

Samik Ghosh

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

3,312
citations

361413
20
h-index

254184
43
g-index

57
all docs

57
docs citations

57
times ranked

5254
citing authors

#	ARTICLE	IF	CITATIONS
1	AI-driven laboratory workflows enable operation in the age of social distancing. <i>SLAS Technology</i> , 2022, 27, 195-203.	1.9	8
2	Toxicity Analysis of Pentachlorophenol Data with a Bioinformatics Tool Set. <i>Methods in Molecular Biology</i> , 2022, 2486, 105-125.	0.9	1
3	Artificial intelligence-based computational framework for drug-target prioritization and inference of novel repositionable drugs for Alzheimer's disease. <i>Alzheimer's Research and Therapy</i> , 2021, 13, 92.	6.2	29
4	A Geometric Clustering Tool (AGCT) to robustly unravel the inner cluster structures of time-series gene expressions. <i>PLoS ONE</i> , 2020, 15, e0233755.	2.5	3
5	Computational Systems Biology Applications. , 2019, , 66-73.		0
6	Computational Systems Biology. , 2019, , 789-795.		4
7	Lenvatinib plus anti-PD-1 antibody combination treatment activates CD8+ T cells through reduction of tumor-associated macrophage and activation of the interferon pathway. <i>PLoS ONE</i> , 2019, 14, e0212513.	2.5	294
8	Multi-dimensional computational pipeline for large-scale deep screening of compound effect assessment: an in silico case study on ageing-related compounds. <i>Npj Systems Biology and Applications</i> , 2019, 5, 42.	3.0	3
9	Sequence homology in eukaryotes (SHOE): interactive visual tool for promoter analysis. <i>BMC Genomics</i> , 2018, 19, 715.	2.8	7
10	Precise Temporal Profiling of Signaling Complexes in Primary Cells Using SWATH Mass Spectrometry. <i>Cell Reports</i> , 2017, 18, 3219-3226.	6.4	28
11	Supporting evidence-based analysis for modified risk tobacco products through a toxicology data-sharing infrastructure. <i>F1000Research</i> , 2017, 6, 12.	1.6	7
12	Supporting evidence-based analysis for modified risk tobacco products through a toxicology data-sharing infrastructure. <i>F1000Research</i> , 2017, 6, 12.	1.6	10
13	A machine learning approach for the identification of key markers involved in brain development from single-cell transcriptomic data. <i>BMC Genomics</i> , 2016, 17, 1025.	2.8	35
14	Network analyses based on comprehensive molecular interaction maps reveal robust control structures in yeast stress response pathways. <i>Npj Systems Biology and Applications</i> , 2016, 2, 15018.	3.0	27
15	Digital health revolution: perfect storm or perfect opportunity for pharmaceutical R&D?. <i>Drug Discovery Today</i> , 2016, 21, 900-911.	6.4	42
16	Elucidation of the molecular mechanisms underlying adverse reactions associated with a kinase inhibitor using systems toxicology. <i>Npj Systems Biology and Applications</i> , 2015, 1, 15005.	3.0	16
17	Application of machine learning approaches in drug target identification and network pharmacology. , 2015, , .		0
18	Oscillation of cAMP and Ca ²⁺ in cardiac myocytes: a systems biology approach. <i>Journal of Physiological Sciences</i> , 2015, 65, 195-200.	2.1	15

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19	Weaving Knowledge into Biological Pathways in a Collaborative Manner. <i>Methods in Pharmacology and Toxicology</i> , 2015, , 181-208.	0.2	1
20	Software Platform for Systems Biology. <i>Drug Delivery System</i> , 2014, 29, 386-396.	0.0	0
21	A Versatile Platform for Multilevel Modeling of Physiological Systems: SBML-PHML Hybrid Modeling and Simulation. <i>Advanced Biomedical Engineering</i> , 2014, 3, 50-58.	0.6	15
22	Identification of drug-target modules in the human protein-protein interaction network. <i>Artificial Life and Robotics</i> , 2014, 19, 406-413.	1.2	4
23	Integrating Pathways of Parkinson's Disease in a Molecular Interaction Map. <i>Molecular Neurobiology</i> , 2014, 49, 88-102.	4.0	231
24	Modeling and Simulation Using CellDesigner. <i>Methods in Molecular Biology</i> , 2014, 1164, 121-145.	0.9	60
25	A comprehensive map of the influenza A virus replication cycle. <i>BMC Systems Biology</i> , 2013, 7, 97.	3.0	97
26	Toward an integrated software platform for systems pharmacology. <i>Biopharmaceutics and Drug Disposition</i> , 2013, 34, 508-526.	1.9	18
27	Software Platform for Metabolic Network Reconstruction of <i>Mycobacterium tuberculosis</i> . , 2013, , 21-35.		1
28	Harnessing Diversity towards the Reconstructing of Large Scale Gene Regulatory Networks. <i>PLoS Computational Biology</i> , 2013, 9, e1003361.	3.2	32
29	A versatile platform for multilevel modeling of physiological systems: Template/instance framework for large-scale modeling and simulation. , 2013, 2013, 5529-32.		7
30	Combining Machine Learning Systems and Multiple Docking Simulation Packages to Improve Docking Prediction Reliability for Network Pharmacology. <i>PLoS ONE</i> , 2013, 8, e83922.	2.5	268
31	CTen: a web-based platform for identifying enriched cell types from heterogeneous microarray data. <i>BMC Genomics</i> , 2012, 13, 460.	2.8	113
32	AlzPathway: a comprehensive map of signaling pathways of Alzheimer's disease. <i>BMC Systems Biology</i> , 2012, 6, 52.	3.0	114
33	Software for systems biology: from tools to integrated platforms. <i>Nature Reviews Genetics</i> , 2011, 12, 821-832.	16.3	228
34	Social engineering for virtual 'big science' in systems biology. <i>Nature Chemical Biology</i> , 2011, 7, 323-326.	8.0	35
35	Discrete diffusion models to study the effects of Mg ²⁺ concentration on the PhoPQ signal transduction system. <i>BMC Genomics</i> , 2010, 11, S3.	2.8	3
36	Connecting the dots: role of standardization and technology sharing in biological simulation. <i>Drug Discovery Today</i> , 2010, 15, 1024-1031.	6.4	6

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37	Payao: a community platform for SBML pathway model curation. <i>Bioinformatics</i> , 2010, 26, 1381-1383.	4.1	50
38	A comprehensive molecular interaction map of the budding yeast cell cycle. <i>Molecular Systems Biology</i> , 2010, 6, 415.	7.2	62
39	A comprehensive map of the mTOR signaling network. <i>Molecular Systems Biology</i> , 2010, 6, 453.	7.2	201
40	Consistent design schematics for biological systems: standardization of representation in biological engineering. <i>Journal of the Royal Society Interface</i> , 2009, 6, S393-404.	3.4	15
41	The Systems Biology Graphical Notation. <i>Nature Biotechnology</i> , 2009, 27, 735-741.	17.5	828
42	Parametric modeling of protein-DNA binding kinetics: A discrete event based simulation approach. <i>Discrete Applied Mathematics</i> , 2009, 157, 2395-2415.	0.9	2
43	Construction and analysis of a modular model of caspase activation in apoptosis. <i>Theoretical Biology and Medical Modelling</i> , 2008, 5, 26.	2.1	89
44	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.	3.8	4
45	Modeling protein-DNA binding time in Stochastic Discrete Event Simulation of Biological Processes. , 2007, , .		5
46	Modeling the Stochastic Dynamics of Gene Expression in Single Cells: A Birth and Death Markov Chain Analysis. , 2007, , .		5
47	Channel Assignment Strategies for Multiradio Wireless Mesh Networks: Issues and Solutions. , 2007, 45, 86-95.		250
48	Towards Optimal Virtual Patients: An Online Adaptive Control Approach. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2007, 2007, 3292-5.	0.5	3
49	Enabling real-time fleet route planning and execution in a pervasive transportation environment. , 2007, , .		3
50	“MeshUp” Self-organizing mesh-based topologies for next generation radio access networks. <i>Ad Hoc Networks</i> , 2007, 5, 652-679.	5.5	6
51	Revisiting the Optimal Partitioning of Zones in Next Generation Cellular Networks: A Network Capacity Impact Perspective. , 2007, , 1011-1023.		0
52	A Computationally Fast and Parametric Model to Estimate Protein-Ligand Docking Time for Stochastic Event Based Simulation. , 2007, , 14-41.		3
53	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.	0.4	3
54	A Stochastic model to estimate the time taken for Protein-Ligand Docking. , 2006, , .		8