Jeremy Gunawardena

List of Publications by Year
in descending order

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	Learning Outside the Brain: Integrating Cognitive Science and Systems Biology. Proceedings of the IEEE, 2022, 110, 590-612.	16.4	7
2	The linear framework: using graph theory to reveal the algebra and thermodynamics of biomolecular systems. Interface Focus, 2022, 12, .	1.5	10
3	Reconsidering the evidence for learning in single cells. ELife, 2021, 10, .	2.8	58
4	Allosteric conformational ensembles have unlimited capacity for integrating information. ELife, 2021, 10, .	2.8	24
5	Robustness and parameter geography in post-translational modification systems. PLoS Computational Biology, 2020, 16, e1007573.	1.5	16
6	Gene Regulation in and out of Equilibrium. Annual Review of Biophysics, 2020, 49, 199-226.	4.5	45
7	Reversal symmetries for cyclic paths away from thermodynamic equilibrium. Physical Review E, 2020, 101, 062125.	0.8	9
8	Robustness and parameter geography in post-translational modification systems. , 2020, 16, e1007573.		0
9	Robustness and parameter geography in post-translational modification systems. , 2020, 16, e1007573.		0
10	Robustness and parameter geography in post-translational modification systems. , 2020, 16, e1007573.		0
11	Robustness and parameter geography in post-translational modification systems. , 2020, 16, e1007573.		0
12	Monostationarity and Multistationarity in Tree Networks of Goldbeter–Koshland Loops. Bulletin of Mathematical Biology, 2019, 81, 2463-2509.	0.9	2
13	A Complex Hierarchy of Avoidance Behaviors in a Single-Cell Eukaryote. Current Biology, 2019, 29, 4323-4329.e2.	1.8	59
14	Negative reciprocity, not ordered assembly, underlies the interaction of Sox2 and Oct4 on DNA. ELife, 2019, 8, .	2.8	26
15	Dissecting the sharp response of a canonical developmental enhancer reveals multiple sources of cooperativity. ELife, 2019, 8, .	2.8	47
16	How many human proteoforms are there?. Nature Chemical Biology, 2018, 14, 206-214.	3.9	580
17	Identification of Non-invasive Cytokine Biomarkers for Polycystic Ovary Syndrome Using Supervised Machine Learning. , 2018, , .		2
18	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

#	Article	IF	Citations
19	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
20	Estimating the Distribution of Protein Post-Translational Modification States by Mass Spectrometry. Journal of Proteome Research, 2018, 17, 2727-2734.	1.8	33
21	Energy-speed-accuracy relation in complex networks for biological discrimination. Physical Review E, 2018, 98, 012420.	0.8	32
22	Model discrimination for Ca^{2+}–dependent regulation of myosin light chain kinase in smooth muscle contraction. FEBS Letters, 2018, 592, 2811-2821.	1.3	3
23	The Macronuclear Genome of Stentor coeruleus Reveals Tiny Introns in a Giant Cell. Current Biology, 2017, 27, 569-575.	1.8	105
24	Predicting oocyte fertilisability in intracytoplasmic sperm injection cycles: a retrospective observational study. Lancet, The, 2017, 389, S75.	6.3	2
25	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
26	Transcription factors, coregulators, and epigenetic marks are linearly correlated and highly redundant. PLoS ONE, 2017, 12, e0186324.	1.1	13
27	Cellular Interrogation: Exploiting Cell-to-Cell Variability to Discriminate Regulatory Mechanisms in Oscillatory Signalling. PLoS Computational Biology, 2016, 12, e1004995.	1.5	5
28	Nac1 Coordinates a Sub-network of Pluripotency Factors to Regulate Embryonic Stem Cell Differentiation. Cell Reports, 2016, 14, 1181-1194.	2.9	29
29	Information Integration and Energy Expenditure in Gene Regulation. Cell, 2016, 166, 234-244.	13.5	127
30	Cybernetics, Redux: An Outside-In Strategy for Unraveling Cellular Function. Developmental Cell, 2016, 36, 2-4.	3.1	7
31	Characterization of Neuronal Tau Protein as a Target of Extracellular Signal-regulated Kinase. Journal of Biological Chemistry, 2016, 291, 7742-7753.	1.6	54
32	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
33	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
34	Invariants reveal multiple forms of robustness in bifunctional enzyme systems. Integrative Biology (United Kingdom), 2015, 7, 883-894.	0.6	16
35	A framework for modelling gene regulation which accommodates non-equilibrium mechanisms. BMC Biology, 2014, 12, 102.	1.7	53
36	Time–scale separation – Michaelis and Menten's old idea, still bearing fruit. FEBS Journal, 2014, 281, 473-488.	2.2	107

#	ARTICLE	IF	CITATIONS
37	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
38	Quantitative profiling of peptides from RNAs classified as noncoding. Nature Communications, 2014, 5, 5429.	5.8	55
39	Paradoxical Results in Perturbation-Based Signaling Network Reconstruction. Biophysical Journal, 2014, 106, 2720-2728.	0.2	23
40	A Fundamental Trade-off in Covalent Switching and Its Circumvention by Enzyme Bifunctionality in Glucose Homeostasis. Journal of Biological Chemistry, 2014, 289, 13010-13025.	1.6	33
41	Models in biology: 'accurate descriptions of our pathetic thinking'. BMC Biology, 2014, 12, 29.	1.7	188
42	Tunable Signal Processing Through Modular Control of Transcription Factor Translocation. Science, 2013, 339, 460-464.	6.0	132
43	Laplacian Dynamics on General Graphs. Bulletin of Mathematical Biology, 2013, 75, 2118-2149.	0.9	87
44	Biology is more theoretical than physics. Molecular Biology of the Cell, 2013, 24, 1827-1829.	0.9	17
45	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
46	Silicon dreams of cells into symbols. Nature Biotechnology, 2012, 30, 838-840.	9.4	10
47	Some lessons about models from Michaelis and Menten. Molecular Biology of the Cell, 2012, 23, 517-519.	0.9	39
48	Proteus: a web-based, context-specific modelling tool for molecular networks. Bioinformatics, 2012, 28, 1284-1286.	1.8	3
49	Complex-linear invariants of biochemical networks. Journal of Theoretical Biology, 2012, 311, 130-138.	0.8	44
50	Realistic enzymology for post-translational modification: Zero-order ultrasensitivity revisited. Journal of Theoretical Biology, 2012, 311, 139-152.	0.8	31
51	Post-translational modification: nature's escape from genetic imprisonment and the basis for dynamic information encoding. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2012, 4, 565-583.	6.6	288
52	A Linear Framework for Time-Scale Separation in Nonlinear Biochemical Systems. PLoS ONE, 2012, 7, e36321.	1.1	112
53	Comparative analysis of Erk phosphorylation suggests a mixed strategy for measuring phospho-form distributions. Molecular Systems Biology, 2011, 7, 482.	3.2	38
54	A phosphatase threshold sets the level of Cdk1 activity in early mitosis in budding yeast. Molecular Biology of the Cell, 2011, 22, 3595-3608.	0.9	66

#	Article	IF	Citations
55	PHOSIDA 2011: the posttranslational modification database. Nucleic Acids Research, 2011, 39, D253-D260.	6.5	366
56	Evolutionary Constraints of Phosphorylation in Eukaryotes, Prokaryotes, and Mitochondria. Molecular and Cellular Proteomics, 2010, 9, 2642-2653.	2.5	83
57	Biological Systems Theory. Science, 2010, 328, 581-582.	6.0	24
58	Unlimited multistability in multisite phosphorylation systems. Nature, 2009, 460, 274-277.	13.7	219
59	The rational parameterisation theorem for multisite post-translational modification systems. Journal of Theoretical Biology, 2009, 261, 626-636.	0.8	84
60	Programming with models: modularity and abstraction provide powerful capabilities for systems biology. Journal of the Royal Society Interface, 2009, 6, 257-270.	1.5	66
61	Signals and Systems: Towards a Systems Biology of Signal Transduction. Proceedings of the IEEE, 2008, 96, 1386-1397.	16.4	13
62	The Geometry of Multisite Phosphorylation. Biophysical Journal, 2008, 95, 5533-5543.	0.2	62
63	Distributivity and Processivity in Multisite Phosphorylation Can Be Distinguished through Steady-State Invariants. Biophysical Journal, 2007, 93, 3828-3834.	0.2	42
64	Multisite protein phosphorylation makes a good threshold but can be a poor switch. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 14617-14622.	3.3	242
65	The Perron-Frobenius theorem for homogeneous, monotone functions. Transactions of the American Mathematical Society, 2004, 356, 4931-4950.	0.5	101
66	A constructive fixed point theorem for min-max functions. Dynamical Systems, 1999, 14, 407-433.	0.7	71
67	Min-max functions. Discrete Event Dynamic Systems: Theory and Applications, 1994, 4, 377-407.	0.6	71