

Chris H Wiggins

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

3,123
citations

279798

23
h-index

345221

36
g-index

38
all docs

38
docs citations

38
times ranked

3814
citing authors

#	ARTICLE	IF	CITATIONS
1	Learning Rates and States from Biophysical Time Series: A Bayesian Approach to Model Selection and Single-Molecule FRET Data. <i>Biophysical Journal</i> , 2009, 97, 3196-3205.	0.5	368
2	Opposing Effects of PKC ζ and WASp on Symmetry Breaking and Relocation of the Immunological Synapse. <i>Cell</i> , 2007, 129, 773-785.	28.9	316
3	Nonmuscle Myosin IIA-Dependent Force Inhibits Cell Spreading and Drives F-Actin Flow. <i>Biophysical Journal</i> , 2006, 91, 3907-3920.	0.5	255
4	Flexive and Propulsive Dynamics of Elastica at Low Reynolds Number. <i>Physical Review Letters</i> , 1998, 80, 3879-3882.	7.8	235
5	Bayesian Approach to Network Modularity. <i>Physical Review Letters</i> , 2008, 100, 258701.	7.8	212
6	Trapping and Wiggling: Elastohydrodynamics of Driven Microfilaments. <i>Biophysical Journal</i> , 1998, 74, 1043-1060.	0.5	186
7	Empirical Bayes Methods Enable Advanced Population-Level Analyses of Single-Molecule FRET Experiments. <i>Biophysical Journal</i> , 2014, 106, 1327-1337.	0.5	172
8	Lateral Membrane Waves Constitute a Universal Dynamic Pattern of Motile Cells. <i>Physical Review Letters</i> , 2006, 97, 038102.	7.8	142
9	Allosteric collaboration between elongation factor G and the ribosomal L1 stalk directs tRNA movements during translation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15702-15707.	7.1	136
10	Quantification of Cell Edge Velocities and Traction Forces Reveals Distinct Motility Modules during Cell Spreading. <i>PLoS ONE</i> , 2008, 3, e3735.	2.5	112
11	Optimal Signal Processing in Small Stochastic Biochemical Networks. <i>PLoS ONE</i> , 2007, 2, e1077.	2.5	107
12	Viscous Nonlinear Dynamics of Twist and Writhe. <i>Physical Review Letters</i> , 1998, 80, 5232-5235.	7.8	105
13	Multimodal transcriptional control of pattern formation in embryonic development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 836-847.	7.1	82
14	Information-theoretic approach to network modularity. <i>Physical Review E</i> , 2005, 71, 046117.	2.1	74
15	Spectral solutions to stochastic models of gene expression with bursts and regulation. <i>Physical Review E</i> , 2009, 80, 041921.	2.1	71
16	The small GTPase R-Ras regulates organization of actin and drives membrane protrusions through the activity of PLC ζ . <i>Journal of Cell Science</i> , 2006, 119, 1307-1319.	2.0	67
17	Pegasus: a comprehensive annotation and prediction tool for detection of driver gene fusions in cancer. <i>BMC Systems Biology</i> , 2014, 8, 97.	3.0	60
18	Dynamic Patterns and Self-Knotting of a Driven Hanging Chain. <i>Physical Review Letters</i> , 2001, 87, 114301.	7.8	57

#	ARTICLE	IF	CITATIONS
19	A stochastic spectral analysis of transcriptional regulatory cascades. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6529-6534.	7.1	52
20	Dynamics of semiflexible polymers in a flow field. Physical Review E, 2006, 74, 041911.	2.1	39
21	Durable Interactions of T Cells with T Cell Receptor Stimuli in the Absence of a Stable Immunological Synapse. Cell Reports, 2018, 22, 340-349.	6.4	36
22	Analytic Methods for Modeling Stochastic Regulatory Networks. Methods in Molecular Biology, 2012, 880, 273-322.	0.9	35
23	Multiple LacI-mediated loops revealed by Bayesian statistics and tethered particle motion. Nucleic Acids Research, 2014, 42, 10265-10277.	14.5	29
24	Noise Expands the Response Range of the Bacillus subtilis Competence Circuit. PLoS Computational Biology, 2016, 12, e1004793.	3.2	20
25	Multiple events on single molecules: Unbiased estimation in single-molecule biophysics. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 1750-1755.	7.1	19
26	Graphical models for inferring single molecule dynamics. BMC Bioinformatics, 2010, 11, S2.	2.6	18
27	Single-molecule dataset (SMD): a generalized storage format for raw and processed single-molecule data. BMC Bioinformatics, 2015, 16, 3.	2.6	17
28	Information-Optimal Transcriptional Response to Oscillatory Driving. Physical Review Letters, 2010, 105, 058101.	7.8	16
29	Hierarchically-coupled hidden Markov models for learning kinetic rates from single-molecule data. JMLR Workshop and Conference Proceedings, 2013, 28, 361-369.	1.4	16
30	A classification-based framework for predicting and analyzing gene regulatory response. BMC Bioinformatics, 2006, 7, S5.	2.6	15
31	Learning Regulatory Programs That Accurately Predict Differential Expression with MEDUSA. Annals of the New York Academy of Sciences, 2007, 1115, 178-202.	3.8	13
32	Motif Discovery Through Predictive Modeling of Gene Regulation. Lecture Notes in Computer Science, 2005, , 538-552.	1.3	12
33	Integrative analysis of T cell motility from multi-channel microscopy data using TIAM. Journal of Immunological Methods, 2015, 416, 84-93.	1.4	10
34	Biopolymer mechanics: stability, dynamics, and statistics. Mathematical Methods in the Applied Sciences, 2001, 24, 1325-1335.	2.3	6
35	Statistical method for revealing form-function relations in biological networks. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 446-451.	7.1	5
36	Statistical Inference for Nanopore Sequencing with a Biased Random Walk Model. Biophysical Journal, 2015, 108, 1852-1855.	0.5	2