

Peter S Swain

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

10,876
citations

201385

27
h-index

276539

41
g-index

50
all docs

50
docs citations

50
times ranked

8870
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiple nutrient transporters enable cells to mitigate a rate-affinity tradeoff. PLoS Computational Biology, 2022, 18, e1010060.	1.5	4
2	Analysing and meta-analysing time-series data of microbial growth and gene expression from plate readers. PLoS Computational Biology, 2022, 18, e1010138.	1.5	4
3	Roadmap on biology in time varying environments. Physical Biology, 2021, 18, 041502.	0.8	23
4	Estimating numbers of intracellular molecules through analysing fluctuations in photobleaching. Scientific Reports, 2019, 9, 15238.	1.6	12
5	Resolving fluorescent species by their brightness and diffusion using correlated photon-counting histograms. PLoS ONE, 2019, 14, e0226063.	1.1	6
6	Morphologically constrained and data informed cell segmentation of budding yeast. Bioinformatics, 2018, 34, 88-96.	1.8	33
7	On-Line Optimal Input Design Increases the Efficiency and Accuracy of the Modelling of an Inducible Synthetic Promoter. Processes, 2018, 6, 148.	1.3	25
8	Distributed and dynamic intracellular organization of extracellular information. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 6088-6093.	3.3	58
9	Transition between fermentation and respiration determines history-dependent behavior in fluctuating carbon sources. ELife, 2018, 7, .	2.8	44
10	Predicting metabolic adaptation from networks of mutational paths. Nature Communications, 2017, 8, 685.	5.8	8
11	Distributing tasks via multiple input pathways increases cellular survival in stress. ELife, 2017, 6, .	2.8	44
12	General calibration of microbial growth in microplate readers. Scientific Reports, 2016, 6, 38828.	1.6	238
13	Inferring time derivatives including cell growth rates using Gaussian processes. Nature Communications, 2016, 7, 13766.	5.8	87
14	A geometric analysis of fast-slow models for stochastic gene expression. Journal of Mathematical Biology, 2016, 72, 87-122.	0.8	25
15	BioJazz: <i>in silico</i> evolution of cellular networks with unbounded complexity using rule-based modeling. Nucleic Acids Research, 2015, 43, e123-e123.	6.5	11
16	Mechanistic links between cellular trade-offs, gene expression, and growth. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1038-47.	3.3	342
17	Unmixing of fluorescence spectra to resolve quantitative time-series measurements of gene expression in plate readers. BMC Biotechnology, 2014, 14, 11.	1.7	42
18	Environmental sensing, information transfer, and cellular decision-making. Current Opinion in Biotechnology, 2014, 28, 149-155.	3.3	107

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19	A Microfluidic System for Studying Ageing and Dynamic Single-Cell Responses in Budding Yeast. PLoS ONE, 2014, 9, e100042.	1.1	123
20	Ultrasensitivity in Phosphorylation-Dephosphorylation Cycles with Little Substrate. PLoS Computational Biology, 2013, 9, e1003175.	1.5	21
21	The Fidelity of Dynamic Signaling by Noisy Biomolecular Networks. PLoS Computational Biology, 2013, 9, e1002965.	1.5	56
22	Identifying sources of variation and the flow of information in biochemical networks. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1320-8.	3.3	120
23	A Bayesian method for inferring quantitative information from FRET data. BMC Biophysics, 2011, 4, 10.	4.4	6
24	Trade-Offs and Constraints in Allosteric Sensing. PLoS Computational Biology, 2011, 7, e1002261.	1.5	38
25	The scaffold protein Ste5 directly controls a switch-like mating decision in yeast. Nature, 2010, 465, 101-105.	13.7	160
26	Scalable Rule-Based Modelling of Allosteric Proteins and Biochemical Networks. PLoS Computational Biology, 2010, 6, e1000975.	1.5	45
27	Strategies for cellular decision-making. Molecular Systems Biology, 2009, 5, 326.	3.2	272
28	Cross-Talk between Signaling Pathways Can Generate Robust Oscillations in Calcium and cAMP. PLoS ONE, 2009, 4, e7189.	1.1	35
29	The stochastic nature of biochemical networks. Current Opinion in Biotechnology, 2008, 19, 369-374.	3.3	177
30	Analytical distributions for stochastic gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17256-17261.	3.3	719
31	Colored extrinsic fluctuations and stochastic gene expression. Molecular Systems Biology, 2008, 4, 196.	3.2	226
32	Noisy information processing through transcriptional regulation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7151-7156.	3.3	83
33	Facile: a command-line network compiler for systems biology. BMC Systems Biology, 2007, 1, 36.	3.0	18
34	A Fluctuation Method to Quantify In Vivo Fluorescence Data. Biophysical Journal, 2006, 91, 759-766.	0.2	69
35	An Entropic Mechanism to Generate Highly Cooperative and Specific Binding from Protein Phosphorylations. Current Biology, 2006, 16, 2150-2155.	1.8	37
36	Noise in genetic and neural networks. Chaos, 2006, 16, 026101.	1.0	46

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37	Gene Regulation at the Single-Cell Level. <i>Science</i> , 2005, 307, 1962-1965.	6.0	973
38	Efficient Attenuation of Stochasticity in Gene Expression Through Post-transcriptional Control. <i>Journal of Molecular Biology</i> , 2004, 344, 965-976.	2.0	189
39	Intrinsic and extrinsic contributions to stochasticity in gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12795-12800.	3.3	1,444
40	Stochastic Gene Expression in a Single Cell. <i>Science</i> , 2002, 297, 1183-1186.	6.0	4,817
41	The Role of Proofreading in Signal Transduction Specificity. <i>Biophysical Journal</i> , 2002, 82, 2928-2933.	0.2	76