Samik Ghosh

List of Publications by Year
in descending order

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	The Systems Biology Graphical Notation. Nature Biotechnology, 2009, 27, 735-741.	17.5	828
2	Lenvatinib plus anti-PD-1 antibody combination treatment activates CD8+ T cells through reduction of tumor-associated macrophage and activation of the interferon pathway. PLoS ONE, 2019, 14, e0212513.	2.5	294
3	Combining Machine Learning Systems and Multiple Docking Simulation Packages to Improve Docking Prediction Reliability for Network Pharmacology. PLoS ONE, 2013, 8, e83922.	2.5	268
4	Channel Assignment Strategies for Multiradio Wireless Mesh Networks: Issues and Solutions. , 2007, 45, 86-95.		250
5	Integrating Pathways of Parkinson's Disease in a Molecular Interaction Map. Molecular Neurobiology, 2014, 49, 88-102.	4.0	231
6	Software for systems biology: from tools to integrated platforms. Nature Reviews Genetics, 2011, 12, 821-832.	16.3	228
7	A comprehensive map of the mTOR signaling network. Molecular Systems Biology, 2010, 6, 453.	7.2	201
8	AlzPathway: a comprehensive map of signaling pathways of Alzheimer's disease. BMC Systems Biology, 2012, 6, 52.	3.0	114
9	CTen: a web-based platform for identifying enriched cell types from heterogeneous microarray data. BMC Genomics, 2012, 13, 460.	2.8	113
10	A comprehensive map of the influenza A virus replication cycle. BMC Systems Biology, 2013, 7, 97.	3.0	97
11	Construction and analysis of a modular model of caspase activation in apoptosis. Theoretical Biology and Medical Modelling, 2008, 5, 26.	2.1	89
12	A comprehensive molecular interaction map of the budding yeast cell cycle. Molecular Systems Biology, 2010, 6, 415.	7.2	62
13	Modeling and Simulation Using CellDesigner. Methods in Molecular Biology, 2014, 1164, 121-145.	0.9	60
14	Payao: a community platform for SBML pathway model curation. Bioinformatics, 2010, 26, 1381-1383.	4.1	50
15	Digital health revolution: perfect storm or perfect opportunity for pharmaceutical R&D?. Drug Discovery Today, 2016, 21, 900-911.	6.4	42
16	Social engineering for virtual 'big science' in systems biology. Nature Chemical Biology, 2011, 7, 323-326.	8.0	35
17	A machine learning approach for the identification of key markers involved in brain development from single-cell transcriptomic data. BMC Genomics, 2016, 17, 1025.	2.8	35
18	Harnessing Diversity towards the Reconstructing of Large Scale Gene Regulatory Networks. PLoS Computational Biology, 2013, 9, e1003361.	3.2	32

#	Article	IF	Citations
19	Artificial intelligence-based computational framework for drug-target prioritization and inference of novel repositionable drugs for Alzheimerâ€™s disease. Alzheimer's Research and Therapy, 2021, 13, 92.	6.2	29
20	Precise Temporal Profiling of Signaling Complexes in Primary Cells Using SWATH Mass Spectrometry. Cell Reports, 2017, 18, 3219-3226.	6.4	28
21	Network analyses based on comprehensive molecular interaction maps reveal robust control structures in yeast stress response pathways. Npj Systems Biology and Applications, 2016, 2, 15018.	3.0	27
22	Toward an integrated software platform for systems pharmacology. Biopharmaceutics and Drug Disposition, 2013, 34, 508-526.	1.9	18
23	Elucidation of the molecular mechanisms underlying adverse reactions associated with a kinase inhibitor using systems toxicology. Npj Systems Biology and Applications, 2015, 1, 15005.	3.0	16
24	Consistent design schematics for biological systems: standardization of representation in biological engineering. Journal of the Royal Society Interface, 2009, 6, S393-404.	3.4	15
25	A Versatile Platform for Multilevel Modeling of Physiological Systems: SBML-PHML Hybrid Modeling and Simulation. Advanced Biomedical Engineering, 2014, 3, 50-58.	0.6	15
26	Oscillation of cAMP and Ca2+ in cardiac myocytes: a systems biology approach. Journal of Physiological Sciences, 2015, 65, 195-200.	2.1	15
27	Supporting evidence-based analysis for modified risk tobacco products through a toxicology data-sharing infrastructure. F1000Research, 2017, 6, 12.	1.6	10
28	A Stochastic model to estimate the time taken for Protein-Ligand Docking. , 2006, , .		8
29	AI-driven laboratory workflows enable operation in the age of social distancing. SLAS Technology, 2022, 27, 195-203.	1.9	8
30	A versatile platform for multilevel modeling of physiological systems: Template/instance framework for large-scale modeling and simulation. , 2013, 2013, 5529-32.		7
31	Sequence homology in eukaryotes (SHOE): interactive visual tool for promoter analysis. BMC Genomics, 2018, 19, 715.	2.8	7
32	Supporting evidence-based analysis for modified risk tobacco products through a toxicology data-sharing infrastructure. F1000Research, 2017, 6, 12.	1.6	7
33	â€œMeshUpâ€ Self-organizing mesh-based topologies for next generation radio access networks. Ad Hoc Networks, 2007, 5, 652-679.	5.5	6
34	Connecting the dots: role of standardization and technology sharing in biological simulation. Drug Discovery Today, 2010, 15, 1024-1031.	6.4	6
35	Modeling protein-DNA binding time in Stochastic Discrete Event Simulation of Biological Processes. , 2007, , .		5
36	Modeling the Stochastic Dynamics of Gene Expression in Single Cells: A Birth and Death Markov Chain Analysis. , 2007, , .		5

#	ARTICLE	IF	CITATIONS
37	Holding time estimation for reactions in stochastic event-based simulation of complex biological systems. Simulation Modelling Practice and Theory, 2008, 16, 1615-1639.	3.8	4
38	Identification of drug-target modules in the human protein–protein interaction network. Artificial Life and Robotics, 2014, 19, 406-413.	1.2	4
39	Computational Systems Biology. , 2019, , 789-795.		4
40	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
41	Enabling real-time fleet route planning and execution in a pervasive transportation environment. , 2007, , .		3
42	Discrete diffusion models to study the effects of Mg2+ concentration on the PhoPQ signal transduction system. BMC Genomics, 2010, 11, S3.	2.8	3
43	Multi-dimensional computational pipeline for large-scale deep screening of compound effect assessment: an in silico case study on ageing-related compounds. Npj Systems Biology and Applications, 2019, 5, 42.	3.0	3
44	A Geometric Clustering Tool (AGCT) to robustly unravel the inner cluster structures of time-series gene expressions. PLoS ONE, 2020, 15, e0233755.	2.5	3
45	A Computationally Fast and Parametric Model to Estimate Protein-Ligand Docking Time for Stochastic Event Based Simulation. , 2007, , 14-41.		3
46	A markov model based analysis of stochastic biochemical systems. Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2007, 6, 121-32.	0.4	3
47	Parametric modeling of protein–DNA binding kinetics: A discrete event based simulation approach. Discrete Applied Mathematics, 2009, 157, 2395-2415.	0.9	2
48	Software Platform for Metabolic Network Reconstruction of Mycobacterium tuberculosis. , 2013, , 21-35.		1
49	Weaving Knowledge into Biological Pathways in a Collaborative Manner. Methods in Pharmacology and Toxicology, 2015, , 181-208.	0.2	1
50	Toxicity Analysis of Pentachlorophenol Data with a Bioinformatics Tool Set. Methods in Molecular Biology, 2022, 2486, 105-125.	0.9	1
51	Software Platform for Systems Biology. Drug Delivery System, 2014, 29, 386-396.	0.0	0
52	Application of machine leaning approaches in drug target identification and network pharmacology. , 2015, , .		0
53	Computational Systems Biology Applications. , 2019, , 66-73.		0
54	Revisiting the Optimal Partitioning of Zones in Next Generation Cellular Networks: A Network Capacity Impact Perspective. , 2007, , 1011-1023.		0