

Pietro Lio

List of Publications by Citations

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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	Hematopoietic stem cells reversibly switch from dormancy to self-renewal during homeostasis and repair. <i>Cell</i> , 2008 , 135, 1118-29	56.2	1335
365	The BioMart community portal: an innovative alternative to large, centralized data repositories. <i>Nucleic Acids Research</i> , 2015 , 43, W589-98	20.1	468
364	Periodic gene expression program of the fission yeast cell cycle. <i>Nature Genetics</i> , 2004 , 36, 809-17	36.3	402
363	Molecular phylogenetics: state-of-the-art methods for looking into the past. <i>Trends in Genetics</i> , 2001 , 17, 262-72	8.5	311
362	Models of molecular evolution and phylogeny. <i>Genome Research</i> , 1998 , 8, 1233-44	9.7	215
361	MeDuSa: a multi-draft based scaffolder. <i>Bioinformatics</i> , 2015 , 31, 2443-51	7.2	203
360	Distinct epigenomic features in end-stage failing human hearts. <i>Circulation</i> , 2011 , 124, 2411-22	16.7	196
359	Towards real-time community detection in large networks. <i>Physical Review E</i> , 2009 , 79, 066107	2.4	190
358	Biometric evidence that sexual selection has shaped the hominin face. <i>PLoS ONE</i> , 2007 , 2, e710	3.7	147
357	Wavelets in bioinformatics and computational biology: state of art and perspectives. <i>Bioinformatics</i> , 2003 , 19, 2-9	7.2	142
356	A novel algorithm and web-based tool for comparing two alternative phylogenetic trees. <i>Bioinformatics</i> , 2006 , 22, 117-9	7.2	140
355	Opportunistic routing through conjugation in bacteria communication nanonetwork. <i>Nano Communication Networks</i> , 2012 , 3, 36-45	2.9	134
354	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
353	Collective human mobility pattern from taxi trips in urban area. <i>PLoS ONE</i> , 2012 , 7, e34487	3.7	128
352	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
351	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
350	Computational Modeling, Formal Analysis, and Tools for Systems Biology. <i>PLoS Computational Biology</i> , 2016 , 12, e1004591	5	115

349	Multiple protein phosphatases are required for mitosis in <i>Drosophila</i> . <i>Current Biology</i> , 2007 , 17, 293-303	6.3	104
348	Risk perception in epidemic modeling. <i>Physical Review E</i> , 2007 , 76, 061904	2.4	102
347	Applications of molecular communications to medicine: A survey. <i>Nano Communication Networks</i> , 2016 , 7, 27-45	2.9	93
346	Multi -omics and metabolic modelling pipelines: challenges and tools for systems microbiology. <i>Microbiological Research</i> , 2015 , 171, 52-64	5.3	90
345	Intra- and inter-chromosomal interactions correlate with CTCF binding genome wide. <i>Molecular Systems Biology</i> , 2010 , 6, 426	12.2	85
344	Single-cell RNA-sequencing uncovers transcriptional states and fate decisions in haematopoiesis. <i>Nature Communications</i> , 2017 , 8, 2045	17.4	78
343	A Variance-Components Model for Distance-Matrix Phylogenetic Reconstruction. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011 , 10,	1.2	78
342	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
341	Network-based analysis of comorbidities risk during an infection: SARS and HIV case studies. <i>BMC Bioinformatics</i> , 2014 , 15, 333	3.6	70
340	Multi-hop conjugation based bacteria nanonetworks. <i>IEEE Transactions on Nanobioscience</i> , 2013 , 12, 47-59	4	69
339	comoR: a software for disease comorbidity risk assessment. <i>Journal of Clinical Bioinformatics</i> , 2014 , 4, 8		65
338	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
337	Parapred: antibody paratope prediction using convolutional and recurrent neural networks. <i>Bioinformatics</i> , 2018 , 34, 2944-2950	7.2	62
336	Selfishness, Altruism and Message Spreading in Mobile Social Networks 2009 ,		60
335	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
334	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
333	How artificial intelligence and machine learning can help healthcare systems respond to COVID-19. <i>Machine Learning</i> , 2020 , 110, 1-14	4	47
332	Privacy-Preserving Asynchronous Federated Learning Mechanism for Edge Network Computing. <i>IEEE Access</i> , 2020 , 8, 48970-48981	3.5	46

331	Comorbidity: a multidimensional approach. <i>Trends in Molecular Medicine</i> , 2013 , 19, 515-21	11.5	46
330	Robust design of microbial strains. <i>Bioinformatics</i> , 2012 , 28, 3097-104	7.2	46
329	How to build personalized multi-omics comorbidity profiles. <i>Frontiers in Cell and Developmental Biology</i> , 2015 , 3, 28	5.7	44
328	Analysis of plasmid genes by phylogenetic profiling and visualization of homology relationships using Blast2Network. <i>BMC Bioinformatics</i> , 2008 , 9, 551	3.6	42
327	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
326	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
325	A review of experimental opportunities for molecular communication. <i>Nano Communication Networks</i> , 2013 , 4, 43-52	2.9	38
324	Machine Learning-Based Models for Early Stage Detection of Autism Spectrum Disorders. <i>IEEE Access</i> , 2019 , 7, 166509-166527	3.5	38
323	Genetic Profiling and Comorbidities of Zika Infection. <i>Journal of Infectious Diseases</i> , 2017 , 216, 703-712	7	37
322	DrugClust: A machine learning approach for drugs side effects prediction. <i>Computational Biology and Chemistry</i> , 2017 , 68, 204-210	3.6	35
321	Bio-inspired multi-agent data harvesting in a proactive urban monitoring environment. <i>Ad Hoc Networks</i> , 2009 , 7, 725-741	4.8	35
320	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
319	Antarctic fish mitochondrial genomes lack ND6 gene. <i>Journal of Molecular Evolution</i> , 2007 , 65, 519-28	3.1	35
318	The Impact of Heterogeneity and Awareness in Modeling Epidemic Spreading on Multiplex Networks. <i>Scientific Reports</i> , 2016 , 6, 37105	4.9	34
317	Predictive analytics of environmental adaptability in multi-omic network models. <i>Scientific Reports</i> , 2015 , 5, 15147	4.9	34
316	CytoCom: a Cytoscape app to visualize, query and analyse disease comorbidity networks. <i>Bioinformatics</i> , 2015 , 31, 969-71	7.2	34
315	EpiChIP: gene-by-gene quantification of epigenetic modification levels. <i>Nucleic Acids Research</i> , 2011 , 39, e27	20.1	34
314	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

313	Phylogenomics and bioinformatics of SARS-CoV. <i>Trends in Microbiology</i> , 2004 , 12, 106-11	12.4	33
312	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
311	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
310	The landscape of DNA repeat elements in human heart failure. <i>Genome Biology</i> , 2012 , 13, R90	18.3	29
309	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
308	Systems medicine of inflammaging. <i>Briefings in Bioinformatics</i> , 2016 , 17, 527-40	13.4	27
307	Variational Autoencoders for Cancer Data Integration: Design Principles and Computational Practice. <i>Frontiers in Genetics</i> , 2019 , 10, 1205	4.5	27
306	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
305	NuChart: an R package to study gene spatial neighbourhoods with multi-omics annotations. <i>PLoS ONE</i> , 2013 , 8, e75146	3.7	26
304	Using Deep Data Augmentation Training to Address Software and Hardware Heterogeneities in Wearable and Smartphone Sensing Devices 2018 ,		26
303	How Can We Make Gan Perform Better in Single Medical Image Super-Resolution? A Lesion Focused Multi-Scale Approach 2019 ,		25
302	Combining a wavelet change point and the Bayes factor for analysing chromosomal interaction data. <i>Molecular BioSystems</i> , 2014 , 10, 1576-85		25
301	FisHiCal: an R package for iterative FISH-based calibration of Hi-C data. <i>Bioinformatics</i> , 2014 , 30, 3120-2	7.2	25
300	Biological principles for future internet architecture design 2011 , 49, 44-52		25
299	Statistical mechanics of rumour spreading in network communities. <i>Procedia Computer Science</i> , 2010 , 1, 2331-2339	1.6	25
298	Identification of DNA regulatory motifs using Bayesian variable selection. <i>Bioinformatics</i> , 2004 , 20, 2553-61		25
297	High statistics block entropy measures of DNA sequences. <i>Journal of Theoretical Biology</i> , 1996 , 180, 151-60		25
296	Modelling osteomyelitis. <i>BMC Bioinformatics</i> , 2012 , 13 Suppl 14, S12	3.6	24

295	Risk perception and disease spread on social networks. <i>Procedia Computer Science</i> , 2010 , 1, 2345-2354	1.6	24
294	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
293	Quantifying the Role of Homophily in Human Cooperation Using Multiplex Evolutionary Game Theory. <i>PLoS ONE</i> , 2015 , 10, e0140646	3.7	23
292	Identification of targeted analyte clusters for studies of schizophrenia. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 510-22	7.6	23
291	Community structure in social networks: applications for epidemiological modelling. <i>PLoS ONE</i> , 2011 , 6, e22220	3.7	23
290	Genetic effects of welding fumes on the progression of neurodegenerative diseases. <i>NeuroToxicology</i> , 2019 , 71, 93-101	4.4	23
289	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
288	Impact of altruism on opportunistic communications 2009 ,		21
287	Bottleneck genes and community structure in the cell cycle network of <i>S. pombe</i> . <i>PLoS Computational Biology</i> , 2007 , 3, e103	5	21
286	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
285	Pathogenetic profiling of COVID-19 and SARS-like viruses. <i>Briefings in Bioinformatics</i> , 2021 , 22, 1175-1196	13.4	20
284	Pathway-based subnetworks enable cross-disease biomarker discovery. <i>Nature Communications</i> , 2018 , 9, 4746	17.4	19
283	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
282	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
281	Information dynamics algorithm for detecting communities in networks. <i>Communications in Nonlinear Science and Numerical Simulation</i> , 2012 , 17, 4294-4303	3.7	18
280	Trends in modeling Biomedical Complex Systems. <i>BMC Bioinformatics</i> , 2009 , 10 Suppl 12, I1	3.6	18
279	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
278	Selection, mutations and codon usage in a bacterial model. <i>Journal of Theoretical Biology</i> , 1995 , 173, 271-81	2.3	18

277	Quantifying the propagation of distress and mental disorders in social networks. <i>Scientific Reports</i> , 2018 , 8, 5005	4.9	17
276	The puzzling role of CXCR4 in human immunodeficiency virus infection. <i>Theranostics</i> , 2013 , 3, 18-25	12.1	17
275	Investigating the evolution and structure of chemokine receptors. <i>Gene</i> , 2003 , 317, 29-37	3.8	17
274	CytoHiC: a cytoscape plugin for visual comparison of Hi-C networks. <i>Bioinformatics</i> , 2013 , 29, 1206-7	7.2	16
273	Genome-scale metabolic network reconstruction. <i>Methods in Molecular Biology</i> , 2015 , 1231, 233-56	1.4	16
272	Emotion Recognition From EEG Signal Focusing on Deep Learning and Shallow Learning Techniques. <i>IEEE Access</i> , 2021 , 9, 94601-94624	3.5	16
271	Pathway-based Bayesian inference of drug-disease interactions. <i>Molecular BioSystems</i> , 2014 , 10, 1538-48		15
270	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
269	Assessing ventilation system performance in isolation rooms. <i>Energy and Buildings</i> , 2011 , 43, 246-252	7	15
268	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
267	Stochastic analysis of a miRNA-protein toggle switch. <i>Molecular BioSystems</i> , 2011 , 7, 2796-803		14
266	Forensic DNA and bioinformatics. <i>Briefings in Bioinformatics</i> , 2007 , 8, 117-28	13.4	14
265	Comorbidity networks: beyond disease correlations. <i>Journal of Complex Networks</i> , 2015 , 3, 319-332	1.7	13
264	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
263	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
262	Modeling HIV quasispecies evolutionary dynamics. <i>BMC Evolutionary Biology</i> , 2007 , 7 Suppl 2, S5	3	13
261	Cancer Markers Selection Using Network-Based Cox Regression: A Methodological and Computational Practice. <i>Frontiers in Physiology</i> , 2016 , 7, 208	4.6	13
260	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

259	Forward and Reverse coding for chromosome transfer in bacterial nanonetworks. <i>Nano Communication Networks</i> , 2014 , 5, 15-24	2.9	12
258	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
257	Modeling Mitochondrial Protein Evolution Using Structural Information. <i>Journal of Molecular Evolution</i> , 2002 , 54, 519-529	3.1	12
256	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
255	Cross-modal Recurrent Models for Weight Objective Prediction from Multimodal Time-series Data 2018 ,		12
254	Systems based analysis of human embryos and gene networks involved in cell lineage allocation. <i>BMC Genomics</i> , 2019 , 20, 171	4.5	11
253	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
252	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
251	Pareto optimality in organelle energy metabolism analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013 , 10, 1032-44	3	11
250	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
249	Size Matters: Variation in Personal Network Size, Personality and Effect on Information Transmission 2009 ,		11
248	Investigating the relationship between genome structure, composition, and ecology in prokaryotes. <i>Molecular Biology and Evolution</i> , 2002 , 19, 789-800	8.3	11
247	ML-SIM: universal reconstruction of structured illumination microscopy images using transfer learning. <i>Biomedical Optics Express</i> , 2021 , 12, 2720-2733	3.5	11
246	Protein Interaction Networks Link Schizophrenia Risk Loci to Synaptic Function. <i>Schizophrenia Bulletin</i> , 2016 , 42, 1334-1342	1.3	11
245	Modelling circulating tumour cells for personalised survival prediction in metastatic breast cancer. <i>PLoS Computational Biology</i> , 2015 , 11, e1004199	5	10
244	How computer science can help in understanding the 3D genome architecture. <i>Briefings in Bioinformatics</i> , 2016 , 17, 733-44	13.4	10
243	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
242	Efficient behavior of photosynthetic organelles via Pareto optimality, identifiability, and sensitivity analysis. <i>ACS Synthetic Biology</i> , 2013 , 2, 274-88	5.7	10

241	Design of robust metabolic pathways 2011 ,		10
240	A Molecular Communication System in Blood Vessels for Tumor Detection 2007 ,		10
239	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
238	Investigating meta-approaches for reconstructing gene networks in a mammalian cellular context. <i>PLoS ONE</i> , 2012 , 7, e28713	3.7	10
237	The onset of type 2 diabetes: proposal for a multi-scale model. <i>JMIR Research Protocols</i> , 2013 , 2, e44	2	10
236	X-CNN: Cross-modal convolutional neural networks for sparse datasets 2016 ,		10
235	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
234	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
233	GenHap: a novel computational method based on genetic algorithms for haplotype assembly. <i>BMC Bioinformatics</i> , 2019 , 20, 172	3.6	9
232	Evidence in cortical folding patterns for prenatal predispositions to hallucinations in schizophrenia. <i>Translational Psychiatry</i> , 2020 , 10, 387	8.6	9
231	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
230	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
229	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
228	Clinical bioinformatics for complex disorders: a schizophrenia case study. <i>BMC Bioinformatics</i> , 2009 , 10 Suppl 12, S6	3.6	9
227	Phylogenetic and structural analysis of mitochondrial complex I proteins. <i>Gene</i> , 2005 , 345, 55-64	3.8	9
226	Forecasting Ultra-early Intensive Care Strain from COVID-19 in England, v1.1.4		9
225	ASSCA: API sequence and statistics features combined architecture for malware detection. <i>Computer Networks</i> , 2019 , 157, 99-111	5.4	8
224	Integrating multi-omic features exploiting Chromosome Conformation Capture data. <i>Frontiers in Genetics</i> , 2015 , 6, 40	4.5	8

223	Unsupervised generative and graph representation learning for modelling cell differentiation. <i>Scientific Reports</i> , 2020 , 10, 9790	4.9	8
222	A design automation framework for computational bioenergetics in biological networks. <i>Molecular BioSystems</i> , 2013 , 9, 2554-64		8
221	Who Wrote This? Textual Modeling with Authorship Attribution in Big Data 2014 ,		8
220	Analysis and Optimization of C3 Photosynthetic Carbon Metabolism 2010 ,		8
219	Social Networking for Pervasive Adaptation 2008 ,		8
218	AI-Based Reconstruction for Fast MRI Systematic Review and Meta-Analysis. <i>Proceedings of the IEEE</i> , 2022 , 110, 224-245	14.3	8
217	Lesion focused super-resolution 2019 ,		8
216	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
215	Social dynamics modeling of chrono-nutrition. <i>PLoS Computational Biology</i> , 2019 , 15, e1006714	5	7
214	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
213	Short and long-term genome stability analysis of prokaryotic genomes. <i>BMC Genomics</i> , 2013 , 14, 309	4.5	7
212	Multi-Target Analysis and Design of Mitochondrial Metabolism. <i>PLoS ONE</i> , 2015 , 10, e0133825	3.7	7
211	Measuring similarity between gene expression profiles: a Bayesian approach. <i>BMC Genomics</i> , 2009 , 10 Suppl 3, S14	4.5	7
210	Cognitive network dynamics in chatlines. <i>Procedia Computer Science</i> , 2010 , 1, 2355-2362	1.6	7
209	Security estimation model with directional antennas 2008 ,		7
208	A Novel Mobility Model from a Heterogeneous Military MANET Trace. <i>Lecture Notes in Computer Science</i> , 2008 , 463-474	0.9	7
207	Multiple Verification in Complex Biological Systems: The Bone Remodelling Case Study. <i>Lecture Notes in Computer Science</i> , 2012 , 53-76	0.9	7
206	Continuous authentication by free-text keystroke based on CNN and RNN. <i>Computers and Security</i> , 2020 , 96, 101861	4.9	7

205	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
204	Arbitrary Scale Super-Resolution for Medical Images. <i>International Journal of Neural Systems</i> , 2021 , 31, 2150037	6.2	7
203	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
202	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
201	PECLIDES Neuro: A Personalisable Clinical Decision Support System for Neurological Diseases. <i>Frontiers in Artificial Intelligence</i> , 2020 , 3, 23	3	6
200	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
199	Channel modelling of molecular communications across blood vessels and nerves 2016 ,		6
198	Modeling TGF- β in early stages of cancer tissue dynamics. <i>PLoS ONE</i> , 2014 , 9, e88533	3.7	6
197	Wavelet Kernel Principal Component Analysis in Noisy Multiscale Data Classification 2012 , 2012, 1-13		6
196	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
195	Transcriptome and proteome analysis of Salmonella enterica serovar Typhimurium systemic infection of wild type and immune-deficient mice. <i>PLoS ONE</i> , 2017 , 12, e0181365	3.7	6
194	Physio-environmental sensing and live modeling. <i>Interactive Journal of Medical Research</i> , 2013 , 2, e3	2.1	6
193	Bayesian Phylogeny on Grid. <i>Communications in Computer and Information Science</i> , 2008 , 404-416	0.3	6
192	Early Detection of Neurological Dysfunction Using Blood Cell Transcript Profiles		6
191	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
190	Deep Graph Mapper: Seeing Graphs Through the Neural Lens. <i>Frontiers in Big Data</i> , 2021 , 4, 680535	2.8	6
189	Multi-omic analysis of signalling factors in inflammatory comorbidities. <i>BMC Bioinformatics</i> , 2018 , 19, 439	3.6	6
188	Proximal Distilled Evolutionary Reinforcement Learning. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2020 , 34, 3283-3290	5	5

187	A study on multi-omic oscillations in Escherichia coli metabolic networks. <i>BMC Bioinformatics</i> , 2018 , 19, 194	3.6	5
186	Combining Pathway Identification and Breast Cancer Survival Prediction via Screening-Network Methods. <i>Frontiers in Genetics</i> , 2018 , 9, 206	4.5	5
185	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
184	Identification of sensitive enzymes in the photosynthetic carbon metabolism. <i>Advances in Experimental Medicine and Biology</i> , 2012 , 736, 441-59	3.6	5
183	Detection Probability Estimation of Directional Antennas and Omni-Directional Antennas. <i>Wireless Personal Communications</i> , 2010 , 55, 51-63	1.9	5
182	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
181	Association of the Gln 27 beta 2-adrenoceptor polymorphism and IgE variability in asthmatic families. <i>Chest</i> , 1997 , 111, 78S-79S	5.3	5
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179	The Bio-Inspired and Social Evolution of Node and Data in a Multilayer Network 2014 ,		5
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