

Jeremy Gunawardena

List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

4,229
citations

159525

30
h-index

123376

61
g-index

78
all docs

78
docs citations

78
times ranked

5773
citing authors

#	ARTICLE	IF	CITATIONS
1	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.	3.9	580
2	PHOSIDA 2011: the posttranslational modification database. <i>Nucleic Acids Research</i> , 2011, 39, D253-D260.	6.5	366
3	Post-translational modification: nature's escape from genetic imprisonment and the basis for dynamic information encoding. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2012, 4, 565-583.	6.6	288
4	Multisite protein phosphorylation makes a good threshold but can be a poor switch. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 14617-14622.	3.3	242
5	Unlimited multistability in multisite phosphorylation systems. <i>Nature</i> , 2009, 460, 274-277.	13.7	219
6	Models in biology: "accurate descriptions of our pathetic thinking"™. <i>BMC Biology</i> , 2014, 12, 29.	1.7	188
7	Tunable Signal Processing Through Modular Control of Transcription Factor Translocation. <i>Science</i> , 2013, 339, 460-464.	6.0	132
8	Information Integration and Energy Expenditure in Gene Regulation. <i>Cell</i> , 2016, 166, 234-244.	13.5	127
9	A Linear Framework for Time-Scale Separation in Nonlinear Biochemical Systems. <i>PLoS ONE</i> , 2012, 7, e36321.	1.1	112
10	Time-scale separation " Michaelis and Menten's old idea, still bearing fruit. <i>FEBS Journal</i> , 2014, 281, 473-488.	2.2	107
11	The Macronuclear Genome of <i>Stentor coeruleus</i> Reveals Tiny Introns in a Giant Cell. <i>Current Biology</i> , 2017, 27, 569-575.	1.8	105
12	The Perron-Frobenius theorem for homogeneous, monotone functions. <i>Transactions of the American Mathematical Society</i> , 2004, 356, 4931-4950.	0.5	101
13	Laplacian Dynamics on General Graphs. <i>Bulletin of Mathematical Biology</i> , 2013, 75, 2118-2149.	0.9	87
14	The rational parameterisation theorem for multisite post-translational modification systems. <i>Journal of Theoretical Biology</i> , 2009, 261, 626-636.	0.8	84
15	Evolutionary Constraints of Phosphorylation in Eukaryotes, Prokaryotes, and Mitochondria. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2642-2653.	2.5	83
16	Min-max functions. <i>Discrete Event Dynamic Systems: Theory and Applications</i> , 1994, 4, 377-407.	0.6	71
17	A constructive fixed point theorem for min-max functions. <i>Dynamical Systems</i> , 1999, 14, 407-433.	0.7	71
18	Programming with models: modularity and abstraction provide powerful capabilities for systems biology. <i>Journal of the Royal Society Interface</i> , 2009, 6, 257-270.	1.5	66

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19	A phosphatase threshold sets the level of Cdk1 activity in early mitosis in budding yeast. <i>Molecular Biology of the Cell</i> , 2011, 22, 3595-3608.	0.9	66
20	The Geometry of Multisite Phosphorylation. <i>Biophysical Journal</i> , 2008, 95, 5533-5543.	0.2	62
21	A Complex Hierarchy of Avoidance Behaviors in a Single-Cell Eukaryote. <i>Current Biology</i> , 2019, 29, 4323-4329.e2.	1.8	59
22	Reconsidering the evidence for learning in single cells. <i>ELife</i> , 2021, 10, .	2.8	58
23	Quantitative profiling of peptides from RNAs classified as noncoding. <i>Nature Communications</i> , 2014, 5, 5429.	5.8	55
24	Characterization of Neuronal Tau Protein as a Target of Extracellular Signal-regulated Kinase. <i>Journal of Biological Chemistry</i> , 2016, 291, 7742-7753.	1.6	54
25	A framework for modelling gene regulation which accommodates non-equilibrium mechanisms. <i>BMC Biology</i> , 2014, 12, 102.	1.7	53
26	Dissecting the sharp response of a canonical developmental enhancer reveals multiple sources of cooperativity. <i>ELife</i> , 2019, 8, .	2.8	47
27	Gene Regulation in and out of Equilibrium. <i>Annual Review of Biophysics</i> , 2020, 49, 199-226.	4.5	45
28	Complex-linear invariants of biochemical networks. <i>Journal of Theoretical Biology</i> , 2012, 311, 130-138.	0.8	44
29	Distributivity and Processivity in Multisite Phosphorylation Can Be Distinguished through Steady-State Invariants. <i>Biophysical Journal</i> , 2007, 93, 3828-3834.	0.2	42
30	Some lessons about models from Michaelis and Menten. <i>Molecular Biology of the Cell</i> , 2012, 23, 517-519.	0.9	39
31	Comparative analysis of Erk phosphorylation suggests a mixed strategy for measuring phosphoform distributions. <i>Molecular Systems Biology</i> , 2011, 7, 482.	3.2	38
32	A Fundamental Trade-off in Covalent Switching and Its Circumvention by Enzyme Bifunctionality in Glucose Homeostasis. <i>Journal of Biological Chemistry</i> , 2014, 289, 13010-13025.	1.6	33
33	Estimating the Distribution of Protein Post-Translational Modification States by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2018, 17, 2727-2734.	1.8	33
34	Energy-speed-accuracy relation in complex networks for biological discrimination. <i>Physical Review E</i> , 2018, 98, 012420.	0.8	32
35	Realistic enzymology for post-translational modification: Zero-order ultrasensitivity revisited. <i>Journal of Theoretical Biology</i> , 2012, 311, 139-152.	0.8	31
36	Nac1 Coordinates a Sub-network of Pluripotency Factors to Regulate Embryonic Stem Cell Differentiation. <i>Cell Reports</i> , 2016, 14, 1181-1194.	2.9	29

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37	Structural conditions on complex networks for the Michaelis-Menten input-output response. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 9738-9743.	3.3	28
38	Negative reciprocity, not ordered assembly, underlies the interaction of Sox2 and Oct4 on DNA. ELife, 2019, 8, .	2.8	26
39	Biological Systems Theory. Science, 2010, 328, 581-582.	6.0	24
40	Dimerization and Bifunctionality Confer Robustness to the Isocitrate Dehydrogenase Regulatory System in Escherichia coli*. Journal of Biological Chemistry, 2013, 288, 5770-5778.	1.6	24
41	Allosteric conformational ensembles have unlimited capacity for integrating information. ELife, 2021, 10, .	2.8	24
42	Paradoxical Results in Perturbation-Based Signaling Network Reconstruction. Biophysical Journal, 2014, 106, 2720-2728.	0.2	23
43	Biology is more theoretical than physics. Molecular Biology of the Cell, 2013, 24, 1827-1829.	0.9	17
44	Invariants reveal multiple forms of robustness in bifunctional enzyme systems. Integrative Biology (United Kingdom), 2015, 7, 883-894.	0.6	16
45	Robustness and parameter geography in post-translational modification systems. PLoS Computational Biology, 2020, 16, e1007573.	1.5	16
46	The Study of Posttranslational Modifications of Tau Protein by Nuclear Magnetic Resonance Spectroscopy: Phosphorylation of Tau Protein by ERK2 Recombinant Kinase and Rat Brain Extract, and Acetylation by Recombinant Creb-Binding Protein. Methods in Molecular Biology, 2017, 1523, 179-213.	0.4	15
47	Signals and Systems: Towards a Systems Biology of Signal Transduction. Proceedings of the IEEE, 2008, 96, 1386-1397.	16.4	13
48	Robust network structure of the Sln1-Ypd1-Ssk1 three-component phospho-relay prevents unintended activation of the HOG MAPK pathway in Saccharomyces cerevisiae. BMC Systems Biology, 2015, 9, 17.	3.0	13
49	Transcription factors, coregulators, and epigenetic marks are linearly correlated and highly redundant. PLoS ONE, 2017, 12, e0186324.	1.1	13
50	Beware the tail that wags the dog: informal and formal models in biology. Molecular Biology of the Cell, 2014, 25, 3441-3444.	0.9	11
51	Lack of evidence for substrate channeling or flux between wildtype and mutant isocitrate dehydrogenase to produce the oncometabolite 2-hydroxyglutarate. Journal of Biological Chemistry, 2018, 293, 20051-20061.	1.6	11
52	Silicon dreams of cells into symbols. Nature Biotechnology, 2012, 30, 838-840.	9.4	10
53	The linear framework: using graph theory to reveal the algebra and thermodynamics of biomolecular systems. Interface Focus, 2022, 12, .	1.5	10
54	Bayesian modeling suggests that IL-12 (p40), IL-13 and MCP-1 drive murine cytokine networks in vivo. BMC Systems Biology, 2015, 9, 76.	3.0	9

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55	Reversal symmetries for cyclic paths away from thermodynamic equilibrium. <i>Physical Review E</i> , 2020, 101, 062125.	0.8	9
56	Cybernetics, Redux: An Outside-In Strategy for Unraveling Cellular Function. <i>Developmental Cell</i> , 2016, 36, 2-4.	3.1	7
57	Learning Outside the Brain: Integrating Cognitive Science and Systems Biology. <i>Proceedings of the IEEE</i> , 2022, 110, 590-612.	16.4	7
58	Cellular Interrogation: Exploiting Cell-to-Cell Variability to Discriminate Regulatory Mechanisms in Oscillatory Signalling. <i>PLoS Computational Biology</i> , 2016, 12, e1004995.	1.5	5
59	Proteus: a web-based, context-specific modelling tool for molecular networks. <i>Bioinformatics</i> , 2012, 28, 1284-1286.	1.8	3
60	Model discrimination for Ca ²⁺ -dependent regulation of myosin light chain kinase in smooth muscle contraction. <i>FEBS Letters</i> , 2018, 592, 2811-2821.	1.3	3
61	Predicting oocyte fertilisability in intracytoplasmic sperm injection cycles: a retrospective observational study. <i>Lancet, The</i> , 2017, 389, S75.	6.3	2
62	Identification of Non-invasive Cytokine Biomarkers for Polycystic Ovary Syndrome Using Supervised Machine Learning. , 2018, , .		2
63	Monostationarity and Multistationarity in Tree Networks of Goldbeter's "Koshland Loops. <i>Bulletin of Mathematical Biology</i> , 2019, 81, 2463-2509.	0.9	2
64	Robustness and parameter geography in post-translational modification systems. , 2020, 16, e1007573.		0
65	Robustness and parameter geography in post-translational modification systems. , 2020, 16, e1007573.		0
66	Robustness and parameter geography in post-translational modification systems. , 2020, 16, e1007573.		0
67	Robustness and parameter geography in post-translational modification systems. , 2020, 16, e1007573.		0