Peter S Swain

List of Publications by Year
in descending order

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41 papers	10,876 citations	201674 27 h-index	276875 41 g-index
50 all docs	50 docs citations	50 times ranked	8870 citing authors

#	Article	IF	Citations
1	Stochastic Gene Expression in a Single Cell. Science, 2002, 297, 1183-1186.	12.6	4,817
2	Intrinsic and extrinsic contributions to stochasticity in gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 12795-12800.	7.1	1,444
3	Gene Regulation at the Single-Cell Level. Science, 2005, 307, 1962-1965.	12.6	973
4	Analytical distributions for stochastic gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17256-17261.	7.1	719
5	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.	7.1	342
6	Strategies for cellular decisionâ€making. Molecular Systems Biology, 2009, 5, 326.	7.2	272
7	General calibration of microbial growth in microplate readers. Scientific Reports, 2016, 6, 38828.	3.3	238
8	Colored extrinsic fluctuations and stochastic gene expression. Molecular Systems Biology, 2008, 4, 196.	7.2	226
9	Efficient Attenuation of Stochasticity in Gene Expression Through Post-transcriptional Control. Journal of Molecular Biology, 2004, 344, 965-976.	4.2	189
10	The stochastic nature of biochemical networks. Current Opinion in Biotechnology, 2008, 19, 369-374.	6.6	177
11	The scaffold protein Ste5 directly controls a switch-like mating decision in yeast. Nature, 2010, 465, 101-105.	27.8	160
12	A Microfluidic System for Studying Ageing and Dynamic Single-Cell Responses in Budding Yeast. PLoS ONE, 2014, 9, e100042.	2.5	123
13	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.	7.1	120
14	Environmental sensing, information transfer, and cellular decision-making. Current Opinion in Biotechnology, 2014, 28, 149-155.	6.6	107
15	Inferring time derivatives including cell growth rates using Gaussian processes. Nature Communications, 2016, 7, 13766.	12.8	87
16	Noisy information processing through transcriptional regulation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7151-7156.	7.1	83
17	The Role of Proofreading in Signal Transduction Specificity. Biophysical Journal, 2002, 82, 2928-2933.	0.5	76
18	A Fluctuation Method to Quantify In Vivo Fluorescence Data. Biophysical Journal, 2006, 91, 759-766.	0.5	69

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19	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.	7.1	58
20	The Fidelity of Dynamic Signaling by Noisy Biomolecular Networks. PLoS Computational Biology, 2013, 9, e1002965.	3.2	56
21	Noise in genetic and neural networks. Chaos, 2006, 16, 026101.	2.5	46
22	Scalable Rule-Based Modelling of Allosteric Proteins and Biochemical Networks. PLoS Computational Biology, 2010, 6, e1000975.	3.2	45
23	Distributing tasks via multiple input pathways increases cellular survival in stress. ELife, 2017, 6, .	6.0	44
24	Transition between fermentation and respiration determines history-dependent behavior in fluctuating carbon sources. ELife, 2018, 7, .	6.0	44
25	Unmixing of fluorescence spectra to resolve quantitative time-series measurements of gene expression in plate readers. BMC Biotechnology, 2014, 14, 11.	3.3	42
26	Trade-Offs and Constraints in Allosteric Sensing. PLoS Computational Biology, 2011, 7, e1002261.	3.2	38
27	An Entropic Mechanism to Generate Highly Cooperative and Specific Binding from Protein Phosphorylations. Current Biology, 2006, 16, 2150-2155.	3.9	37
28	Cross-Talk between Signaling Pathways Can Generate Robust Oscillations in Calcium and cAMP. PLoS ONE, 2009, 4, e7189.	2.5	35
29	Morphologically constrained and data informed cell segmentation of budding yeast. Bioinformatics, 2018, 34, 88-96.	4.1	33
30	A geometric analysis of fast-slow models for stochastic gene expression. Journal of Mathematical Biology, 2016, 72, 87-122.	1.9	25
31	On-Line Optimal Input Design Increases the Efficiency and Accuracy of the Modelling of an Inducible Synthetic Promoter. Processes, 2018, 6, 148.	2.8	25
32	Roadmap on biology in time varying environments. Physical Biology, 2021, 18, 041502.	1.8	23
33	Ultrasensitivity in Phosphorylation-Dephosphorylation Cycles with Little Substrate. PLoS Computational Biology, 2013, 9, e1003175.	3.2	21
34	Facile: a command-line network compiler for systems biology. BMC Systems Biology, 2007, 1, 36.	3.0	18
35	Estimating numbers of intracellular molecules through analysing fluctuations in photobleaching. Scientific Reports, 2019, 9, 15238.	3.3	12
36	BioJazz:in silicoevolution of cellular networks with unbounded complexity using rule-based modeling. Nucleic Acids Research, 2015, 43, e123-e123.	14.5	11

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37	Predicting metabolic adaptation from networks of mutational paths. Nature Communications, 2017, 8, 685.	12.8	8
38	A Bayesian method for inferring quantitative information from FRET data. BMC Biophysics, 2011, 4, 10.	4.4	6
39	Resolving fluorescent species by their brightness and diffusion using correlated photon-counting histograms. PLoS ONE, 2019, 14, e0226063.	2.5	6
40	Multiple nutrient transporters enable cells to mitigate a rate-affinity tradeoff. PLoS Computational Biology, 2022, 18, e1010060.	3.2	4
41	Analysing and meta-analysing time-series data of microbial growth and gene expression from plate readers. PLoS Computational Biology, 2022, 18, e1010138.	3.2	4