

Preetam Ghosh

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167
papers

1,607
citations

22
h-index

31
g-index

198
ext. papers

2,323
ext. citations

3.8
avg, IF

5.38
L-index

#	Paper	IF	Citations
167	Two-Component Signal Transduction Systems of Pathogenic Bacteria As Targets for Antimicrobial Therapy: An Overview. <i>Frontiers in Microbiology</i> , 2017 , 8, 1878	5.7	106
166	Long-COVID and Post-COVID Health Complications: An Up-to-Date Review on Clinical Conditions and Their Possible Molecular Mechanisms. <i>Viruses</i> , 2021 , 13,	6.2	56
165	Factors affecting COVID-19 infected and death rates inform lockdown-related policymaking. <i>PLoS ONE</i> , 2020 , 15, e0241165	3.7	47
164	BARHL1 Is Downregulated in Alzheimer's Disease and May Regulate Cognitive Functions through ESR1 and Multiple Pathways. <i>Genes</i> , 2017 , 8,	4.2	46
163	Insight of Genus : Ascertaining the Role of Pathogenic and Non-pathogenic Species. <i>Frontiers in Microbiology</i> , 2017 , 8, 1937	5.7	45
162	Multi-omics-based identification of SARS-CoV-2 infection biology and candidate drugs against COVID-19. <i>Computers in Biology and Medicine</i> , 2020 , 126, 104051	7	45
161	Clinical Applications of Antimicrobial Peptides (AMPs): Where do we Stand Now?. <i>Protein and Peptide Letters</i> , 2020 , 27, 120-134	1.9	43
160	A pricing strategy for job allocation in mobile grids using a non-cooperative bargaining theory framework. <i>Journal of Parallel and Distributed Computing</i> , 2005 , 65, 1366-1383	4.4	40
159	Comparative mangrove metagenome reveals global prevalence of heavy metals and antibiotic resistome across different ecosystems. <i>Scientific Reports</i> , 2018 , 8, 11187	4.9	38
158	Searching for signatures across microbial communities: Metagenomic analysis of soil samples from mangrove and other ecosystems. <i>Scientific Reports</i> , 2017 , 7, 8859	4.9	37
157	A Game Theory-Based Pricing Strategy to Support Single/Multiclass Job Allocation Schemes for Bandwidth-Constrained Distributed Computing Systems. <i>IEEE Transactions on Parallel and Distributed Systems</i> , 2007 , 18, 289-306	3.7	35
156	Potential chimeric peptides to block the SARS-CoV-2 spike receptor-binding domain. <i>F1000Research</i> , 2020 , 9, 576	3.6	28
155	Dynamics of protofibril elongation and association involved in A β 2 peptide aggregation in Alzheimer's disease. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 6, S24	3.6	27
154	Strain-specific Fibril Propagation by an A β Dodecamer. <i>Scientific Reports</i> , 2017 , 7, 40787	4.9	26
153	Lanatoside C Induces G2/M Cell Cycle Arrest and Suppresses Cancer Cell Growth by Attenuating MAPK, Wnt, JAK-STAT, and PI3K/AKT/mTOR Signaling Pathways. <i>Biomolecules</i> , 2019 , 9,	5.9	26
152	An integrative in-silico approach for therapeutic target identification in the human pathogen <i>Corynebacterium diphtheriae</i> . <i>PLoS ONE</i> , 2017 , 12, e0186401	3.7	25
151	Cause and consequence of A β Lipid interactions in Alzheimer disease pathogenesis. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2018 , 1860, 1652-1662	3.8	25

150	Recent advances on constraint-based models by integrating machine learning. <i>Current Opinion in Biotechnology</i> , 2020 , 64, 85-91	11.4	23
149	Strophanthidin Attenuates MAPK, PI3K/AKT/mTOR, and Wnt/ β Catenin Signaling Pathways in Human Cancers. <i>Frontiers in Oncology</i> , 2019 , 9, 1469	5.3	22
148	Mobility-aware cost-efficient job scheduling for single-class grid jobs in a generic mobile grid architecture. <i>Future Generation Computer Systems</i> , 2010 , 26, 1356-1367	7.5	22
147	A novel gene network inference algorithm using predictive minimum description length approach. <i>BMC Systems Biology</i> , 2010 , 4 Suppl 1, S7	3.5	22
146	Anticancer and Antiviral Properties of Cardiac Glycosides: A Review to Explore the Mechanism of Actions. <i>Molecules</i> , 2020 , 25,	4.8	22
145	Reverse vaccinology and subtractive genomics reveal new therapeutic targets against : a causative agent of pneumonia. <i>Royal Society Open Science</i> , 2019 , 6, 190907	3.3	21
144	Determination of critical nucleation number for a single nucleation amyloid- β aggregation model. <i>Mathematical Biosciences</i> , 2016 , 273, 70-9	3.9	20
143	Mobility-Aware Efficient Job Scheduling in Mobile Grids 2007 ,		19
142	Conserved host-pathogen PPIs. Globally conserved inter-species bacterial PPIs based conserved host-pathogen interactome derived novel target in <i>C. pseudotuberculosis</i> , <i>C. diphtheriae</i> , <i>M. tuberculosis</i> , <i>C. ulcerans</i> , <i>Y. pestis</i> , and <i>E. coli</i> targeted by Piper betel compounds. <i>Integrative Biology (United Kingdom)</i> , 2013 , 5, 495-509	3.7	18
141	Deployment of robust wireless sensor networks using gene regulatory networks: An isomorphism-based approach. <i>Pervasive and Mobile Computing</i> , 2014 , 13, 246-257	3.5	17
140	Leveraging the robustness of genetic networks: a case study on bio-inspired wireless sensor network topologies. <i>Journal of Ambient Intelligence and Humanized Computing</i> , 2014 , 5, 323-339	3.7	16
139	Complete genome sequence of <i>Corynebacterium pseudotuberculosis</i> strain CIP 52.97, isolated from a horse in Kenya. <i>Journal of Bacteriology</i> , 2011 , 193, 7025-6	3.5	16
138	Time lagged information theoretic approaches to the reverse engineering of gene regulatory networks. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 6, S19	3.6	16
137	QoS-aware data reporting control in cluster-based wireless sensor networks. <i>Computer Communications</i> , 2010 , 33, 1244-1254	5.1	16
136	In silico identification of essential proteins in <i>Corynebacterium pseudotuberculosis</i> based on protein-protein interaction networks. <i>BMC Systems Biology</i> , 2016 , 10, 103	3.5	15
135	The genome anatomy of <i>Corynebacterium pseudotuberculosis</i> VD57 a highly virulent strain causing Caseous lymphadenitis. <i>Standards in Genomic Sciences</i> , 2016 , 11, 29		15
134	DISMIRA: Prioritization of disease candidates in miRNA-disease associations based on maximum weighted matching inference model and motif-based analysis. <i>BMC Genomics</i> , 2015 , 16 Suppl 5, S12	4.5	15
133	miRsig: a consensus-based network inference methodology to identify pan-cancer miRNA-miRNA interaction signatures. <i>Scientific Reports</i> , 2017 , 7, 39684	4.9	14

132	2011,			14
131	Optimal Time-Varying Vaccine Allocation Amid Pandemics With Uncertain Immunity Ratios. <i>IEEE Access</i> , 2021 , 9, 15110-15121	3.5		14
130	Long-range degree correlations in complex networks. <i>Computational Social Networks</i> , 2015 , 2,	5.8		13
129	Motif Participation by Genes in E. coli Transcriptional Networks. <i>Frontiers in Physiology</i> , 2012 , 3, 357	4.6		13
128	A novel multi-omics-based highly accurate prediction of symptoms, comorbid conditions, and possible long-term complications of COVID-19. <i>Molecular Omics</i> , 2021 , 17, 317-337	4.4		13
127	MapRepeat: an approach for effective assembly of repetitive regions in prokaryotic genomes. <i>Bioinformatics</i> , 2015 , 11, 276-9	1.1		12
126	Multiple Infection Sources Identification with Provable Guarantees 2016,			11
125	Efficient Communications in Wireless Sensor Networks Based on Biological Robustness 2016,			11
124	Recreational and philanthropic sectors are the worst-hit US industries in the COVID-19 aftermath. <i>Social Sciences & Humanities Open</i> , 2021 , 3, 100098	1.9		11
123	16S rRNA Gene Amplicon Based Metagenomic Signatures of Rhizobiome Community in Rice Field During Various Growth Stages. <i>Frontiers in Microbiology</i> , 2019 , 10, 2103	5.7		10
122	miRegulome: a knowledge-base of miRNA regulomics and analysis. <i>Scientific Reports</i> , 2015 , 5, 12832	4.9		10
121	Transcriptional Network Growing Models Using Motif-Based Preferential Attachment. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015 , 3, 157	5.8		10
120	2012,			10
119	Robust Deployment of Wireless Sensor Networks Using Gene Regulatory Networks. <i>Lecture Notes in Computer Science</i> , 2013 , 192-207	0.9		10
118	Bacterial Cellulose Retains Robustness but Its Synthesis Declines After Exposure to a Mars-like Environment Simulated Outside the International Space Station. <i>Astrobiology</i> , 2021 , 21, 706-717	3.7		10
117	Transcriptome profile of <i>Corynebacterium pseudotuberculosis</i> in response to iron limitation. <i>BMC Genomics</i> , 2019 , 20, 663	4.5		9
116	A novel in silico reverse-transcriptomics-based identification and blood-based validation of a panel of sub-type specific biomarkers in lung cancer. <i>BMC Genomics</i> , 2013 , 14 Suppl 6, S5	4.5		9
115	A modified Stokes-Einstein equation for A β aggregation. <i>BMC Bioinformatics</i> , 2011 , 12 Suppl 10, S13	3.6		9

114	Comparing 2-nt 3'overhangs against blunt-ended siRNAs: a systems biology based study. <i>BMC Genomics</i> , 2009 , 10 Suppl 1, S17	4.5	9
113	Whole-genome sequence of <i>Corynebacterium pseudotuberculosis</i> strain Cp162, isolated from camel. <i>Journal of Bacteriology</i> , 2012 , 194, 5718-9	3.5	9
112	Computational screening for potential drug candidates against the SARS-CoV-2 main protease. <i>F1000Research</i> , 2020 , 9,	3.6	9
111	Role of motifs in topological robustness of gene regulatory networks 2017 ,		8
110	Improving end-to-end quality-of-service in online multi-player wireless gaming networks. <i>Computer Communications</i> , 2008 , 31, 2685-2698	5.1	8
109	bioMCS 2020 ,		8
108	Analysis of the microarray gene expression for breast cancer progression after the application modified logistic regression. <i>Gene</i> , 2020 , 726, 144168	3.8	8
107	Performance Comparison of Deep Learning Autoencoders for Cancer Subtype Detection Using Multi-Omics Data. <i>Cancers</i> , 2021 , 13,	6.6	8
106	<i>Corynebacterium pseudotuberculosis</i> may be under anagenesis and biovar <i>Equi</i> forms biovar <i>Ovis</i> : a phylogenetic inference from sequence and structural analysis. <i>BMC Microbiology</i> , 2016 , 16, 100	4.5	8
105	Crosstalk and the Dynamical Modularity of Feed-Forward Loops in Transcriptional Regulatory Networks. <i>Biophysical Journal</i> , 2017 , 112, 1539-1550	2.9	7
104	Potential Chimeric Peptides to Block the SARS-CoV-2 Spike RBD 2020 ,		7
103	Fitness of Outer Membrane Vesicles From Is Altered Under the Impact of Simulated Mars-like Stressors Outside the International Space Station. <i>Frontiers in Microbiology</i> , 2020 , 11, 1268	5.7	7
102	Complete genome analysis of <i>Glutamicibacter creatinolyticus</i> from mare abscess and comparative genomics provide insight of diversity and adaptation for <i>Glutamicibacter</i> . <i>Gene</i> , 2020 , 741, 144566	3.8	7
101	SIMBA: a web tool for managing bacterial genome assembly generated by Ion PGM sequencing technology. <i>BMC Bioinformatics</i> , 2016 , 17, 456	3.6	7
100	Insights into Antagonistic Interactions of Multidrug Resistant Bacteria in Mangrove Sediments from the South Indian State of Kerala. <i>Microorganisms</i> , 2019 , 7,	4.9	7
99	Leveraging Network Science for Social Distancing to Curb Pandemic Spread. <i>IEEE Access</i> , 2021 , 9, 26196-26207	3.5	7
98	Quantitative Proteomic Analysis of the Response of Probiotic Putative NCDO 2118 Strain to Different Oxygen Availability Under Temperature Variation. <i>Frontiers in Microbiology</i> , 2019 , 10, 759	5.7	6
97	Social Influence Spectrum with Guarantees: Computing More in Less Time. <i>Lecture Notes in Computer Science</i> , 2015 , 84-103	0.9	6

96	Ontologies in radiation oncology. <i>Physica Medica</i> , 2020 , 72, 103-113	2.7	6
95	Propagation of an Aβ Dodecamer Strain Involves a Three-Step Mechanism and a Key Intermediate. <i>Biophysical Journal</i> , 2018 , 114, 539-549	2.9	6
94	Social Influence Spectrum at Scale. <i>ACM Transactions on Information Systems</i> , 2017 , 36, 1-26	4.8	6
93	Determining causal miRNAs and their signaling cascade in diseases using an influence diffusion model. <i>Scientific Reports</i> , 2017 , 7, 8133	4.9	6
92	Fatty Acid Concentration and Phase Transitions Modulate Aβ Aggregation Pathways. <i>Scientific Reports</i> , 2017 , 7, 10370	4.9	6
91	In Silico Protein-Protein Interactions: Avoiding Data and Method Biases Over Sensitivity and Specificity. <i>Current Protein and Peptide Science</i> , 2015 , 16, 689-700	2.8	6
90	The pan-genome of <i>Treponema pallidum</i> reveals differences in genome plasticity between subspecies related to venereal and non-venereal syphilis. <i>BMC Genomics</i> , 2020 , 21, 33	4.5	6
89	Motifs enable communication efficiency and fault-tolerance in transcriptional networks. <i>Scientific Reports</i> , 2020 , 10, 9628	4.9	6
88	Towards Dynamic lockdown strategies controlling pandemic spread under healthcare resource budget. <i>Applied Network Science</i> , 2021 , 6, 2	2.9	6
87	Compounds Piperidine, Eugenyl Acetate, and Chlorogenic Acid Are Broad-Spectrum Anti-Compounds that Are Also Effective on MDR Strains of the Pathogen. <i>Pathogens</i> , 2019 , 8,	4.5	5
86	The Druggable Pocketome of : A New Approach for Putative Druggable Targets. <i>Frontiers in Genetics</i> , 2018 , 9, 44	4.5	5
85	Evaluation of the Common Molecular Basis in Alzheimer's and Parkinson's Diseases. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	5
84	Exploiting Gene Regulatory Networks for Robust Wireless Sensor Networking 2015 ,		5
83	In silico functional prediction of hypothetical proteins from the core genome of biovar. <i>PeerJ</i> , 2020 , 8, e9643	3.1	5
82	Automatic Incident Triage in Radiation Oncology Incident Learning System. <i>Healthcare (Switzerland)</i> , 2020 , 8,	3.4	5
81	A Comparative Study on Distancing, Mask and Vaccine Adoption Rates from Global Twitter Trends. <i>Healthcare (Switzerland)</i> , 2021 , 9,	3.4	5
80	Artificial intelligence methods in computer-aided diagnostic tools and decision support analytics for clinical informatics 2020 , 31-59		5
79	Multiple environmental stressors induce complex transcriptomic responses indicative of phenotypic outcomes in Western fence lizard. <i>BMC Genomics</i> , 2018 , 19, 877	4.5	5

78	Cross-layer design for adaptive data reporting in wireless sensor networks 2009 ,		4
77	A Stochastic model to estimate the time taken for Protein-Ligand Docking 2006 ,		4
76	Acetate Kinase (AcK) is Essential for Microbial Growth and Betel-derived Compounds Potentially Target AcK, PhoP and MDR Proteins in <i>M. tuberculosis</i> , <i>V. cholerae</i> and Pathogenic <i>E. coli</i> : An in silico and in vitro Study. <i>Current Topics in Medicinal Chemistry</i> , 2018 , 18, 2731-2740	3	4
75	Linking common non-coding RNAs of human lung cancer and <i>M. tuberculosis</i> . <i>Bioinformatics</i> , 2018 , 14, 337-345	1.1	4
74	First genome sequencing and comparative analyses of strains from Mexico. <i>Standards in Genomic Sciences</i> , 2018 , 13, 21		4
73	Emergence of Cardiac Glycosides as Potential Drugs: Current and Future Scope for Cancer Therapeutics. <i>Biomolecules</i> , 2021 , 11,	5.9	4
72	A Survey on Recent Named Entity Recognition and Relationship Extraction Techniques on Clinical Texts. <i>Applied Sciences (Switzerland)</i> , 2021 , 11, 8319	2.6	4
71	Cost-Optimal Job Allocation Schemes for Bandwidth-Constrained Distributed Computing Systems. <i>Lecture Notes in Computer Science</i> , 2005 , 40-50	0.9	4
70	Integrated Natural Language Processing and Machine Learning Models for Standardizing Radiotherapy Structure Names. <i>Healthcare (Switzerland)</i> , 2020 , 8,	3.4	3
69	In Silico Models 2014 , 385-404		3
68	First-passage time analysis of a one-dimensional diffusion-reaction model: application to protein transport along DNA. <i>BMC Bioinformatics</i> , 2011 , 12 Suppl 10, S18	3.6	3
67	Gene Regulatory Network Inference Using Predictive Minimum Description Length Principle and Conditional Mutual Information 2009 ,		3
66	A Case Study-based Performance Evaluation Framework for CSCF Processes on a Blade-Server 2007 ,		3
65	Modeling protein-DNA binding time in Stochastic Discrete Event Simulation of Biological Processes 2007 ,		3
64	Modeling the Stochastic Dynamics of Gene Expression in Single Cells: A Birth and Death Markov Chain Analysis 2007 ,		3
63	Current Trends in Experimental and Computational Approaches to Combat Antimicrobial Resistance. <i>Frontiers in Genetics</i> , 2020 , 11, 563975	4.5	3
62	A Machine Learning method for relabeling arbitrary DICOM structure sets to TG-263 defined labels. <i>Journal of Biomedical Informatics</i> , 2020 , 109, 103527	10.2	3
61	bioMCS 2.0: A distributed, energy-aware fog-based framework for data forwarding in mobile crowdsensing. <i>Pervasive and Mobile Computing</i> , 2021 , 73, 101381	3.5	3

60	Identifying key indicators of job loss trends during COVID-19 and beyond. <i>Social Sciences & Humanities Open</i> , 2021 , 4, 100163	1.9	3
59	A Comparative NLP-Based Study on the Current Trends and Future Directions in COVID-19 Research. <i>IEEE Access</i> , 2021 , 9, 78341-78355	3.5	3
58	A markov model based analysis of stochastic biochemical systems. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2007 , 6, 121-32		3
57	Contribution of canonical feed-forward loop motifs on the fault-tolerance and information transport efficiency of transcriptional regulatory networks. <i>Nano Communication Networks</i> , 2015 , 6, 133-144	2.9	2
56	A game-theoretic approach to deciphering the dynamics of amyloid- aggregation along competing pathways. <i>Royal Society Open Science</i> , 2020 , 7, 191814	3.3	2
55	The Structural Role of Feed-Forward Loop Motif in Transcriptional Regulatory Networks. <i>Mobile Networks and Applications</i> , 2016 , 21, 191-205	2.9	2
54	Top-level dynamics and the regulated gene response of feed-forward loop transcriptional motifs. <i>Physical Review E</i> , 2014 , 90, 032706	2.4	2
53	Determining miRNA-disease associations using bipartite graph modelling 2013 ,		2
52	Discrete diffusion models to study the effects of Mg ²⁺ concentration on the PhoPQ signal transduction system. <i>BMC Genomics</i> , 2010 , 11 Suppl 3, S3	4.5	2
51	CoCONet: A collision-free container-based core optical network. <i>Computer Networks</i> , 2008 , 52, 2013-2032	3.4	2
50	Holding time estimation for reactions in stochastic event-based simulation of complex biological systems. <i>Simulation Modelling Practice and Theory</i> , 2008 , 16, 1615-1639	3.9	2
49	Two Phase Scheduling Algorithm for Maximizing the Number of Satisfied Users in Multi-Rate Wireless Systems 2007 ,		2
48	Dynamical impacts from structural redundancy of transcriptional motifs in gene-regulatory networks 2015 ,		2
47	Feature ranking in transcriptional networks: Packet receipt as a dynamical metric 2015 ,		2
46	Taxonomic classification of strain PO100/5 shows a broader geographic distribution and genetic markers of the recently described <i>Corynebacterium silvaticum</i> . <i>PLoS ONE</i> , 2020 , 15, e0244210	3.7	2
45	Mixed Degree-Degree Correlations in Directed Social Networks. <i>Lecture Notes in Computer Science</i> , 2014 , 571-580	0.9	2
44	A novel multi-omics-based identification of symptoms, comorbid conditions, and possible long-term complications in COVID-19		2
43	Pan-Resistome Insights into the Multidrug Resistance of. <i>Antibiotics</i> , 2021 , 10,	4.9	2

42	Quantifying Mobility and Mixing Propensity in the Spatiotemporal Context of a Pandemic Spread. <i>IEEE Transactions on Emerging Topics in Computational Intelligence</i> , 2021 , 5, 321-331	4.1	2
41	The Spike of SARS-CoV-2: Uniqueness and Applications. <i>Frontiers in Immunology</i> , 2021 , 12, 663912	8.4	2
40	Re-sequencing and optical mapping reveals misassemblies and real inversions on <i>Corynebacterium pseudotuberculosis</i> genomes. <i>Scientific Reports</i> , 2019 , 9, 16387	4.9	2
39	Novel frameshift mutation in gene in a Russian family with complete congenital stationary night blindness. <i>Ophthalmic Genetics</i> , 2019 , 40, 558-563	1.2	2
38	Adaptive Motif-based Topology Control in Mobile Software Defined Wireless Sensor Networks 2021 ,		2
37	Benchmarking the communication fidelity of biomolecular signaling cascades featuring pseudo-one-dimensional transport. <i>AIP Advances</i> , 2018 , 8, 055220	1.5	2
36	Comparative genomics and in silico gene evaluation involved in the probiotic potential of <i>Bifidobacterium longum</i> 5. <i>Gene</i> , 2021 , 795, 145781	3.8	2
35	Relevant and Non-Redundant Feature Selection for Cancer Classification and Subtype Detection. <i>Cancers</i> , 2021 , 13,	6.6	2
34	Stochastic Modeling of Cytoplasmic Reactions in Complex Biological Systems. <i>Lecture Notes in Computer Science</i> , 2006 , 566-576	0.9	2
33	Estimating the dynamics of protofibril elongation involved in A β 2 peptide aggregation in Alzheimer's disease 2010 ,		1
32	2009 ,		1
31	A Novel Photonic Container Switched Architecture and Scheduler to Design the Core Transport Network. <i>IEEE Transactions on Computers</i> , 2007 , 56, 1087-1104	2.5	1
30	A diffusion model to estimate the inter-arrival time of charged molecules in stochastic event based modeling of complex biological networks		1
29	A Clustering Approach to Identify Candidates to Housekeeping Genes Based on RNA-seq Data. <i>Lecture Notes in Computer Science</i> , 2020 , 83-95	0.9	1
28	Bacteriocins as an alternative in the treatment of infections by <i>Staphylococcus aureus</i> . <i>Anais Da Academia Brasileira De Ciencias</i> , 2020 , 92, e20201216	1.4	1
27	Transcriptional Regulatory Network Topology with Applications to Bio-inspired Networking: A Survey. <i>ACM Computing Surveys</i> , 2022 , 54, 1-36	13.4	1
26	Treatment Practice Analysis of Intermediate or High Risk Localized Prostate Cancer: A Multi-center Study with Veterans Health Administration Data. <i>Lecture Notes in Computer Science</i> , 2020 , 134-146	0.9	1
25	A game theoretic approach to deciphering the dynamics of amyloid- β aggregation along competing pathways		1

24	Quantifying Robustness in Biological Networks Using NS-2. <i>Modeling and Optimization in Science and Technologies</i> , 2017 , 273-290	0.6	1
23	Predictive minimum description length principle approach to inferring gene regulatory networks. <i>Advances in Experimental Medicine and Biology</i> , 2011 , 696, 37-43	3.6	1
22	Characterization of the first vaginal genomes isolated in Brazil. <i>PeerJ</i> , 2021 , 9, e11079	3.1	1
21	Automated data abstraction for quality surveillance and outcome assessment in radiation oncology. <i>Journal of Applied Clinical Medical Physics</i> , 2021 , 22, 177-187	2.3	1
20	Computational identification of putative common genomic drug and vaccine targets in <i>Mycoplasma genitalium</i> . <i>Genomics</i> , 2021 , 113, 2730-2743	4.3	1
19	Reverse vaccinology and subtractive genomics approaches for identifying common therapeutics against and. <i>Journal of Venomous Animals and Toxins Including Tropical Diseases</i> , 2021 , 27, e20200027	2.2	1
18	Comparative genomics with a multidrug-resistant <i>Klebsiella pneumoniae</i> isolate reveals the panorama of unexplored diversity in Northeast Brazil. <i>Gene</i> , 2021 , 772, 145386	3.8	1
17	Bioinformatics and Systems Biology in Bioengineering 2018 , 223-243		1
16	Deep neural network models to automate incident triage in the radiation oncology incident learning system 2021 ,		1
15	Spatiotemporal tracing of pandemic spread from infection data. <i>Scientific Reports</i> , 2021 , 11, 17689	4.9	1
14	Potential Molecular Mechanisms of Rare Anti-Tumor Immune Response by SARS-CoV-2 in Isolated Cases of Lymphomas. <i>Viruses</i> , 2021 , 13,	6.2	1
13	In silico disease model: from simple networks to complex diseases 2020 , 441-460		0
12	Parametric modeling of protein-DNA binding kinetics: A discrete event based simulation approach. <i>Discrete Applied Mathematics</i> , 2009 , 157, 2395-2415	1	0
11	Machine-Learning Models for Multicenter Prostate Cancer Treatment Plans. <i>Journal of Computational Biology</i> , 2021 , 28, 166-184	1.7	0
10	Effectiveness of Network Interdiction Strategies to Limit Contagion During a Pandemic. <i>IEEE Access</i> , 2021 , 9, 95862-95871	3.5	0
9	Genomic Characterization of Multidrug-Resistant BH100 Sub-strains. <i>Frontiers in Microbiology</i> , 2020 , 11, 549254	5.7	0
8	Natural selection versus creation: a review on the origin of SARS-COV-2. <i>Infezioni in Medicina</i> , 2020 , 28, 302-311	3.6	0
7	A Bridging Centrality Plugin for GEPHI and a Case Study for <i>Mycobacterium Tuberculosis</i> H37Rv. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 2741-2746	3	0

- 6 Scalable and distributed strategies for socially distanced human mobility.. *Applied Network Science*, **2021**, 6, 95 2.9 0
- 5 Application of Social Network Analytics to Assessing Different Care Coordination Metrics. *Lecture Notes in Computer Science*, **2018**, 151-160 0.9
- 4 An integrated parametric model for MT self-assembly formation analysis. *BioSystems*, **2019**, 176, 6-12 1.9
- 3 Similar Feed-forward Loop Crosstalk Patterns may Impact Robust Information Transport Across E. coli and S. Cerevisiae Transcriptional Networks. *Mobile Networks and Applications*, **2020**, 25, 1970-1982 2.9
- 2 Intrinsic and Simplified Complex Network Embedding Model. *Lecture Notes in Networks and Systems*, **2021**, 269-288 0.5
- 1 Characterization of a new multidrug-resistant Brazilian isolate and 172 spp. sequenced strains: Genomic island, multilocus sequence typing and capsule locus dataset. *Data in Brief*, **2021**, 34, 106746 1.2