

Preetam Ghosh

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.

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	Transcriptional Regulatory Network Topology with Applications to Bio-inspired Networking: A Survey. <i>ACM Computing Surveys</i> , 2022 , 54, 1-36	13.4	1
166	Characterization of the first vaginal genomes isolated in Brazil. <i>PeerJ</i> , 2021 , 9, e11079	3.1	1
165	A Comparative Study on Distancing, Mask and Vaccine Adoption Rates from Global Twitter Trends. <i>Healthcare (Switzerland)</i> , 2021 , 9,	3.4	5
164	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
163	Performance Comparison of Deep Learning Autoencoders for Cancer Subtype Detection Using Multi-Omics Data. <i>Cancers</i> , 2021 , 13,	6.6	8
162	Pan-Resistome Insights into the Multidrug Resistance of. <i>Antibiotics</i> , 2021 , 10,	4.9	2
161	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
160	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
159	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
158	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
157	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
156	The Spike of SARS-CoV-2: Uniqueness and Applications. <i>Frontiers in Immunology</i> , 2021 , 12, 663912	8.4	2
155	Machine-Learning Models for Multicenter Prostate Cancer Treatment Plans. <i>Journal of Computational Biology</i> , 2021 , 28, 166-184	1.7	0
154	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
153	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
152	Effectiveness of Network Interdiction Strategies to Limit Contagion During a Pandemic. <i>IEEE Access</i> , 2021 , 9, 95862-95871	3.5	0
151	Identifying key indicators of job loss trends during COVID-19 and beyond. <i>Social Sciences & Humanities Open</i> , 2021 , 4, 100163	1.9	3

150	Optimal Time-Varying Vaccine Allocation Amid Pandemics With Uncertain Immunity Ratios. <i>IEEE Access</i> , 2021 , 9, 15110-15121	3.5	14
149	Leveraging Network Science for Social Distancing to Curb Pandemic Spread. <i>IEEE Access</i> , 2021 , 9, 26196-26207	3.5	7
148	Intrinsic and Simplified Complex Network Embedding Model. <i>Lecture Notes in Networks and Systems</i> , 2021 , 269-288	0.5	
147	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
146	Adaptive Motif-based Topology Control in Mobile Software Defined Wireless Sensor Networks 2021 ,		2
145	Characterization of a new multidrug-resistant Brazilian isolate and 172 spp. sequenced strains: Genomic island, multilocus sequence typing and capsule locus dataset. <i>Data in Brief</i> , 2021 , 34, 106746	1.2	
144	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
143	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
142	Emergence of Cardiac Glycosides as Potential Drugs: Current and Future Scope for Cancer Therapeutics. <i>Biomolecules</i> , 2021 , 11,	5.9	4
141	Relevant and Non-Redundant Feature Selection for Cancer Classification and Subtype Detection. <i>Cancers</i> , 2021 , 13,	6.6	2
140	Deep neural network models to automate incident triage in the radiation oncology incident learning system 2021 ,		1
139	Spatiotemporal tracing of pandemic spread from infection data. <i>Scientific Reports</i> , 2021 , 11, 17689	4.9	1
138	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
137	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
136	Towards Dynamic lockdown strategies controlling pandemic spread under healthcare resource budget. <i>Applied Network Science</i> , 2021 , 6, 2	2.9	6
135	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
134	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
133	Scalable and distributed strategies for socially distanced human mobility.. <i>Applied Network Science</i> , 2021 , 6, 95	2.9	0

132	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
131	Integrated Natural Language Processing and Machine Learning Models for Standardizing Radiotherapy Structure Names. <i>Healthcare (Switzerland)</i> , 2020 , 8,	3.4	3
130	Potential Chimeric Peptides to Block the SARS-CoV-2 Spike RBD 2020 ,		7
129	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
128	In silico disease model: from simple networks to complex diseases 2020 , 441-460		0
127	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
126	Ontologies in radiation oncology. <i>Physica Medica</i> , 2020 , 72, 103-113	2.7	6
125	bioMCS 2020 ,		8
124	Computational screening for potential drug candidates against the SARS-CoV-2 main protease. <i>F1000Research</i> , 2020 , 9,	3.6	9
123	Potential chimeric peptides to block the SARS-CoV-2 spike receptor-binding domain. <i>F1000Research</i> , 2020 , 9, 576	3.6	28
122	Factors affecting COVID-19 infected and death rates inform lockdown-related policymaking. <i>PLoS ONE</i> , 2020 , 15, e0241165	3.7	47
121	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
120	Clinical Applications of Antimicrobial Peptides (AMPs): Where do we Stand Now?. <i>Protein and Peptide Letters</i> , 2020 , 27, 120-134	1.9	43
119	In silico functional prediction of hypothetical proteins from the core genome of biovar. <i>PeerJ</i> , 2020 , 8, e9643	3.1	5
118	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
117	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
116	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
115	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

114	Recent advances on constraint-based models by integrating machine learning. <i>Current Opinion in Biotechnology</i> , 2020 , 64, 85-91	11.4	23
113	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
112	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
111	Motifs enable communication efficiency and fault-tolerance in transcriptional networks. <i>Scientific Reports</i> , 2020 , 10, 9628	4.9	6
110	Current Trends in Experimental and Computational Approaches to Combat Antimicrobial Resistance. <i>Frontiers in Genetics</i> , 2020 , 11, 563975	4.5	3
109	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
108	Anticancer and Antiviral Properties of Cardiac Glycosides: A Review to Explore the Mechanism of Actions. <i>Molecules</i> , 2020 , 25,	4.8	22
107	Automatic Incident Triage in Radiation Oncology Incident Learning System. <i>Healthcare (Switzerland)</i> , 2020 , 8,	3.4	5
106	Similar Feed-forward Loop Crosstalk Patterns may Impact Robust Information Transport Across E. coli and S. Cerevisiae Transcriptional Networks. <i>Mobile Networks and Applications</i> , 2020 , 25, 1970-1982	2.9	
105	Artificial intelligence methods in computer-aided diagnostic tools and decision support analytics for clinical informatics 2020 , 31-59		5
104	Genomic Characterization of Multidrug-Resistant BH100 Sub-strains. <i>Frontiers in Microbiology</i> , 2020 , 11, 549254	5.7	0
103	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
102	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
101	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
100	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
99	Strophanthidin Attenuates MAPK, PI3K/AKT/mTOR, and Wnt/ECatenin Signaling Pathways in Human Cancers. <i>Frontiers in Oncology</i> , 2019 , 9, 1469	5.3	22
98	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
97	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

96	Transcriptome profile of <i>Corynebacterium pseudotuberculosis</i> in response to iron limitation. <i>BMC Genomics</i> , 2019 , 20, 663	4.5	9
95	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
94	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
93	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
92	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
91	An integrated parametric model for MT self-assembly formation analysis. <i>BioSystems</i> , 2019 , 176, 6-12	1.9	
90	Propagation of an A β Dodecamer Strain Involves a Three-Step Mechanism and a Key Intermediate. <i>Biophysical Journal</i> , 2018 , 114, 539-549	2.9	6
89	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
88	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
87	The Druggable Pocketome of : A New Approach for Putative Druggable Targets. <i>Frontiers in Genetics</i> , 2018 , 9, 44	4.5	5
86	Application of Social Network Analytics to Assessing Different Care Coordination Metrics. <i>Lecture Notes in Computer Science</i> , 2018 , 151-160	0.9	
85	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
84	Linking common non-coding RNAs of human lung cancer and <i>M. tuberculosis</i> . <i>Bioinformatics</i> , 2018 , 14, 337-345	1.1	4
83	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
82	Benchmarking the communication fidelity of biomolecular signaling cascades featuring pseudo-one-dimensional transport. <i>AIP Advances</i> , 2018 , 8, 055220	1.5	2
81	First genome sequencing and comparative analyses of strains from Mexico. <i>Standards in Genomic Sciences</i> , 2018 , 13, 21		4
80	Bioinformatics and Systems Biology in Bioengineering 2018 , 223-243		1
79	Strain-specific Fibril Propagation by an A β Dodecamer. <i>Scientific Reports</i> , 2017 , 7, 40787	4.9	26

78	Crosstalk and the Dynamical Modularity of Feed-Forward Loops in Transcriptional Regulatory Networks. <i>Biophysical Journal</i> , 2017 , 112, 1539-1550	2.9	7
77	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
76	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
75	Social Influence Spectrum at Scale. <i>ACM Transactions on Information Systems</i> , 2017 , 36, 1-26	4.8	6
74	Determining causal miRNAs and their signaling cascade in diseases using an influence diffusion model. <i>Scientific Reports</i> , 2017 , 7, 8133	4.9	6
73	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
72	Fatty Acid Concentration and Phase Transitions Modulate Amyloid Aggregation Pathways. <i>Scientific Reports</i> , 2017 , 7, 10370	4.9	6
71	Role of motifs in topological robustness of gene regulatory networks 2017 ,		8
70	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
69	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
68	Insight of Genus : Ascertaining the Role of Pathogenic and Non-pathogenic Species. <i>Frontiers in Microbiology</i> , 2017 , 8, 1937	5.7	45
67	Quantifying Robustness in Biological Networks Using NS-2. <i>Modeling and Optimization in Science and Technologies</i> , 2017 , 273-290	0.6	1
66	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
65	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
64	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
63	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
62	Determination of critical nucleation number for a single nucleation amyloid aggregation model. <i>Mathematical Biosciences</i> , 2016 , 273, 70-9	3.9	20
61	Multiple Infection Sources Identification with Provable Guarantees 2016 ,		11

60	Corynebacterium pseudotuberculosis may be under anagenesis and biovar Equi forms biovar Ovis: a phylogenetic inference from sequence and structural analysis. <i>BMC Microbiology</i> , 2016 , 16, 100	4.5	8
59	Efficient Communications in Wireless Sensor Networks Based on Biological Robustness 2016 ,		11
58	Long-range degree correlations in complex networks. <i>Computational Social Networks</i> , 2015 , 2,	5.8	13
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	Social Influence Spectrum with Guarantees: Computing More in Less Time. <i>Lecture Notes in Computer Science</i> , 2015 , 84-103	0.9	6
55	miRegulome: a knowledge-base of miRNA regulomics and analysis. <i>Scientific Reports</i> , 2015 , 5, 12832	4.9	10
54	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
53	Transcriptional Network Growing Models Using Motif-Based Preferential Attachment. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015 , 3, 157	5.8	10
52	Exploiting Gene Regulatory Networks for Robust Wireless Sensor Networking 2015 ,		5
51	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
50	Dynamical impacts from structural redundancy of transcriptional motifs in gene-regulatory networks 2015 ,		2
49	Feature ranking in transcriptional networks: Packet receipt as a dynamical metric 2015 ,		2
48	MapRepeat: an approach for effective assembly of repetitive regions in prokaryotic genomes. <i>Bioinformatics</i> , 2015 , 11, 276-9	1.1	12
47	In Silico Models 2014 , 385-404		3
46	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
45	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
44	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
43	Mixed Degree-Degree Correlations in Directed Social Networks. <i>Lecture Notes in Computer Science</i> , 2014 , 571-580	0.9	2

42	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
41	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
40	Determining miRNA-disease associations using bipartite graph modelling 2013 ,		2
39	Robust Deployment of Wireless Sensor Networks Using Gene Regulatory Networks. <i>Lecture Notes in Computer Science</i> , 2013 , 192-207	0.9	10
38	2012 ,		10
37	Motif Participation by Genes in <i>E. coli</i> Transcriptional Networks. <i>Frontiers in Physiology</i> , 2012 , 3, 357	4.6	13
36	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
35	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
34	A modified Stokes-Einstein equation for A β aggregation. <i>BMC Bioinformatics</i> , 2011 , 12 Suppl 10, S13	3.6	9
33	2011 ,		14
32	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
31	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
30	Estimating the dynamics of protofibril elongation involved in A β 2 peptide aggregation in Alzheimer's disease 2010 ,		1
29	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
28	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
27	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
26	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
25	QoS-aware data reporting control in cluster-based wireless sensor networks. <i>Computer Communications</i> , 2010 , 33, 1244-1254	5.1	16

24	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
23	Gene Regulatory Network Inference Using Predictive Minimum Description Length Principle and Conditional Mutual Information 2009 ,		3
22	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
21	Parametric modeling of protein-DNA binding kinetics: A discrete event based simulation approach. <i>Discrete Applied Mathematics</i> , 2009 , 157, 2395-2415	1	0
20	2009 ,		1
19	Cross-layer design for adaptive data reporting in wireless sensor networks 2009 ,		4
18	CoCONet: A collision-free container-based core optical network. <i>Computer Networks</i> , 2008 , 52, 2013-2032	3.4	2
17	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
16	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
15	Mobility-Aware Efficient Job Scheduling in Mobile Grids 2007 ,		19
14	A Case Study-based Performance Evaluation Framework for CSCF Processes on a Blade-Server 2007 ,		3
13	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
12	Modeling protein-DNA binding time in Stochastic Discrete Event Simulation of Biological Processes 2007 ,		3
11	Modeling the Stochastic Dynamics of Gene Expression in Single Cells: A Birth and Death Markov Chain Analysis 2007 ,		3
10	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
9	Two Phase Scheduling Algorithm for Maximizing the Number of Satisfied Users in Multi-Rate Wireless Systems 2007 ,		2
8	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
7	A Stochastic model to estimate the time taken for Protein-Ligand Docking 2006 ,		4

6	Stochastic Modeling of Cytoplasmic Reactions in Complex Biological Systems. <i>Lecture Notes in Computer Science</i> , 2006 , 566-576	0.9	2
5	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	4 ⁰
4	Cost-Optimal Job Allocation Schemes for Bandwidth-Constrained Distributed Computing Systems. <i>Lecture Notes in Computer Science</i> , 2005 , 40-50	0.9	4
3	A diffusion model to estimate the inter-arrival time of charged molecules in stochastic event based modeling of complex biological networks		1
2	A novel multi-omics-based identification of symptoms, comorbid conditions, and possible long-term complications in COVID-19		2
1	A game theoretic approach to deciphering the dynamics of amyloid- β aggregation along competing pathways		1