real-time community detection in large networks. Physical Review E, 2009, 79, 066107.	0.8	223
11	Opportunistic routing through conjugation in bacteria communication nanonetwork. Nano Communication Networks, 2012, 3, 36-45.	1.6	223
12	Biometric Evidence that Sexual Selection Has Shaped the Hominin Face. PLoS ONE, 2007, 2, e710.	1.1	182
13	Predicting factors for survival of breast cancer patients using machine learning techniques. BMC Medical Informatics and Decision Making, 2019, 19, 48.	1.5	166
14	A novel algorithm and web-based tool for comparing two alternative phylogenetic trees. Bioinformatics, 2006, 22, 117-119.	1.8	163
15	Computational Modeling, Formal Analysis, and Tools for Systems Biology. PLoS Computational Biology, 2016, 12, e1004591.	1.5	162
16	Collective Human Mobility Pattern from Taxi Trips in Urban Area. PLoS ONE, 2012, 7, e34487.	1.1	150
17	Single-cell RNA-sequencing uncovers transcriptional states and fate decisions in haematopoiesis. Nature Communications, 2017, 8, 2045.	5.8	147
18	Molecular Evolution of Nitrogen Fixation: The Evolutionary History of the nifD, nifK, nifE, and nifN Genes. Journal of Molecular Evolution, 2000, 51, 1-11.	0.8	141

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19	Phylogenetic analysis of mitochondrial protein coding genes confirms the reciprocal paraphyly of Hexapoda and Crustacea. BMC Evolutionary Biology, 2007, 7, S8.	3.2	137
20	Applications of molecular communications to medicine: A survey. Nano Communication Networks, 2016, 7, 27-45.	1.6	128
21	Multi -omics and metabolic modelling pipelines: Challenges and tools for systems microbiology. Microbiological Research, 2015, 171, 52-64.	2.5	125
22	Parapred: antibody paratope prediction using convolutional and recurrent neural networks. Bioinformatics, 2018, 34, 2944-2950.	1.8	124
23	A machine learning model to identify early stage symptoms of SARS-Cov-2 infected patients. Expert Systems With Applications, 2020, 160, 113661.	4.4	120
24	Risk perception in epidemic modeling. Physical Review E, 2007, 76, 061904.	0.8	119
25	Multiple Protein Phosphatases Are Required for Mitosis in Drosophila. Current Biology, 2007, 17, 293-303.	1.8	119
26	How artificial intelligence and machine learning can help healthcare systems respond to COVID-19. Machine Learning, 2021, 110, 1-14.	3.4	102
27	Machine Learning-Based Models for Early Stage Detection of Autism Spectrum Disorders. IEEE Access, 2019, 7, 166509-166527.	2.6	101
28	Network-based analysis of comorbidities risk during an infection: SARS and HIV case studies. BMC Bioinformatics, 2014, 15, 333.	1.2	93
29	Intraâ€•and interâ€•chromosomal interactions correlate with CTCF binding genome wide. Molecular Systems Biology, 2010, 6, 426.	3.2	92
30	Multi-Hop Conjugation Based Bacteria Nanonetworks. IEEE Transactions on Nanobioscience, 2013, 12, 47-59.	2.2	89
31	Privacy-Preserving Asynchronous Federated Learning Mechanism for Edge Network Computing. IEEE Access, 2020, 8, 48970-48981.	2.6	88
32	comoR: a software for disease comorbidity risk assessment. Journal of Clinical Bioinformatics, 2014, 4, 8.	1.2	81
33	Emotion Recognition From EEG Signal Focusing on Deep Learning and Shallow Learning Techniques. IEEE Access, 2021, 9, 94601-94624.	2.6	77
34	Variational Autoencoders for Cancer Data Integration: Design Principles and Computational Practice. Frontiers in Genetics, 2019, 10, 1205.	1.1	76
35	Estimating Dormant and Active Hematopoietic Stem Cell Kinetics through Extensive Modeling of Bromodeoxyuridine Label-Retaining Cell Dynamics. PLoS ONE, 2009, 4, e6972.	1.1	71
36	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

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37	Selfishness, Altruism and Message Spreading in Mobile Social Networks. , 2009, , .		69
38	A review of experimental opportunities for molecular communication. Nano Communication Networks, 2013, 4, 43-52.	1.6	67
39	The role of gene fusions in the evolution of metabolic pathways: the histidine biosynthesis case. BMC Evolutionary Biology, 2007, 7, S4.	3.2	59
40	Analysis of plasmid genes by phylogenetic profiling and visualization of homology relationships using Blast2Network. BMC Bioinformatics, 2008, 9, 551.	1.2	57
41	AI-Based Reconstruction for Fast MRIâ€"A Systematic Review and Meta-Analysis. Proceedings of the IEEE, 2022, 110, 224-245.	16.4	57
42	Comorbidity: a multidimensional approach. Trends in Molecular Medicine, 2013, 19, 515-521.	3.5	54
43	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
44	Robust design of microbial strains. Bioinformatics, 2012, 28, 3097-3104.	1.8	53
45	How to build personalized multi-omics comorbidity profiles. Frontiers in Cell and Developmental Biology, 2015, 3, 28.	1.8	53
46	Genomeâ€scale metabolic reconstruction and constraintâ€based modelling of the Antarctic bacterium <scp><i>P</i></scp><i>seudoalteromonas haloplanktis</i>â€…<scp>TAC</scp>125. Environmental Microbiology, 2015, 17, 751-766.	1.8	53
47	The Origin and Evolution of Operons: The Piecewise Building of the Proteobacterial Histidine Operon. Journal of Molecular Evolution, 2005, 60, 378-390.	0.8	52
48	DrugClust: A machine learning approach for drugs side effects prediction. Computational Biology and Chemistry, 2017, 68, 204-210.	1.1	51
49	Genetic Profiling and Comorbidities of Zika Infection. Journal of Infectious Diseases, 2017, 216, 703-712.	1.9	48
50	Using Deep Data Augmentation Training to Address Software and Hardware Heterogeneities in Wearable and Smartphone Sensing Devices. , 2018, , .		47
51	Combining a wavelet change point and the Bayes factor for analysing chromosomal interaction data. Molecular BioSystems, 2014, 10, 1576-1585.	2.9	46
52	The Impact of Heterogeneity and Awareness in Modeling Epidemic Spreading on Multiplex Networks. Scientific Reports, 2016, 6, 37105.	1.6	45
53	Predictive analytics of environmental adaptability in multi-omic network models. Scientific Reports, 2015, 5, 15147.	1.6	43
54	How Can We Make Gan Perform Better in Single Medical Image Super-Resolution? A Lesion Focused Multi-Scale Approach. , 2019, , .		43

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55	NuChart: An R Package to Study Gene Spatial Neighbourhoods with Multi-Omics Annotations. PLoS ONE, 2013, 8, e75146.	1.1	42
56	CytoCom: a Cytoscape app to visualize, query and analyse disease comorbidity networks. Bioinformatics, 2015, 31, 969-971.	1.8	42
57	Pathogenetic profiling of COVID-19 and SARS-like viruses. Briefings in Bioinformatics, 2021, 22, 1175-1196.	3.2	42
58	ML-SIM: universal reconstruction of structured illumination microscopy images using transfer learning. Biomedical Optics Express, 2021, 12, 2720.	1.5	42
59	Bio-inspired multi-agent data harvesting in a proactive urban monitoring environment. Ad Hoc Networks, 2009, 7, 725-741.	3.4	41
60	Antarctic Fish Mitochondrial Genomes Lack ND6 Gene. Journal of Molecular Evolution, 2007, 65, 519-528.	0.8	38
61	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
62	Multiplex methods provide effective integration of multi-omic data in genome-scale models. BMC Bioinformatics, 2016, 17, 83.	1.2	37
63	Genetic effects of welding fumes on the progression of neurodegenerative diseases. NeuroToxicology, 2019, 71, 93-101.	1.4	37
64	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
65	Phylogenomics and bioinformatics of SARS-CoV. Trends in Microbiology, 2004, 12, 106-111.	3.5	36
66	EpiChIP: gene-by-gene quantification of epigenetic modification levels. Nucleic Acids Research, 2011, 39, e27-e27.	6.5	36
67	Offloading mobile data from cellular networks through peer-to-peer WiFi communication: A subscribe-and-send architecture. China Communications, 2013, 10, 35-46.	2.0	36
68	FisHiCal: an R package for iterative FISH-based calibration of Hi-C data. Bioinformatics, 2014, 30, 3120-3122.	1.8	35
69	Systems medicine of inflammaging. Briefings in Bioinformatics, 2016, 17, 527-540.	3.2	35
70	From Infection to Immunity: Understanding the Response to SARS-CoV2 Through In-Silico Modeling. Frontiers in Immunology, 2021, 12, 646972.	2.2	35
71	Continuous authentication by free-text keystroke based on CNN and RNN. Computers and Security, 2020, 96, 101861.	4.0	35
72	A Multi-modal Convolutional Neural Network Framework for the Prediction of Alzheimerâ€™s Disease. , 2018, 2018, 1271-1274.		34

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73	StackDPPIV: A novel computational approach for accurate prediction of dipeptidyl peptidase IV (DPP-IV) inhibitory peptides. Methods, 2022, 204, 189-198.	1.9	34
74	Identification of DNA regulatory motifs using Bayesian variable selection. Bioinformatics, 2004, 20, 2553-2561.	1.8	33
75	The landscape of DNA repeat elements in human heart failure. Genome Biology, 2012, 13, R90.	13.9	33
76	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
77	High Statistics Block Entropy Measures of DNA Sequences. Journal of Theoretical Biology, 1996, 180, 151-160.	0.8	31
78	Biological principles for future internet architecture design. , 2011, 49, 44-52.		31
79	Modelling osteomyelitis. BMC Bioinformatics, 2012, 13, S12.	1.2	31
80	Analyzing seasonality of tuberculosis across Indian states and union territories. Journal of Epidemiology and Global Health, 2015, 5, 337.	1.1	31
81	Combining evolutionary game theory and network theory to analyze human cooperation patterns. Chaos, Solitons and Fractals, 2016, 91, 17-24.	2.5	31
82	Community Structure in Social Networks: Applications for Epidemiological Modelling. PLoS ONE, 2011, 6, e22220.	1.1	31
83	Risk perception and disease spread on social networks. Procedia Computer Science, 2010, 1, 2345-2354.	1.2	30
84	Pathway-based subnetworks enable cross-disease biomarker discovery. Nature Communications, 2018, 9, 4746.	5.8	30
85	ASSCA: API sequence and statistics features combined architecture for malware detection. Computer Networks, 2019, 157, 99-111.	3.2	30
86	Genetic effects of welding fumes on the development of respiratory system diseases. Computers in Biology and Medicine, 2019, 108, 142-149.	3.9	30
87	Quantifying the Role of Homophily in Human Cooperation Using Multiplex Evolutionary Game Theory. PLoS ONE, 2015, 10, e0140646.	1.1	29
88	Statistical mechanics of rumour spreading in network communities. Procedia Computer Science, 2010, 1, 2331-2339.	1.2	28
89	Identification of Targeted Analyte Clusters for Studies of Schizophrenia. Molecular and Cellular Proteomics, 2010, 9, 510-522.	2.5	28
90	Cancer Markers Selection Using Network-Based Cox Regression: A Methodological and Computational Practice. Frontiers in Physiology, 2016, 7, 208.	1.3	27

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91	iBitter-Fuse: A Novel Sequence-Based Bitter Peptide Predictor by Fusing Multi-View Features. International Journal of Molecular Sciences, 2021, 22, 8958.	1.8	27
92	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
93	GenHap: a novel computational method based on genetic algorithms for haplotype assembly. BMC Bioinformatics, 2019, 20, 172.	1.2	26
94	Trends in modeling Biomedical Complex Systems. BMC Bioinformatics, 2009, 10, I1.	1.2	25
95	Quantifying the propagation of distress and mental disorders in social networks. Scientific Reports, 2018, 8, 5005.	1.6	25
96	Proximal Distilled Evolutionary Reinforcement Learning. Proceedings of the AAAI Conference on Artificial Intelligence, 2020, 34, 3283-3290.	3.6	25
97	A Molecular Communication System in Blood Vessels for Tumor Detection. , 2014, , .		24
98	Deep convolutional neural networks based ECG beats classification to diagnose cardiovascular conditions. Biomedical Engineering Letters, 2021, 11, 147-162.	2.1	24
99	Temporal pointwise convolutional networks for length of stay prediction in the intensive care unit. , 2021, , .		24
100	Arbitrary Scale Super-Resolution for Medical Images. International Journal of Neural Systems, 2021, 31, 2150037.	3.2	24
101	Genome-Scale Metabolic Network Reconstruction. Methods in Molecular Biology, 2015, 1231, 233-256.	0.4	24
102	Bottleneck Genes and Community Structure in the Cell Cycle Network of S. pombe. PLoS Computational Biology, 2007, 3, e103.	1.5	23
103	Impact of altruism on opportunistic communications. , 2009, , .		23
104	The Puzzling Role of CXCR4 in Human Immunodeficiency Virus Infection. Theranostics, 2013, 3, 18-25.	4.6	23
105	Machine Learning and Bioinformatics Models to Identify Pathways that Mediate Influences of Welding Fumes on Cancer Progression. Scientific Reports, 2020, 10, 2795.	1.6	23
106	Adversarial generation of gene expression data. Bioinformatics, 2022, 38, 730-737.	1.8	23
107	Pareto Optimality in Organelle Energy Metabolism Analysis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1032-1044.	1.9	22
108	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

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109	Making life difficult for Clostridium difficile: augmenting the pathogenâ€™s metabolic model with transcriptomic and codon usage data for better therapeutic target characterization. BMC Systems Biology, 2017, 11, 25.	3.0	22
110	Horizontal gene transfer and silver nanoparticles production in a new Marinomonas strain isolated from the Antarctic psychrophilic ciliate Euplotes focardii. Scientific Reports, 2020, 10, 10218.	1.6	22
111	Cell graph neural networks enable the precise prediction of patient survival in gastric cancer. Npj Precision Oncology, 2022, 6, .	2.3	22
112	Investigating the evolution and structure of chemokine receptors. Gene, 2003, 317, 29-37.	1.0	21
113	Forensic DNA and bioinformatics. Briefings in Bioinformatics, 2006, 8, 117-128.	3.2	21
114	Assessing ventilation system performance in isolation rooms. Energy and Buildings, 2011, 43, 246-252.	3.1	21
115	SCORPION is a stacking-based ensemble learning framework for accurate prediction of phage virion proteins. Scientific Reports, 2022, 12, 4106.	1.6	21
116	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
117	Selection, mutations and codon usage in a bacterial model. Journal of Theoretical Biology, 1995, 173, 271-281.	0.8	20
118	Information dynamics algorithm for detecting communities in networks. Communications in Nonlinear Science and Numerical Simulation, 2012, 17, 4294-4303.	1.7	20
119	Graph Representation Forecasting of Patient's Medical Conditions: Toward a Digital Twin. Frontiers in Genetics, 2021, 12, 652907.	1.1	20
120	A deep graph neural network architecture for modelling spatio-temporal dynamics in resting-state functional MRI data. Medical Image Analysis, 2022, 79, 102471.	7.0	20
121	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
122	Forward and Reverse coding for chromosome transfer in bacterial nanonetworks. Nano Communication Networks, 2014, 5, 15-24.	1.6	19
123	Teaching sustainability as complex systems approach: a sustainable development goals workshop. International Journal of Sustainability in Higher Education, 2021, 22, 25-41.	1.6	19
124	Modeling HIV quasispecies evolutionary dynamics. BMC Evolutionary Biology, 2007, 7, S5.	3.2	18
125	Comorbidity networks: beyond disease correlations. Journal of Complex Networks, 2015, 3, 319-332.	1.1	18
126	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

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127	Integration of Machine Learning Methods to Dissect Genetically Imputed Transcriptomic Profiles in Alzheimerâ€™s Disease. Frontiers in Genetics, 2019, 10, 726.	1.1	18
128	CytoHiC: a cytoscape plugin for visual comparison of Hi-C networks. Bioinformatics, 2013, 29, 1206-1207.	1.8	17
129	Pathway-based Bayesian inference of drugâ€“disease interactions. Molecular BioSystems, 2014, 10, 1538-1548.	2.9	17
130	Draft genomes of three Antarctic Psychrobacter strains producing antimicrobial compounds against Burkholderia cepacia complex, opportunistic human pathogens. Marine Genomics, 2014, 13, 37-38.	0.4	17
131	Cross-modal Recurrent Models for Weight Objective Prediction from Multimodal Time-series Data. , 2018, , .		17
132	XFlow: Cross-Modal Deep Neural Networks for Audiovisual Classification. IEEE Transactions on Neural Networks and Learning Systems, 2020, 31, 3711-3720.	7.2	17
133	Evidence in cortical folding patterns for prenatal predispositions to hallucinations in schizophrenia. Translational Psychiatry, 2020, 10, 387.	2.4	17
134	Stochastic analysis of a miRNAâ€“protein toggle switch. Molecular BioSystems, 2011, 7, 2796.	2.9	16
135	Multilevel Computational Modeling and Quantitative Analysis of Bone Remodeling. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1366-1378.	1.9	16
136	Exploring the complexity of pathwayâ€“drug relationships using latent Dirichlet allocation. Computational Biology and Chemistry, 2014, 53, 144-152.	1.1	16
137	Protein Interaction Networks Link Schizophrenia Risk Loci to Synaptic Function. Schizophrenia Bulletin, 2016, 42, 1334-1342.	2.3	16
138	Identification of strategic molecules for future circular supply chains using large reaction networks. Reaction Chemistry and Engineering, 2019, 4, 1969-1981.	1.9	16
139	Systems based analysis of human embryos and gene networks involved in cell lineage allocation. BMC Genomics, 2019, 20, 171.	1.2	16
140	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
141	CellVGAE: an unsupervised scRNA-seq analysis workflow with graph attention networks. Bioinformatics, 2022, 38, 1277-1286.	1.8	16
142	Bioaccumulation modelling and sensitivity analysis for discovering key players in contaminated food webs: The case study of PCBs in the Adriatic Sea. Ecological Modelling, 2015, 306, 205-215.	1.2	15
143	Analysis of single-cell RNA sequencing data based on autoencoders. BMC Bioinformatics, 2021, 22, 309.	1.2	15
144	Optimization of Multi-Omic Genome-Scale Models: Methodologies, Hands-on Tutorial, and Perspectives. Methods in Molecular Biology, 2018, 1716, 389-408.	0.4	14

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145	How to integrate wet lab and bioinformatics procedures for wine DNA admixture analysis and compositional profiling: Case studies and perspectives. PLoS ONE, 2019, 14, e0211962.	1.1	14
146	A geroscience approach for Parkinsonâ€™s disease: Conceptual framework and design of PROPAG-AGEING project. Mechanisms of Ageing and Development, 2021, 194, 111426.	2.2	14
147	Deep Learning Enables Fast and Accurate Imputation of Gene Expression. Frontiers in Genetics, 2021, 12, 624128.	1.1	14
148	Early downregulation of hsa-miR-144-3p in serum from drug-naÃ¯ve Parkinsonâ€™s disease patients. Scientific Reports, 2022, 12, 1330.	1.6	14
149	Size Matters: Variation in Personal Network Size, Personality and Effect on Information Transmission. , 2009, , .		13
150	It measures like me: An IoTs algorithm in WSNs based on heuristics behavior and clustering methods. Ad Hoc Networks, 2013, 11, 2637-2647.	3.4	13
151	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
152	A Novel Mobility Model from a Heterogeneous Military MANET Trace. Lecture Notes in Computer Science, 2008, , 463-474.	1.0	13
153	The Onset of Type 2 Diabetes: Proposal for a Multi-Scale Model. JMIR Research Protocols, 2013, 2, e44.	0.5	13
154	Modeling Mitochondrial Protein Evolution Using Structural Information. Journal of Molecular Evolution, 2002, 54, 519-529.	0.8	12
155	Clinical bioinformatics for complex disorders: a schizophrenia case study. BMC Bioinformatics, 2009, 10, S6.	1.2	12
156	Alterations of primary fatty acid amides in serum of patients with severe mental illness. Frontiers in Bioscience - Elite, 2011, E3, 308-314.	0.9	12
157	Design of robust metabolic pathways. , 2011, , .		12
158	Modelling Circulating Tumour Cells for Personalised Survival Prediction in Metastatic Breast Cancer. PLoS Computational Biology, 2015, 11, e1004199.	1.5	12
159	Analysis of Genomic Patchiness ofHaemophilus influenzaeandSaccharomyces cerevisiaeChromosomes. Journal of Theoretical Biology, 1996, 183, 455-469.	0.8	11
160	Investigating the Relationship Between Genome Structure, Composition, and Ecology in Prokaryotes. Molecular Biology and Evolution, 2002, 19, 789-800.	3.5	11
161	Social Networking for Pervasive Adaptation. , 2008, , .		11
162	Measuring similarity between gene expression profiles: a Bayesian approach. BMC Genomics, 2009, 10, S14.	1.2	11

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163	Minimizing Detection Probability Routing in Ad Hoc Networks Using Directional Antennas. Eurasip Journal on Wireless Communications and Networking, 2009, 2009, .	1.5	11
164	Analysis and Optimization of C3 Photosynthetic Carbon Metabolism. , 2010, , .		11
165	Bioremediation in marine ecosystems: a computational study combining ecological modeling and flux balance analysis. Frontiers in Genetics, 2014, 5, 319.	1.1	11
166	Who Wrote This? Textual Modeling with Authorship Attribution in Big Data. , 2014, , .		11
167	Integrating multi-omic features exploiting Chromosome Conformation Capture data. Frontiers in Genetics, 2015, 6, 40.	1.1	11
168	X-CNN: Cross-modal convolutional neural networks for sparse datasets. , 2016, , .		11
169	Neural network fusion: a novel CT-MR aortic aneurysm image segmentation method. , 2018, 10574, .		11
170	Multiâ€“omic analysis of signalling factors in inflammatory comorbidities. BMC Bioinformatics, 2018, 19, 439.	1.2	11
171	Stochastic Channel Switching of Frequency-Encoded Signals in Molecular Communication Networks. IEEE Communications Letters, 2018, 22, 332-335.	2.5	11
172	PECLIDES Neuro: A Personalisable Clinical Decision Support System for Neurological Diseases. Frontiers in Artificial Intelligence, 2020, 3, 23.	2.0	11
173	Unsupervised generative and graph representation learning for modelling cell differentiation. Scientific Reports, 2020, 10, 9790.	1.6	11
174	Deep Graph Mapper: Seeing Graphs Through the Neural Lens. Frontiers in Big Data, 2021, 4, 680535.	1.8	11
175	A Fine-Grained IoT Data Access Control Scheme Combining Attribute-Based Encryption and Blockchain. Security and Communication Networks, 2021, 2021, 1-13.	1.0	11
176	Lesion focused super-resolution. , 2019, , .		11
177	Investigating Meta-Approaches for Reconstructing Gene Networks in a Mammalian Cellular Context. PLoS ONE, 2012, 7, e28713.	1.1	11
178	Metabolite and lipoprotein profiles reveal sex-related oxidative stress imbalance in de novo drug-naive Parkinsonâ€™s disease patients. Npj Parkinson's Disease, 2022, 8, 14.	2.5	11
179	Security estimation model with directional antennas. , 2008, , .		10
180	Efficient Behavior of Photosynthetic Organelles via Pareto Optimality, Identifiability, and Sensitivity Analysis. ACS Synthetic Biology, 2013, 2, 274-288.	1.9	10

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181	How computer science can help in understanding the 3D genome architecture. Briefings in Bioinformatics, 2016, 17, 733-744.	3.2	10
182	Combining Pathway Identification and Breast Cancer Survival Prediction via Screening-Network Methods. Frontiers in Genetics, 2018, 9, 206.	1.1	10
183	Deep Learning for Proteinâ€“Protein Interaction Site Prediction. Methods in Molecular Biology, 2021, 2361, 263-288.	0.4	10
184	Heterogeneous Model Fusion Federated Learning Mechanism Based on Model Mapping. IEEE Internet of Things Journal, 2022, 9, 6058-6068.	5.5	10
185	Arbitrary Scale Super-Resolution forÂBrain MRI Images. IFIP Advances in Information and Communication Technology, 2020, , 165-176.	0.5	10
186	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
187	Phylogenetic and structural analysis of mitochondrial complex I proteins. Gene, 2005, 345, 55-64.	1.0	9
188	An adaptive directional MAC protocol for ad hoc networks using directional antennas. Science China Information Sciences, 2012, 55, 1360-1371.	2.7	9
189	Short and long-term genome stability analysis of prokaryotic genomes. BMC Genomics, 2013, 14, 309.	1.2	9
190	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
191	Channel modelling of molecular communications across blood vessels and nerves. , 2016, , .		9
192	Social dynamics modeling of chrono-nutrition. PLoS Computational Biology, 2019, 15, e1006714.	1.5	9
193	Bayesian Phylogeny on Grid. Communications in Computer and Information Science, 2008, , 404-416.	0.4	9
194	NEPTUNE: A novel computational approach for accurate and large-scale identification of tumor homing peptides. Computers in Biology and Medicine, 2022, 148, 105700.	3.9	9
195	MotifScorer: using a compendium of microarrays to identify regulatory motifs. Bioinformatics, 2007, 23, 493-495.	1.8	8
196	Detection Probability Estimation of Directional Antennas and Omni-Directional Antennas. Wireless Personal Communications, 2010, 55, 51-63.	1.8	8
197	A design automation framework for computational bioenergetics in biological networks. Molecular BioSystems, 2013, 9, 2554.	2.9	8
198	Multi-Target Analysis and Design of Mitochondrial Metabolism. PLoS ONE, 2015, 10, e0133825.	1.1	8

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199	Computational Models for Trapping Ebola Virus Using Engineered Bacteria. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 2017-2027.	1.9	8
200	Comparative Study of Inference Methods for Bayesian Nonnegative Matrix Factorisation. Lecture Notes in Computer Science, 2017, , 513-529.	1.0	8
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