

Karthik Raman

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

2,526
citations

304602

22
h-index

223716

46
g-index

88
all docs

88
docs citations

88
times ranked

3675
citing authors

#	ARTICLE	IF	CITATIONS
1	Discovering adaptation-capable biological network structures using control-theoretic approaches. PLoS Computational Biology, 2022, 18, e1009769.	1.5	11
2	Novel ratio-metric features enable the identification of new driver genes across cancer types. Scientific Reports, 2022, 12, 5.	1.6	10
3	Designing Biological Circuits: From Principles to Applications. ACS Synthetic Biology, 2022, 11, 1377-1388.	1.9	9
4	Multi-Omic Data Improve Prediction of Personalized Tumor Suppressors and Oncogenes. Frontiers in Genetics, 2022, 13, .	1.1	1
5	Effect of dormant spare capacity on the attack tolerance of complex networks. Physica A: Statistical Mechanics and Its Applications, 2022, 598, 127419.	1.2	0
6	Introduction to modelling. , 2021, , 1-26.		3
7	Sequence Neighborhoods Enable Reliable Prediction of Pathogenic Mutations in Cancer Genomes. Cancers, 2021, 13, 2366.	1.7	6
8	The art of molecular computing: Whence and whither. BioEssays, 2021, 43, e2100051.	1.2	5
9	NetGenes: A Database of Essential Genes Predicted Using Features From Interaction Networks. Frontiers in Genetics, 2021, 12, 722198.	1.1	5
10	Modelling microbial communities: Harnessing consortia for biotechnological applications. Computational and Structural Biotechnology Journal, 2021, 19, 3892-3907.	1.9	24
11	Systems-Theoretic Approaches to Design Biological Networks with Desired Functionalities. Methods in Molecular Biology, 2021, 2189, 133-155.	0.4	7
12	Synthetic biology beyond borders. Microbial Biotechnology, 2021, 14, 2254-2256.	2.0	0
13	Two-species community design of lactic acid bacteria for optimal production of lactate. Computational and Structural Biotechnology Journal, 2021, 19, 6039-6049.	1.9	6
14	A Computational Framework to Identify Metabolic Engineering Strategies for the Co-Production of Metabolites. Frontiers in Bioengineering and Biotechnology, 2021, 9, 779405.	2.0	3
15	A new index for information gain in the Bayesian framework. IFAC-PapersOnLine, 2020, 53, 634-639.	0.5	5
16	Mycobacterium tuberculosis (Mtb) lipid mediated lysosomal rewiring in infected macrophages modulates intracellular Mtb trafficking and survival. Journal of Biological Chemistry, 2020, 295, 9192-9210.	1.6	20
17	<scp>MinReact</scp>: a systematic approach for identifying minimal metabolic networks. Bioinformatics, 2020, 36, 4309-4315.	1.8	4
18	Machine Learning Applications for Mass Spectrometry-Based Metabolomics. Metabolites, 2020, 10, 243.	1.3	164

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19	Investigating metabolic interactions in a microbial co-culture through integrated modelling and experiments. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1249-1258.	1.9	24
20	Metagenome-wide association analysis identifies microbial determinants of post-antibiotic ecological recovery in the gut. <i>Nature Ecology and Evolution</i> , 2020, 4, 1256-1267.	3.4	98
21	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	3.2	178
22	Special issue on theory and application of network algorithms in biology. <i>International Journal of Advances in Engineering Sciences and Applied Mathematics</i> , 2019, 11, 89-90.	0.7	0
23	Assessment of network module identification across complex diseases. <i>Nature Methods</i> , 2019, 16, 843-852.	9.0	213
24	Rational metabolic engineering for enhanced alpha-tocopherol production in <i>Helianthus annuus</i> cell culture. <i>Biochemical Engineering Journal</i> , 2019, 151, 107256.	1.8	14
25	Uncovering Novel Pathways for Enhancing Hyaluronan Synthesis in Recombinant <i>Lactococcus lactis</i> : Genome-Scale Metabolic Modeling and Experimental Validation. <i>Processes</i> , 2019, 7, 343.	1.3	13
26	Adapting Community Detection Algorithms for Disease Module Identification in Heterogeneous Biological Networks. <i>Frontiers in Genetics</i> , 2019, 10, 164.	1.1	38
27	Evolutionary design principles in metabolism. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190098.	1.2	15
28	Deciphering the metabolic capabilities of Bifidobacteria using genome-scale metabolic models. <i>Scientific Reports</i> , 2019, 9, 18222.	1.6	56
29	Metabolite systems profiling identifies exploitable weaknesses in retinoblastoma. <i>FEBS Letters</i> , 2019, 593, 23-41.	1.3	11
30	Computational Prediction of Synthetic Lethals in Genome-Scale Metabolic Models Using Fast-SL. <i>Methods in Molecular Biology</i> , 2018, 1716, 315-336.	0.4	4
31	Network-based features enable prediction of essential genes across diverse organisms. <i>PLoS ONE</i> , 2018, 13, e0208722.	1.1	28
32	A systems-theoretic approach towards designing biological networks for perfect adaptation. <i>IFAC-PapersOnLine</i> , 2018, 51, 307-312.	0.5	7
33	Understanding the evolution of functional redundancy in metabolic networks. <i>Bioinformatics</i> , 2018, 34, i981-i987.	1.8	27
34	Enumerating all possible biosynthetic pathways in metabolic networks. <i>Scientific Reports</i> , 2018, 8, 9932.	1.6	28
35	Elucidating the biosynthetic pathways of volatile organic compounds in <i>Mycobacterium tuberculosis</i> through a computational approach. <i>Molecular BioSystems</i> , 2017, 13, 750-755.	2.9	6
36	A General Mechanism for the Propagation of Mutational Effects in Proteins. <i>Biochemistry</i> , 2017, 56, 294-305.	1.2	53

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37	Predicting novel metabolic pathways through subgraph mining. <i>Bioinformatics</i> , 2017, 33, 3955-3963.	1.8	13
38	In Silico Approaches to Metabolic Engineering. , 2017, , 161-200.		3
39	Fast-SL: an efficient algorithm to identify synthetic lethal sets in metabolic networks. <i>Bioinformatics</i> , 2015, 31, 3299-3305.	1.8	66
40	Critical assessment of genome-scale metabolic networks: the need for a unified standard. <i>Briefings in Bioinformatics</i> , 2015, 16, 1057-1068.	3.2	62
41	Revisiting Robustness and Evolvability: Evolution in Weighted Genotype Spaces. <i>PLoS ONE</i> , 2014, 9, e112792.	1.1	1
42	The organisational structure of protein networks: revisiting the centralityâ€“lethality hypothesis. <i>Systems and Synthetic Biology</i> , 2014, 8, 73-81.	1.0	80
43	A Systems Theoretic Approach to Systems and Synthetic Biology II: Analysis and Design of Cellular Systems. , 2014, ,		0
44	Identification of putative and potential cross-reactive chickpea (<i>Cicer arietinum</i>) allergens through an in silico approach. <i>Computational Biology and Chemistry</i> , 2013, 47, 149-155.	1.1	15
45	Evolvability and robustness in a complex signalling circuit. <i>Molecular BioSystems</i> , 2011, 7, 1081.	2.9	23
46	Systems Biology of Tuberculosis: Insights for Drug Discovery. , 2011, , 83-110.		1
47	The evolvability of programmable hardware. <i>Journal of the Royal Society Interface</i> , 2011, 8, 269-281.	1.5	37
48	Systems biology. <i>Resonance</i> , 2010, 15, 131-153.	0.2	6
49	Construction and analysis of proteinâ€“protein interaction networks. <i>Automated Experimentation</i> , 2010, 2, 2.	2.0	139
50	A systems perspective of hostâ€“pathogen interactions: predicting disease outcome in tuberculosis. <i>Molecular BioSystems</i> , 2010, 6, 516-530.	2.9	47
51	Flux balance analysis of biological systems: applications and challenges. <i>Briefings in Bioinformatics</i> , 2009, 10, 435-449.	3.2	354
52	Strategies for efficient disruption of metabolism in <i>Mycobacterium tuberculosis</i> from network analysis. <i>Molecular BioSystems</i> , 2009, 5, 1740.	2.9	35
53	<i>Mycobacterium tuberculosis</i> interactome analysis unravels potential pathways to drug resistance. <i>BMC Microbiology</i> , 2008, 8, 234.	1.3	86
54	targetTB: A target identification pipeline for <i>Mycobacterium tuberculosis</i> through an interactome, reactome and genome-scale structural analysis. <i>BMC Systems Biology</i> , 2008, 2, 109.	3.0	222

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55	M. tuberculosis interactome analysis unravels potential pathways to drug resistance. Nature Precedings, 2008, , .	0.1	1
56	PathwayAnalyser: A Systems Biology Tool for Flux Analysis of Metabolic Pathways. Nature Precedings, 2008, , .	0.1	4
57	Hallmarks of mycolic acid biosynthesis: A comparative genomics study. Proteins: Structure, Function and Bioinformatics, 2007, 69, 358-368.	1.5	11
58	Metabolome Based Reaction Graphs of M. tuberculosis and M. leprae: A Comparative Network Analysis. PLoS ONE, 2007, 2, e881.	1.1	38
59	Principles and Practices of Pathway Modelling. Current Bioinformatics, 2006, 1, 147-160.	0.7	9
60	Flux Balance Analysis of Mycolic Acid Pathway: Targets for Anti-Tubercular Drugs. PLoS Computational Biology, 2005, 1, e46.	1.5	127
61	Flux Balance Analysis of Mycolic Acid Pathway: Targets for Anti-tubercular Drugs. PLoS Computational Biology, 2005, preprint, e46.	1.5	1
62	An Introduction to Computational Systems Biology. , 0, , .		5
63	PathwayAnalyser: A Systems Biology Tool for Flux Analysis of Metabolic Pathways. Nature Precedings, 0, , .	0.1	1
64	Systems-Level Modelling of Microbial Communities. , 0, , .		13