

Pietro Lio

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

366
papers

8,583
citations

40
h-index

85
g-index

421
ext. papers

10,770
ext. citations

4.7
avg, IF

6.45
L-index

#	Paper	IF	Citations
366	Early downregulation of hsa-miR-144-3p in serum from drug-naïve Parkinson's disease patients.. <i>Scientific Reports</i> , 2022 , 12, 1330	4.9	1
365	System Neural Network: Evolution and Change based Structure Learning. <i>IEEE Transactions on Artificial Intelligence</i> , 2022 , 1-1	4.7	0
364	Metabolite and lipoprotein profiles reveal sex-related oxidative stress imbalance in de novo drug-naïve Parkinson's disease patients.. <i>Npj Parkinsons Disease</i> , 2022 , 8, 14	9.7	1
363	Metabolically Driven Latent Space Learning for Gene Expression Data 2022 , 131-155		
362	AI-Based Reconstruction for Fast MRI: Systematic Review and Meta-Analysis. <i>Proceedings of the IEEE</i> , 2022 , 110, 224-245	14.3	8
361	Transcriptional biomarkers of response to pharmacological treatments in severe mental disorders: A systematic review.. <i>European Neuropsychopharmacology</i> , 2022 , 55, 112-157	1.2	2
360	SCORPION is a stacking-based ensemble learning framework for accurate prediction of phage virion proteins.. <i>Scientific Reports</i> , 2022 , 12, 4106	4.9	1
359	Molecular Markers and Genomics for Food and Beverages Characterization 2022 , 889-909		
358	End-to-End Deep Learning of Non-rigid Groupwise Registration and Reconstruction of Dynamic MRI.. <i>Frontiers in Cardiovascular Medicine</i> , 2022 , 9, 880186	5.4	
357	AMYPred-FRL is a novel approach for accurate prediction of amyloid proteins by using feature representation learning.. <i>Scientific Reports</i> , 2022 , 12, 7697	4.9	1
356	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	15.4	0
355	Molecular Markers and Genomics for Food and Beverages Characterization 2021 , 1-21		
354	Modeling Brain-Heart Crosstalk Information in Patients with Traumatic Brain Injury. <i>Neurocritical Care</i> , 2021 , 1	3.3	1
353	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,	11.5	2
352	Signal metrics analysis of oscillatory patterns in bacterial multi-omic networks. <i>Bioinformatics</i> , 2021 , 37, 1411-1419	7.2	
351	Teaching sustainability as complex systems approach: a sustainable development goals workshop. <i>International Journal of Sustainability in Higher Education</i> , 2021 , 22, 25-41	3.9	8
350	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	5.6	6

349	Advantages of using graph databases to explore chromatin conformation capture experiments. <i>BMC Bioinformatics</i> , 2021 , 22, 43	3.6	
348	ML-SIM: universal reconstruction of structured illumination microscopy images using transfer learning. <i>Biomedical Optics Express</i> , 2021 , 12, 2720-2733	3.5	11
347	Temporal pointwise convolutional networks for length of stay prediction in the intensive care unit 2021 ,		3
346	Deep Learning Enables Fast and Accurate Imputation of Gene Expression. <i>Frontiers in Genetics</i> , 2021 , 12, 624128	4.5	0
345	Multilayer modelling of the human transcriptome and biological mechanisms of complex diseases and traits. <i>Npj Systems Biology and Applications</i> , 2021 , 7, 24	5	0
344	Analysis of single-cell RNA sequencing data based on autoencoders. <i>BMC Bioinformatics</i> , 2021 , 22, 309	3.6	3
343	Deep Graph Mapper: Seeing Graphs Through the Neural Lens. <i>Frontiers in Big Data</i> , 2021 , 4, 680535	2.8	6
342	Arbitrary Scale Super-Resolution for Medical Images. <i>International Journal of Neural Systems</i> , 2021 , 31, 2150037	6.2	7
341	Pathogenetic profiling of COVID-19 and SARS-like viruses. <i>Briefings in Bioinformatics</i> , 2021 , 22, 1175-1196	3.4	20
340	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	6.6	1
339	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	2
338	Emotion Recognition From EEG Signal Focusing on Deep Learning and Shallow Learning Techniques. <i>IEEE Access</i> , 2021 , 9, 94601-94624	3.5	16
337	Deep Learning for Protein-Protein Interaction Site Prediction. <i>Methods in Molecular Biology</i> , 2021 , 2361, 263-288	1.4	3
336	Heterogeneous Model Fusion Federated Learning Mechanism based on Model Mapping. <i>IEEE Internet of Things Journal</i> , 2021 , 1-1	10.7	1
335	Deep convolutional neural networks based ECG beats classification to diagnose cardiovascular conditions. <i>Biomedical Engineering Letters</i> , 2021 , 11, 147-162	3.6	5
334	iBitter-Fuse: A Novel Sequence-Based Bitter Peptide Predictor by Fusing Multi-View Features. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	4
333	A Fine-Grained IoT Data Access Control Scheme Combining Attribute-Based Encryption and Blockchain. <i>Security and Communication Networks</i> , 2021 , 2021, 1-13	1.9	5
332	From Infection to Immunity: Understanding the Response to SARS-CoV2 Through Modeling. <i>Frontiers in Immunology</i> , 2021 , 12, 646972	8.4	4

331	Graph Representation Forecasting of Patient's Medical Conditions: Toward a Digital Twin. <i>Frontiers in Genetics</i> , 2021 , 12, 652907	4.5	4
330	Heterogeneity of prodromal Parkinson symptoms in siblings of Parkinson disease patients. <i>Npj Parkinsons Disease</i> , 2021 , 7, 78	9.7	0
329	Analysis of Cardio-Cerebral Crosstalk Events in an Adult Cohort from the CENTER-TBI Study. <i>Acta Neurochirurgica Supplementum</i> , 2021 , 131, 39-42	1.7	1
328	Adversarial generation of gene expression data. <i>Bioinformatics</i> , 2021 ,	7.2	3
327	A class-contrastive human-interpretable machine learning approach to predict mortality in severe mental illness. <i>NPJ Schizophrenia</i> , 2021 , 7, 60	5.5	0
326	CellVGAE: an unsupervised scRNA-seq analysis workflow with graph attention networks. <i>Bioinformatics</i> , 2021 ,	7.2	1
325	A Universal Malicious Documents Static Detection Framework Based on Feature Generalization. <i>Applied Sciences (Switzerland)</i> , 2021 , 11, 12134	2.6	1
324	StackDPPIV: a novel computational approach for accurate prediction of dipeptidyl peptidase IV (DPP-IV) inhibitory peptides. <i>Methods</i> , 2021 ,	4.6	3
323	COSMONET: An R Package for Survival Analysis Using Screening-Network Methods. <i>Mathematics</i> , 2021 , 9, 3262	2.3	1
322	Evidence in cortical folding patterns for prenatal predispositions to hallucinations in schizophrenia. <i>Translational Psychiatry</i> , 2020 , 10, 387	8.6	9
321	PECLIDES Neuro: A Personalisable Clinical Decision Support System for Neurological Diseases. <i>Frontiers in Artificial Intelligence</i> , 2020 , 3, 23	3	6
320	A machine learning model to identify early stage symptoms of SARS-Cov-2 infected patients. <i>Expert Systems With Applications</i> , 2020 , 160, 113661	7.8	57
319	Domain-Oriented Topic Discovery Based on Features Extraction and Topic Clustering. <i>IEEE Access</i> , 2020 , 8, 93648-93662	3.5	2
318	Privacy-Preserving Asynchronous Federated Learning Mechanism for Edge Network Computing. <i>IEEE Access</i> , 2020 , 8, 48970-48981	3.5	46
317	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	4.9	7
316	Unsupervised generative and graph representation learning for modelling cell differentiation. <i>Scientific Reports</i> , 2020 , 10, 9790	4.9	8
315	Proximal Distilled Evolutionary Reinforcement Learning. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2020 , 34, 3283-3290	5	5
314	ChronoMID-Cross-modal neural networks for 3-D temporal medical imaging data. <i>PLoS ONE</i> , 2020 , 15, e0228962	3.7	

313	Machine Learning and Bioinformatics Models to Identify Pathways that Mediate Influences of Welding Fumes on Cancer Progression. <i>Scientific Reports</i> , 2020 , 10, 2795	4.9	11
312	Dynamic survival prediction in intensive care units from heterogeneous time series without the need for variable selection or curation. <i>Scientific Reports</i> , 2020 , 10, 22129	4.9	5
311	Neural Models for Brain Networks Connectivity Analysis. <i>Lecture Notes in Computer Science</i> , 2020 , 212-226	0	
310	Arbitrary Scale Super-Resolution for Brain MRI Images. <i>IFIP Advances in Information and Communication Technology</i> , 2020 , 165-176	0.5	5
309	NeoHiC: A Web Application for the Analysis of Hi-C Data. <i>Lecture Notes in Computer Science</i> , 2020 , 98-107	0.9	1
308	Continuous authentication by free-text keystroke based on CNN and RNN. <i>Computers and Security</i> , 2020 , 96, 101861	4.9	7
307	XFlow: Cross-Modal Deep Neural Networks for Audiovisual Classification. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2020 , 31, 3711-3720	10.3	7
306	A Novel Methodology for designing Policies in Mobile Crowdsensing Systems. <i>Pervasive and Mobile Computing</i> , 2020 , 67, 101230	3.5	2
305	Unsupervised stratification in neuroimaging through deep latent embeddings. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2020 , 2020, 1568-1571	0.9	1
304	DADIM: A distance adjustment dynamic influence map model. <i>Future Generation Computer Systems</i> , 2020 , 112, 1122-1130	7.5	1
303	A deep spatiotemporal graph learning architecture for brain connectivity analysis. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2020 , 2020, 1120-1123	0.9	1
302	A novel Graph Attention Network Architecture for modeling multimodal brain connectivity. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2020 , 2020, 1071-1074	0.9	1
301	How artificial intelligence and machine learning can help healthcare systems respond to COVID-19. <i>Machine Learning</i> , 2020 , 110, 1-14	4	47
300	How Can We Make Gan Perform Better in Single Medical Image Super-Resolution? A Lesion Focused Multi-Scale Approach 2019 ,		25
299	Improving QoE in Multi-layer Social Sensing 2019 ,		1
298	Integration of Machine Learning Methods to Dissect Genetically Imputed Transcriptomic Profiles in Alzheimer's Disease. <i>Frontiers in Genetics</i> , 2019 , 10, 726	4.5	9
297	Social dynamics modeling of chrono-nutrition. <i>PLoS Computational Biology</i> , 2019 , 15, e1006714	5	7
296	A Logical Framework for Modelling Breast Cancer Progression. <i>Lecture Notes in Computer Science</i> , 2019 , 121-141	0.9	2

295	GenHap: a novel computational method based on genetic algorithms for haplotype assembly. <i>BMC Bioinformatics</i> , 2019 , 20, 172	3.6	9
294	A Machine Learning Tool for Interpreting Differences in Cognition Using Brain Features. <i>IFIP Advances in Information and Communication Technology</i> , 2019 , 475-486	0.5	1
293	ASSCA: API sequence and statistics features combined architecture for malware detection. <i>Computer Networks</i> , 2019 , 157, 99-111	5.4	8
292	Predicting factors for survival of breast cancer patients using machine learning techniques. <i>BMC Medical Informatics and Decision Making</i> , 2019 , 19, 48	3.6	70
291	Hierarchical Block Matrix Approach for Multi-view Clustering. <i>Lecture Notes in Computer Science</i> , 2019 , 200-212	0.9	
290	Systems based analysis of human embryos and gene networks involved in cell lineage allocation. <i>BMC Genomics</i> , 2019 , 20, 171	4.5	11
289	Genetic effects of welding fumes on the development of respiratory system diseases. <i>Computers in Biology and Medicine</i> , 2019 , 108, 142-149	7	11
288	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	3.7	6
287	Identification of strategic molecules for future circular supply chains using large reaction networks. <i>Reaction Chemistry and Engineering</i> , 2019 , 4, 1969-1981	4.9	9
286	Modeling breast cancer progression to bone: how driver mutation order and metabolism matter. <i>BMC Medical Genomics</i> , 2019 , 12, 106	3.7	4
285	Variational Autoencoders for Cancer Data Integration: Design Principles and Computational Practice. <i>Frontiers in Genetics</i> , 2019 , 10, 1205	4.5	27
284	Lesion focused super-resolution 2019 ,		8
283	Modelling Trait-dependent Speciation with Approximate Bayesian Computation. <i>Acta Physica Polonica B, Proceedings Supplement</i> , 2019 , 12, 25	1.8	3
282	High Performance Computing for Haplotyping: Models and Platforms. <i>Lecture Notes in Computer Science</i> , 2019 , 650-661	0.9	1
281	Machine Learning-Based Models for Early Stage Detection of Autism Spectrum Disorders. <i>IEEE Access</i> , 2019 , 7, 166509-166527	3.5	38
280	Integrating Petri Nets and Flux Balance Methods in Computational Biology Models: a Methodological and Computational Practice. <i>Fundamenta Informaticae</i> , 2019 , 171, 367-392	1	4
279	Genetic effects of welding fumes on the progression of neurodegenerative diseases. <i>NeuroToxicology</i> , 2019 , 71, 93-101	4.4	23
278	A parameter-efficient deep learning approach to predict conversion from mild cognitive impairment to Alzheimer's disease. <i>NeuroImage</i> , 2019 , 189, 276-287	7.9	129

277	Multi-omic Network Regression: Methodology, Tool and Case Study. <i>Studies in Computational Intelligence</i> , 2019 , 611-624	0.8	
276	Seeing the wood for the trees: a forest of methods for optimization and omic-network integration in metabolic modelling. <i>Briefings in Bioinformatics</i> , 2018 , 19, 1218-1235	13.4	23
275	Parapred: antibody paratope prediction using convolutional and recurrent neural networks. <i>Bioinformatics</i> , 2018 , 34, 2944-2950	7.2	62
274	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	7.5	2
273	Quantifying the propagation of distress and mental disorders in social networks. <i>Scientific Reports</i> , 2018 , 8, 5005	4.9	17
272	A study on multi-omic oscillations in Escherichia coli metabolic networks. <i>BMC Bioinformatics</i> , 2018 , 19, 194	3.6	5
271	Combining Pathway Identification and Breast Cancer Survival Prediction via Screening-Network Methods. <i>Frontiers in Genetics</i> , 2018 , 9, 206	4.5	5
270	Investigating Diagrammatic Reasoning with Deep Neural Networks. <i>Lecture Notes in Computer Science</i> , 2018 , 390-398	0.9	
269	Simultaneous Transients of Intracranial Pressure and Heart Rate in Traumatic Brain Injury: Methods of Analysis. <i>Acta Neurochirurgica Supplementum</i> , 2018 , 126, 147-151	1.7	4
268	Automatic Inference of Cross-Modal Connection Topologies for X-CNNs. <i>Lecture Notes in Computer Science</i> , 2018 , 54-63	0.9	1
267	Optimization of Multi-Omic Genome-Scale Models: Methodologies, Hands-on Tutorial, and Perspectives. <i>Methods in Molecular Biology</i> , 2018 , 1716, 389-408	1.4	10
266	Bioinformatics methodologies for coeliac disease and its comorbidities. <i>Briefings in Bioinformatics</i> , 2018 ,	13.4	5
265	Guest Editors 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	3	
264	A Multi-modal Convolutional Neural Network Framework for the Prediction of Alzheimer's Disease. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2018 , 2018, 1271-1274	0.9	12
263	Pathway-based subnetworks enable cross-disease biomarker discovery. <i>Nature Communications</i> , 2018 , 9, 4746	17.4	19
262	Neural network fusion: a novel CT-MR Aortic Aneurysm image segmentation method. <i>Proceedings of SPIE</i> , 2018 , 10574,	1.7	5
261	Multi-omic analysis of signalling factors in inflammatory comorbidities. <i>BMC Bioinformatics</i> , 2018 , 19, 439	3.6	6
260	CiliateGEM: an open-project and a tool for predictions of ciliate metabolic variations and experimental condition design. <i>BMC Bioinformatics</i> , 2018 , 19, 442	3.6	1

259	Using Deep Data Augmentation Training to Address Software and Hardware Heterogeneities in Wearable and Smartphone Sensing Devices 2018 ,		26
258	Cross-modal Recurrent Models for Weight Objective Prediction from Multimodal Time-series Data 2018 ,		12
257	STable: a novel approach to de novo assembly of RNA-seq data and its application in a metabolic model network based metatranscriptomic workflow. <i>BMC Bioinformatics</i> , 2018 , 19, 184	3.6	1
256	Computational Models for Trapping Ebola Virus Using Engineered Bacteria. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018 , 15, 2017-2027	3	7
255	Stochastic Channel Switching of Frequency-Encoded Signals in Molecular Communication Networks. <i>IEEE Communications Letters</i> , 2018 , 22, 332-335	3.8	4
254	Making life difficult for <i>Clostridium difficile</i> : augmenting the pathogen's metabolic model with transcriptomic and codon usage data for better therapeutic target characterization. <i>BMC Systems Biology</i> , 2017 , 11, 25	3.5	18
253	DrugClust: A machine learning approach for drugs side effects prediction. <i>Computational Biology and Chemistry</i> , 2017 , 68, 204-210	3.6	35
252	A big-data layered architecture for analyzing molecular communications systems in blood vessels 2017 ,		1
251	A multiplex network approach for the analysis of intracranial pressure and heart rate data in traumatic brain injured patients. <i>Applied Network Science</i> , 2017 , 2, 29	2.9	6
250	Global gene expression profiling and senescence biomarker analysis of hESC exposed to HO induced non-cytotoxic oxidative stress. <i>Stem Cell Research and Therapy</i> , 2017 , 8, 160	8.3	4
249	Opportunities for community awareness platforms in personal genomics and bioinformatics education. <i>Briefings in Bioinformatics</i> , 2017 , 18, 1082-1090	13.4	1
248	Genetic Profiling and Comorbidities of Zika Infection. <i>Journal of Infectious Diseases</i> , 2017 , 216, 703-712	7	37
247	Single-cell RNA-sequencing uncovers transcriptional states and fate decisions in haematopoiesis. <i>Nature Communications</i> , 2017 , 8, 2045	17.4	78
246	NuChart-II: The road to a fast and scalable tool for Hi-C data analysis. <i>International Journal of High Performance Computing Applications</i> , 2017 , 31, 196-211	1.8	3
245	Transcriptome and proteome analysis of <i>Salmonella enterica</i> serovar Typhimurium systemic infection of wild type and immune-deficient mice. <i>PLoS ONE</i> , 2017 , 12, e0181365	3.7	6
244	Comparative Study of Inference Methods for Bayesian Nonnegative Matrix Factorisation. <i>Lecture Notes in Computer Science</i> , 2017 , 513-529	0.9	5
243	Effect of Aging, Disease Versus Health Conditions in the Design of Nano-communications in Blood Vessels. <i>Modeling and Optimization in Science and Technologies</i> , 2017 , 447-471	0.6	1
242	Multilayer Data and Document Stratification for Comorbidity Analysis. <i>Lecture Notes in Computer Science</i> , 2017 , 209-219	0.9	

241	Bio-Inspired ICT for Big Data Management in Healthcare. <i>Studies in Big Data</i> , 2016 , 1-26	0.9	2
240	Applications of molecular communications to medicine: A survey. <i>Nano Communication Networks</i> , 2016 , 7, 27-45	2.9	93
239	NuchaRt: Embedding High-Level Parallel Computing in R for Augmented Hi-C Data Analysis. <i>Lecture Notes in Computer Science</i> , 2016 , 259-272	0.9	2
238	Channel modelling of molecular communications across blood vessels and nerves 2016 ,		6
237	The Impact of Heterogeneity and Awareness in Modeling Epidemic Spreading on Multiplex Networks. <i>Scientific Reports</i> , 2016 , 6, 37105	4.9	34
236	Bioinformatics Challenges and Potentialities in Studying Extreme Environments. <i>Lecture Notes in Computer Science</i> , 2016 , 205-219	0.9	
235	MolComML 2016 ,		3
234	Muxstep: an open-source C ++ multiplex HMM library for making inferences on multiple data types. <i>Bioinformatics</i> , 2016 , 32, 2562-4	7.2	1
233	Multiplex methods provide effective integration of multi-omic data in genome-scale models. <i>BMC Bioinformatics</i> , 2016 , 17 Suppl 4, 83	3.6	30
232	Metabolic disorders: how can systems modelling help?. <i>Lancet Diabetes and Endocrinology</i> , 2016 , 4, 306	18.1	2
231	Systems medicine of inflammaging. <i>Briefings in Bioinformatics</i> , 2016 , 17, 527-40	13.4	27
230	Hierarchical block matrices as efficient representations of chromosome topologies and their application for 3C data integration. <i>Bioinformatics</i> , 2016 , 32, 1121-9	7.2	4
229	How computer science can help in understanding the 3D genome architecture. <i>Briefings in Bioinformatics</i> , 2016 , 17, 733-44	13.4	10
228	Iterative Multi Level Calibration of Metabolic Networks. <i>Current Bioinformatics</i> , 2016 , 11, 93-105	4.7	4
227	The Genome Conformation As an Integrator of Multi-Omic Data: The Example of Damage Spreading in Cancer. <i>Frontiers in Genetics</i> , 2016 , 7, 194	4.5	15
226	Distance-Based Opportunistic Mobile Data Offloading. <i>Sensors</i> , 2016 , 16,	3.8	5
225	Computational Modeling, Formal Analysis, and Tools for Systems Biology. <i>PLoS Computational Biology</i> , 2016 , 12, e1004591	5	115
224	Cancer Markers Selection Using Network-Based Cox Regression: A Methodological and Computational Practice. <i>Frontiers in Physiology</i> , 2016 , 7, 208	4.6	13

223	X-CNN: Cross-modal convolutional neural networks for sparse datasets 2016 ,		10
222	Parameter estimation of tuberculosis transmission model using Ensemble Kalman filter across Indian states and union territories. <i>Infection, Disease and Health</i> , 2016 , 21, 184-191	4.6	5
221	Animal inference on human mitochondrial diseases. <i>Computational Biology and Chemistry</i> , 2016 , 62, 17-28	3.6	3
220	Combining evolutionary game theory and network theory to analyze human cooperation patterns. <i>Chaos, Solitons and Fractals</i> , 2016 , 91, 17-24	9.3	21
219	Protein Interaction Networks Link Schizophrenia Risk Loci to Synaptic Function. <i>Schizophrenia Bulletin</i> , 2016 , 42, 1334-1342	1.3	11
218	Warped Matrix Factorisation for Multi-view Data Integration. <i>Lecture Notes in Computer Science</i> , 2016 , 789-804	0.9	1
217	Comorbidity networks: beyond disease correlations. <i>Journal of Complex Networks</i> , 2015 , 3, 319-332	1.7	13
216	Analysis and design of molecular machines. <i>Theoretical Computer Science</i> , 2015 , 599, 102-117	1.1	3
215	Modelling circulating tumour cells for personalised survival prediction in metastatic breast cancer. <i>PLoS Computational Biology</i> , 2015 , 11, e1004199	5	10
214	Integrating multi-omic features exploiting Chromosome Conformation Capture data. <i>Frontiers in Genetics</i> , 2015 , 6, 40	4.5	8
213	Analyzing seasonality of tuberculosis across Indian states and union territories. <i>Journal of Epidemiology and Global Health</i> , 2015 , 5, 337-46	5.5	22
212	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	3	12
211	MeDuSa: a multi-draft based scaffolder. <i>Bioinformatics</i> , 2015 , 31, 2443-51	7.2	203
210	Improving Literature-Based Discovery with Advanced Text Mining. <i>Lecture Notes in Computer Science</i> , 2015 , 89-98	0.9	4
209	Automated Detection of Fluorescent Probes in Molecular Imaging. <i>Lecture Notes in Computer Science</i> , 2015 , 68-75	0.9	1
208	Network regularised Cox regression and multiplex network models to predict disease comorbidities and survival of cancer. <i>Computational Biology and Chemistry</i> , 2015 , 59 Pt B, 15-31	3.6	28
207	Drug Repurposing by Optimizing Mining of Genes Target Association. <i>Lecture Notes in Computer Science</i> , 2015 , 209-218	0.9	
206	A Hybrid of Metabolic Flux Analysis and Bayesian Factor Modeling for Multiomic Temporal Pathway Activation. <i>ACS Synthetic Biology</i> , 2015 , 4, 880-9	5.7	18

205	Bayesian Melding Approach to Estimate the Reproduction Number for Tuberculosis Transmission in Indian States and Union Territories. <i>Asia-Pacific Journal of Public Health</i> , 2015 , 27, 723-32	2	3
204	Genome-scale metabolic reconstruction and constraint-based modelling of the Antarctic bacterium <i>Pseudoalteromonas haloplanktis</i> TAC125. <i>Environmental Microbiology</i> , 2015 , 17, 751-66	5.2	33
203	Predictive analytics of environmental adaptability in multi-omic network models. <i>Scientific Reports</i> , 2015 , 5, 15147	4.9	34
202	DAPPER: a data-mining resource for protein-protein interactions. <i>BioData Mining</i> , 2015 , 8, 30	4.3	4
201	How to build personalized multi-omics comorbidity profiles. <i>Frontiers in Cell and Developmental Biology</i> , 2015 , 3, 28	5.7	44
200	Multi-Target Analysis and Design of Mitochondrial Metabolism. <i>PLoS ONE</i> , 2015 , 10, e0133825	3.7	7
199	Quantifying the Role of Homophily in Human Cooperation Using Multiplex Evolutionary Game Theory. <i>PLoS ONE</i> , 2015 , 10, e0140646	3.7	23
198	Parallel Exploration of the Nuclear Chromosome Conformation with NuChart-II 2015 ,		3
197	CytoCom: a Cytoscape app to visualize, query and analyse disease comorbidity networks. <i>Bioinformatics</i> , 2015 , 31, 969-71	7.2	34
196	The BioMart community portal: an innovative alternative to large, centralized data repositories. <i>Nucleic Acids Research</i> , 2015 , 43, W589-98	20.1	468
195	Molecular multiplex network inference using Gaussian mixture hidden Markov models. <i>Journal of Complex Networks</i> , 2015 , cnv029	1.7	3
194	Advances in Artificial Life: Synthesis and Simulation of Living Systems: Editorial. <i>Artificial Life</i> , 2015 , 21, 395-7	1.4	2
193	Multi -omics and metabolic modelling pipelines: challenges and tools for systems microbiology. <i>Microbiological Research</i> , 2015 , 171, 52-64	5.3	90
192	Genome-scale metabolic network reconstruction. <i>Methods in Molecular Biology</i> , 2015 , 1231, 233-56	1.4	16
191	Applications of Network-based Survival Analysis Methods for Pathways Detection in Cancer. <i>Lecture Notes in Computer Science</i> , 2015 , 76-88	0.9	1
190	NuChart-II: A Graph-Based Approach for Analysis and Interpretation of Hi-C Data. <i>Lecture Notes in Computer Science</i> , 2015 , 298-311	0.9	
189	A content dissemination model for mobile internet to minimize load on cellular network 2015 , 289-294		
188	Advances in translational biomedicine from systems approaches. <i>Frontiers in Genetics</i> , 2014 , 5, 273	4.5	3

187	MtPAN(3): site-class specific amino acid replacement matrices for mitochondrial proteins of Pancrustacea and Collembola. <i>Molecular Phylogenetics and Evolution</i> , 2014 , 75, 239-44	4.1	1
186	Exploring the complexity of pathway-drug relationships using latent Dirichlet allocation. <i>Computational Biology and Chemistry</i> , 2014 , 53 Pt A, 144-52	3.6	13
185	Combining a wavelet change point and the Bayes factor for analysing chromosomal interaction data. <i>Molecular BioSystems</i> , 2014 , 10, 1576-85		25
184	FisHiCal: an R package for iterative FISH-based calibration of Hi-C data. <i>Bioinformatics</i> , 2014 , 30, 3120-2	7.2	25
183	Directional communication with movement prediction in mobile wireless sensor networks. <i>Personal and Ubiquitous Computing</i> , 2014 , 18, 1941-1953	2.1	3
182	comoR: a software for disease comorbidity risk assessment. <i>Journal of Clinical Bioinformatics</i> , 2014 , 4, 8		65
181	Pathway-based Bayesian inference of drug-disease interactions. <i>Molecular BioSystems</i> , 2014 , 10, 1538-48		15
180	Forward and Reverse coding for chromosome transfer in bacterial nanonetworks. <i>Nano Communication Networks</i> , 2014 , 5, 15-24	2.9	12
179	Draft genomes of three Antarctic Psychrobacter strains producing antimicrobial compounds against Burkholderia cepacia complex, opportunistic human pathogens. <i>Marine Genomics</i> , 2014 , 13, 37-8	1.9	15
178	Modeling TGF- β in early stages of cancer tissue dynamics. <i>PLoS ONE</i> , 2014 , 9, e88533	3.7	6
177	Bioremediation in marine ecosystems: a computational study combining ecological modeling and flux balance analysis. <i>Frontiers in Genetics</i> , 2014 , 5, 319	4.5	10
176	Who Wrote This? Textual Modeling with Authorship Attribution in Big Data 2014 ,		8
175	Network-based analysis of comorbidities risk during an infection: SARS and HIV case studies. <i>BMC Bioinformatics</i> , 2014 , 15, 333	3.6	70
174	The Bio-Inspired and Social Evolution of Node and Data in a Multilayer Network 2014 ,		5
173	Short and long-term genome stability analysis of prokaryotic genomes. <i>BMC Genomics</i> , 2013 , 14, 309	4.5	7
172	Comorbidity: a multidimensional approach. <i>Trends in Molecular Medicine</i> , 2013 , 19, 515-21	11.5	46
171	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	3	27
170	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	4.8	9

169	CytoHiC: a cytoscape plugin for visual comparison of Hi-C networks. <i>Bioinformatics</i> , 2013 , 29, 1206-7	7.2	16
168	Design and strain selection criteria for bacterial communication networks. <i>Nano Communication Networks</i> , 2013 , 4, 155-163	2.9	1
167	Differential impacts of R5 vs. X4 HIV-1 on the transcriptome of primary CD4+ T cells. <i>Retrovirology</i> , 2013 , 10,	3.6	1
166	Speeding up the transition to collective awareness 2013 ,		3
165	A design automation framework for computational bioenergetics in biological networks. <i>Molecular BioSystems</i> , 2013 , 9, 2554-64		8
164	Pareto optimality in organelle energy metabolism analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013 , 10, 1032-44	3	11
163	A review of experimental opportunities for molecular communication. <i>Nano Communication Networks</i> , 2013 , 4, 43-52	2.9	38
162	Efficient behavior of photosynthetic organelles via Pareto optimality, identifiability, and sensitivity analysis. <i>ACS Synthetic Biology</i> , 2013 , 2, 274-88	5.7	10
161	Multi-hop conjugation based bacteria nanonetworks. <i>IEEE Transactions on Nanobioscience</i> , 2013 , 12, 47-59	5.4	69
160	Pareto epsilon-dominance and identifiable solutions for BioCAD modeling 2013 ,		3
159	A Location Prediction Algorithm for Mobile Communications Using Directional Antennas. <i>International Journal of Distributed Sensor Networks</i> , 2013 , 9, 418606	1.7	2
158	The puzzling role of CXCR4 in human immunodeficiency virus infection. <i>Theranostics</i> , 2013 , 3, 18-25	12.1	17
157	NuChart: an R package to study gene spatial neighbourhoods with multi-omics annotations. <i>PLoS ONE</i> , 2013 , 8, e75146	3.7	26
156	Physio-environmental sensing and live modeling. <i>Interactive Journal of Medical Research</i> , 2013 , 2, e3	2.1	6
155	The onset of type 2 diabetes: proposal for a multi-scale model. <i>JMIR Research Protocols</i> , 2013 , 2, e44	2	10
154	The Role of the Genome in the Evolution of the Complexity of Metabolic Machines. <i>Springer Proceedings in Complexity</i> , 2013 , 1063-1069	0.3	
153	Risk Perception, Heuristics and Epidemic Spread 2013 , 139-152		4
152	Opportunistic routing through conjugation in bacteria communication nanonetwork. <i>Nano Communication Networks</i> , 2012 , 3, 36-45	2.9	134

151	Multilevel computational modeling and quantitative analysis of bone remodeling. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012 , 9, 1366-78	3	13
150	The landscape of DNA repeat elements in human heart failure. <i>Genome Biology</i> , 2012 , 13, R90	18.3	29
149	Robust design of microbial strains. <i>Bioinformatics</i> , 2012 , 28, 3097-104	7.2	46
148	Information dynamics algorithm for detecting communities in networks. <i>Communications in Nonlinear Science and Numerical Simulation</i> , 2012 , 17, 4294-4303	3.7	18
147	Modelling osteomyelitis. <i>BMC Bioinformatics</i> , 2012 , 13 Suppl 14, S12	3.6	24
146	Statistical approaches to use a model organism for regulatory sequences annotation of newly sequenced species. <i>PLoS ONE</i> , 2012 , 7, e42489	3.7	1
145	An adaptive directional MAC protocol for ad hoc networks using directional antennas. <i>Science China Information Sciences</i> , 2012 , 55, 1360-1371	3.4	9
144	Identification of sensitive enzymes in the photosynthetic carbon metabolism. <i>Advances in Experimental Medicine and Biology</i> , 2012 , 736, 441-59	3.6	5
143	Wavelet Kernel Principal Component Analysis in Noisy Multiscale Data Classification 2012 , 2012, 1-13		6
142	Modeling TGF- β signaling pathway in epithelial-mesenchymal transition. <i>AIP Advances</i> , 2012 , 2, 011201	1.5	2
141	Disease processes as hybrid dynamical systems. <i>Electronic Proceedings in Theoretical Computer Science, EPTCS</i> , 2012 , 92, 152-166		
140	Investigating meta-approaches for reconstructing gene networks in a mammalian cellular context. <i>PLoS ONE</i> , 2012 , 7, e28713	3.7	10
139	Collective human mobility pattern from taxi trips in urban area. <i>PLoS ONE</i> , 2012 , 7, e34487	3.7	128
138	Rational design of organelle compartments in cells. <i>EMBnet Journal</i> , 2012 , 18, 20	2.3	2
137	Multi-objective Optimisation, Sensitivity and Robustness Analysis in FBA Modelling. <i>Lecture Notes in Computer Science</i> , 2012 , 127-147	0.9	5
136	Multiple Verification in Complex Biological Systems: The Bone Remodelling Case Study. <i>Lecture Notes in Computer Science</i> , 2012 , 53-76	0.9	7
135	Stochastic analysis of a miRNA-protein toggle switch. <i>Molecular BioSystems</i> , 2011 , 7, 2796-803		14
134	Alterations of primary fatty acid amides in serum of patients with severe mental illness. <i>Frontiers in Bioscience - Elite</i> , 2011 , 3, 308-14	1.6	11

133	Message from the workshop on the future of social networking. <i>Computer Communication Review</i> , 2011 , 41, 14-18	1.4	
132	Methodological Bridges for Multi-Level Systems. <i>Procedia Computer Science</i> , 2011 , 7, 180-182	1.6	
131	Biological principles for future internet architecture design 2011 , 49, 44-52		25
130	A Combined Process Algebraic and Stochastic Approach to Bone Remodeling. <i>Electronic Notes in Theoretical Computer Science</i> , 2011 , 277, 41-52	0.7	5
129	Unity in Diversity: Phylogenetic-inspired Techniques for Reverse Engineering and Detection of Malware Families 2011 ,		3
128	How the Mutational-Selection Interplay Organizes the Fitness Landscape. <i>Journal of Nonlinear Mathematical Physics</i> , 2011 , 18, 265	0.9	
127	Evolving Model of Opportunistic Routing in Delay Tolerant Networks 2011 ,		3
126	Assessing ventilation system performance in isolation rooms. <i>Energy and Buildings</i> , 2011 , 43, 246-252	7	15
125	Design of robust metabolic pathways 2011 ,		10
124	Epileptic EEG Detection via a Novel Pattern Recognition Framework 2011 ,		4
123	EpiChIP: gene-by-gene quantification of epigenetic modification levels. <i>Nucleic Acids Research</i> , 2011 , 39, e27	20.1	34
122	Distinct epigenomic features in end-stage failing human hearts. <i>Circulation</i> , 2011 , 124, 2411-22	16.7	196
121	A Variance-Components Model for Distance-Matrix Phylogenetic Reconstruction. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011 , 10,	1.2	78
120	Community structure in social networks: applications for epidemiological modelling. <i>PLoS ONE</i> , 2011 , 6, e22220	3.7	23
119	StochKit-FF: Efficient Systems Biology on Multicore Architectures. <i>Lecture Notes in Computer Science</i> , 2011 , 167-175	0.9	5
118	Identification of targeted analyte clusters for studies of schizophrenia. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 510-22	7.6	23
117	Features extraction via wavelet kernel PCA for data classification 2010 ,		2
116	Generic spaced DNA motif discovery using Genetic Algorithm 2010 ,		3

115	Feature extraction via dynamic PCA for epilepsy diagnosis and epileptic seizure detection 2010 ,		1
114	Analysis and Optimization of C3 Photosynthetic Carbon Metabolism 2010 ,		8
113	Biologically inspired networking [Guest Editorial]. <i>IEEE Network</i> , 2010 , 24, 4-4	11.4	4
112	Intra- and inter-chromosomal interactions correlate with CTCF binding genome wide. <i>Molecular Systems Biology</i> , 2010 , 6, 426	12.2	85
111	An integrated modelling approach for R5X4 mutation and HAART therapy assessment. <i>Swarm Intelligence</i> , 2010 , 4, 319-340		3
110	Detection Probability Estimation of Directional Antennas and Omni-Directional Antennas. <i>Wireless Personal Communications</i> , 2010 , 55, 51-63	1.9	5
109	Formal reasoning on qualitative models of coinfection of HIV and Tuberculosis and HAART therapy. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 1, S67	3.6	5
108	Statistical mechanics of rumour spreading in network communities. <i>Procedia Computer Science</i> , 2010 , 1, 2331-2339	1.6	25
107	Risk perception and disease spread on social networks. <i>Procedia Computer Science</i> , 2010 , 1, 2345-2354	1.6	24
106	Cognitive network dynamics in chatlines. <i>Procedia Computer Science</i> , 2010 , 1, 2355-2362	1.6	7
105	Evolution of Metabolic Pathways and Evolution of Genomes 2010 , 37-68		1
104	Combining Replicates and Nearby Species Data: A Bayesian Approach. <i>Lecture Notes in Computer Science</i> , 2010 , 191-205	0.9	
103	Noise and non-linearities in high-throughput data. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2009 , 2009, P01014	1.9	1
102	Estimating dormant and active hematopoietic stem cell kinetics through extensive modeling of bromodeoxyuridine label-retaining cell dynamics. <i>PLoS ONE</i> , 2009 , 4, e6972	3.7	65
101	Towards real-time community detection in large networks. <i>Physical Review E</i> , 2009 , 79, 066107	2.4	190
100	A comparative study of noise effect on wavelet based de-noising methods 2009 ,		1
99	Trends in modeling Biomedical Complex Systems. <i>BMC Bioinformatics</i> , 2009 , 10 Suppl 12, I1	3.6	18
98	Clinical bioinformatics for complex disorders: a schizophrenia case study. <i>BMC Bioinformatics</i> , 2009 , 10 Suppl 12, S6	3.6	9

97	Measuring similarity between gene expression profiles: a Bayesian approach. <i>BMC Genomics</i> , 2009 , 10 Suppl 3, S14	4.5	7
96	The evolution of histidine biosynthesis in archaea: insights into the his genes structure and organization in LUCA. <i>Journal of Molecular Evolution</i> , 2009 , 69, 512-26	3.1	12
95	Bio-inspired multi-agent data harvesting in a proactive urban monitoring environment. <i>Ad Hoc Networks</i> , 2009 , 7, 725-741	4.8	35
94	Hematopoietic Stem Cells Reversibly Switch from Dormancy to Self-Renewal during Homeostasis and Repair. <i>Cell</i> , 2009 , 138, 209	56.2	2
93	Size Matters: Variation in Personal Network Size, Personality and Effect on Information Transmission 2009 ,		11
92	Impact of altruism on opportunistic communications 2009 ,		21
91	Selfishness, Altruism and Message Spreading in Mobile Social Networks 2009 ,		60
90	Minimizing Detection Probability Routing in Ad Hoc Networks Using Directional Antennas. <i>Eurasip Journal on Wireless Communications and Networking</i> , 2009 , 2009,	3.2	6
89	Information Processing and Timing Mechanisms in Vision. <i>Lecture Notes in Computer Science</i> , 2009 , 325-334	3.9	
88	Mathematical Model of HIV Superinfection and Comparative Drug Therapy. <i>Lecture Notes in Computer Science</i> , 2009 , 41-53	0.9	
87	Formal Analysis of the Genetic Toggle. <i>Lecture Notes in Computer Science</i> , 2009 , 96-110	0.9	
86	Searching for Glycomics Role in Stem Cell Development. <i>Lecture Notes in Computer Science</i> , 2009 , 198-209	0.9	
85	Substitution Matrices and Mutual Information Approaches to Modeling Evolution. <i>Lecture Notes in Computer Science</i> , 2009 , 259-272	0.9	0
84	A Case Study of ICA with Multi-scale PCA of Simulated Traffic Data. <i>Lecture Notes in Computer Science</i> , 2009 , 358-367	0.9	
83	The Structural Network Properties of Biological Systems. <i>World Scientific Lecture Notes in Complex Systems</i> , 2009 , 9-31		
82	Analysis of plasmid genes by phylogenetic profiling and visualization of homology relationships using Blast2Network. <i>BMC Bioinformatics</i> , 2008 , 9, 551	3.6	42
81	Hematopoietic stem cells reversibly switch from dormancy to self-renewal during homeostasis and repair. <i>Cell</i> , 2008 , 135, 1118-29	56.2	1335
80	Security estimation model with directional antennas 2008 ,		7

79	Bio-Inspired Multi-agent Collaboration for Urban Monitoring Applications. <i>Lecture Notes in Computer Science</i> , 2008 , 204-216	0.9	5
78	Combining Experimental Evidences from Replicates and Nearby Species Data for Annotating Novel Genomes. <i>AIP Conference Proceedings</i> , 2008 ,	0	1
77	Prediction by graph theoretic measures of structural effects in proteins arising from non-synonymous single nucleotide polymorphisms. <i>PLoS Computational Biology</i> , 2008 , 4, e1000135	5	41
76	A Location Prediction Algorithm for Directional Communication 2008 ,		4
75	Social Networking for Pervasive Adaptation 2008 ,		8
74	Modeling sequence evolution. <i>Methods in Molecular Biology</i> , 2008 , 452, 255-85	1.4	4
73	Current trends in the bioinformatic sequence analysis of metabolic pathways in prokaryotes. <i>Briefings in Bioinformatics</i> , 2008 , 9, 34-45	13.4	4
72	Contact Network Modeling of Flu Epidemics. <i>Lecture Notes in Computer Science</i> , 2008 , 354-361	0.9	
71	Wavelet-Domain Statistics of Packet Switching Networks Near Traffic Congestion. <i>Lecture Notes in Computer Science</i> , 2008 , 268-279	0.9	
70	Topological Metrics in Blast Data Mining: Plasmid and Nitrogen-Fixing Proteins Case Studies. <i>Communications in Computer and Information Science</i> , 2008 , 207-220	0.3	
69	A Stochastic Multi-agent Model of Stem Cell Proliferation. <i>Lecture Notes in Computer Science</i> , 2008 , 500-505		5
68	Bayesian Inference on Hidden Knowledge in High-Throughput Molecular Biology Data. <i>Lecture Notes in Computer Science</i> , 2008 , 829-838	0.9	1
67	Combining Molecular and Physiological Data of Complex Disorders. <i>Communications in Computer and Information Science</i> , 2008 , 362-376	0.3	1
66	Bayesian Phylogeny on Grid. <i>Communications in Computer and Information Science</i> , 2008 , 404-416	0.3	6
65	Inference on Missing Values in Genetic Networks Using High-Throughput Data 2008 , 106-116		1
64	A Novel Mobility Model from a Heterogeneous Military MANET Trace. <i>Lecture Notes in Computer Science</i> , 2008 , 463-474	0.9	7
63	Human Heuristics for Autonomous Agents. <i>Lecture Notes in Computer Science</i> , 2008 , 340-351	0.9	1
62	Grid methodology for identifying co-regulated genes and transcription factor binding sites. <i>IEEE Transactions on Nanobioscience</i> , 2007 , 6, 162-7	3.4	2

61	Phylogenetics and Computational Biology of Multigene Families 2007 , 191-205		1
60	Topological and dynamical properties of genetic and social networks. <i>Proceedings in Applied Mathematics and Mechanics</i> , 2007 , 7, 2070007-2070008	0.2	
59	The role of gene fusions in the evolution of metabolic pathways: the histidine biosynthesis case. <i>BMC Evolutionary Biology</i> , 2007 , 7 Suppl 2, S4	3	35
58	Modeling HIV quasispecies evolutionary dynamics. <i>BMC Evolutionary Biology</i> , 2007 , 7 Suppl 2, S5	3	13
57	Phylogenetic analysis of mitochondrial protein coding genes confirms the reciprocal paraphyly of Hexapoda and Crustacea. <i>BMC Evolutionary Biology</i> , 2007 , 7 Suppl 2, S8	3	121
56	Multiple protein phosphatases are required for mitosis in Drosophila. <i>Current Biology</i> , 2007 , 17, 293-303	6.3	104
55	Antarctic fish mitochondrial genomes lack ND6 gene. <i>Journal of Molecular Evolution</i> , 2007 , 65, 519-28	3.1	35
54	Forensic DNA and bioinformatics. <i>Briefings in Bioinformatics</i> , 2007 , 8, 117-28	13.4	14
53	Bottleneck genes and community structure in the cell cycle network of S. pombe. <i>PLoS Computational Biology</i> , 2007 , 3, e103	5	21
52	MotifScorer: using a compendium of microarrays to identify regulatory motifs. <i>Bioinformatics</i> , 2007 , 23, 493-5	7.2	4
51	A Molecular Communication System in Blood Vessels for Tumor Detection 2007 ,		10
50	Risk perception in epidemic modeling. <i>Physical Review E</i> , 2007 , 76, 061904	2.4	102
49	Wavelet Spectral Analysis of Packet Traffic Near Phase Transition Point from Free Flow to Congestion in Data Network Model 2007 ,		2
48	Biometric evidence that sexual selection has shaped the hominin face. <i>PLoS ONE</i> , 2007 , 2, e710	3.7	147
47	Computational framework for the prediction of transcription factor binding sites by multiple data integration. <i>BMC Neuroscience</i> , 2006 , 7 Suppl 1, S8	3.2	3
46	A novel algorithm and web-based tool for comparing two alternative phylogenetic trees. <i>Bioinformatics</i> , 2006 , 22, 117-9	7.2	140
45	Modeling Evolutionary Dynamics of HIV Infection. <i>Lecture Notes in Computer Science</i> , 2006 , 196-211	0.9	
44	The Influence of Risk Perception in Epidemics: A Cellular Agent Model. <i>Lecture Notes in Computer Science</i> , 2006 , 321-329	0.9	3

43	Phylogenetic and structural analysis of mitochondrial complex I proteins. <i>Gene</i> , 2005 , 345, 55-64	3.8	9
42	The origin and evolution of operons: the piecewise building of the proteobacterial histidine operon. <i>Journal of Molecular Evolution</i> , 2005 , 60, 378-90	3.1	40
41	Identification of DNA regulatory motifs using Bayesian variable selection. <i>Bioinformatics</i> , 2004 , 20, 2553-61	3.1	25
40	Periodic gene expression program of the fission yeast cell cycle. <i>Nature Genetics</i> , 2004 , 36, 809-17	36.3	402
39	Phylogenomics and bioinformatics of SARS-CoV. <i>Trends in Microbiology</i> , 2004 , 12, 106-11	12.4	33
38	Statistical bioinformatic methods in microbial genome analysis. <i>BioEssays</i> , 2003 , 25, 266-73	4.1	4
37	Wavelets in bioinformatics and computational biology: state of art and perspectives. <i>Bioinformatics</i> , 2003 , 19, 2-9	7.2	142
36	Investigating the evolution and structure of chemokine receptors. <i>Gene</i> , 2003 , 317, 29-37	3.8	17
35	Dimensionality and dependence problems in statistical genomics. <i>Briefings in Bioinformatics</i> , 2003 , 4, 168-77	13.4	2
34	Modeling Mitochondrial Protein Evolution Using Structural Information. <i>Journal of Molecular Evolution</i> , 2002 , 54, 519-529	3.1	12
33	Modeling mitochondrial protein evolution using structural information. <i>Journal of Molecular Evolution</i> , 2002 , 54, 519-29	3.1	4
32	Investigating the relationship between genome structure, composition, and ecology in prokaryotes. <i>Molecular Biology and Evolution</i> , 2002 , 19, 789-800	8.3	11
31	Molecular phylogenetics: state-of-the-art methods for looking into the past. <i>Trends in Genetics</i> , 2001 , 17, 262-72	8.5	311
30	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	3.1	116
29	Models of molecular evolution and phylogeny. <i>Genome Research</i> , 1998 , 8, 1233-44	9.7	215
28	Association of the Gln 27 beta 2-adrenoceptor polymorphism and IgE variability in asthmatic families. <i>Chest</i> , 1997 , 111, 785-795	5.3	5
27	Genome flux in tomato cell clones cultured in vitro in different physiological equilibria. II. A RAPD analysis of variability. <i>Genome</i> , 1996 , 39, 846-53	2.4	33
26	High statistics block entropy measures of DNA sequences. <i>Journal of Theoretical Biology</i> , 1996 , 180, 151-60	2.4	25

25	Analysis of genomic patchiness of <i>Haemophilus influenzae</i> and <i>Saccharomyces cerevisiae</i> chromosomes. <i>Journal of Theoretical Biology</i> , 1996 , 183, 455-69	2.3	10
24	Selection, mutations and codon usage in a bacterial model. <i>Journal of Theoretical Biology</i> , 1995 , 173, 271-81	2.3	18
23	The evolution of the histidine biosynthetic genes in prokaryotes: a common ancestor for the hisA and hisF genes. <i>Journal of Molecular Evolution</i> , 1994 , 38, 489-95	3.1	59
22	Third codon G + C periodicity as a possible signal for an "internal" selective constraint. <i>Journal of Theoretical Biology</i> , 1994 , 171, 215-23	2.3	18
21	Transcription factors and gene regulatory networks36-52		
20	A Deep Graph Neural Network Architecture for Modelling Spatio-temporal Dynamics in resting-state functional MRI Data		1
19	Graph representation forecasting of patient's medical conditions: towards a digital twin		1
18	Multiple verification in computational modeling of bone pathologies. <i>Electronic Proceedings in Theoretical Computer Science, EPTCS</i> ,67, 82-96		3
17	Variational autoencoders for cancer data integration: design principles and computational practice		2
16	Unseen Word Representation by Aligning Heterogeneous Lexical Semantic Spaces. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> ,33, 6900-6907	5	2
15	Analysis of single-cell RNA sequencing data based on autoencoders		1
14	CellVGAE: An unsupervised scRNA-seq analysis workflow with graph attention networks		1
13	Forecasting Ultra-early Intensive Care Strain from COVID-19 in England, v1.1.4		9
12	Gene Expression Imputation with Generative Adversarial Imputation Nets		1
11	The computational Patient has diabetes and a COVID		2
10	Population Graph GNNs for Brain Age Prediction		3
9	Grapphein - a Python Library for Geometric Deep Learning and Network Analysis on Protein Structures		5
8	GEESE: Metabolically driven latent space learning for gene expression data		3

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3	Volumetric Segmentation and Characterisation of the Paracingulate Sulcus on MRI Scans	2
2	Paratope Prediction using Convolutional and Recurrent Neural Networks	1
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