Nicolas E Buchler

List of Publications by Year
in descending order

39 papers	3,714 citations	257450 24 h-index	315739 38 g-index
54 all docs	54 docs citations	54 times ranked	4215 citing authors

#	Article	IF	Citations
1	Competition for DNA binding between paralogous transcription factors determines their genomic occupancy and regulatory functions. Genome Research, 2021, 31, 1216-1229.	5.5	14
2	Chytrid fungi. Current Biology, 2020, 30, R516-R520.	3.9	24
3	Genetic transformation of Spizellomyces punctatus, a resource for studying chytrid biology and evolutionary cell biology. ELife, 2020, 9, .	6.0	29
4	Exact and efficient hybrid Monte Carlo algorithm for accelerated Bayesian inference of gene expression models from snapshots of single-cell transcripts. Journal of Chemical Physics, 2019, 151, 024106.	3.0	9
5	Evolutionary innovation, fungal cell biology, and the lateral gene transfer of a viral KilA-N domain. Current Opinion in Genetics and Development, 2019, 58-59, 103-110.	3.3	10
6	Recognition of Histone Crotonylation by Taf14 Links Metabolic State to Gene Expression. Molecular Cell, 2019, 76, 909-921.e3.	9.7	83
7	Epigenetic switching as a strategy for quick adaptation while attenuating biochemical noise. PLoS Computational Biology, 2019, 15, e1007364.	3.2	17
8	Enhancer Histone Acetylation Modulates Transcriptional Bursting Dynamics of Neuronal Activity-Inducible Genes. Cell Reports, 2019, 26, 1174-1188.e5.	6.4	111
9	The evolution of a G1/S transcriptional network in yeasts. Current Genetics, 2018, 64, 81-86.	1.7	12
10	Daily humidity oscillation regulates the circadian clock to influence plant physiology. Nature Communications, 2018, 9, 4290.	12.8	38
11	Efficient analysis of stochastic gene dynamics in the non-adiabatic regime using piecewise deterministic Markov processes. Journal of the Royal Society Interface, 2018, 15, 20170804.	3.4	25
12	Conservation and divergence of C-terminal domain structure in the retinoblastoma protein family. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4942-4947.	7.1	33
13	Long-term growth data of Escherichia coli at a single-cell level. Scientific Data, 2017, 4, 170036.	5.3	23
14	BayFish: Bayesian inference of transcription dynamics from population snapshots of single-molecule RNA FISH in single cells. Genome Biology, 2017, 18, 164.	8.8	37
15	Gene duplication and co-evolution of G1/S transcription factor specificity in fungi are essential for optimizing cell fitness. PLoS Genetics, 2017, 13, e1006778.	3.5	11
16	Cell cycle Start is coupled to entry into the yeast metabolic cycle across diverse strains and growth rates. Molecular Biology of the Cell, 2016, 27, 64-74.	2.1	52
17	The *Physarum polycephalum* Genome Reveals Extensive Use of Prokaryotic Two-Component and Metazoan-Type Tyrosine Kinase Signaling. Genome Biology and Evolution, 2016, 8, 109-125.	2.5	87
18	Punctuated evolution and transitional hybrid network in an ancestral cell cycle of fungi. ELife, 2016, 5, .	6.0	52

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19	Role of DNA binding sites and slow unbinding kinetics in titration-based oscillators. Physical Review E, 2015, 92, 062712.	2.1	16
20	A noisy linear map underlies oscillations in cell size and gene expression in bacteria. Nature, 2015, 523, 357-360.	27.8	209
21	Redox rhythm reinforces the circadian clock to gate immune response. Nature, 2015, 523, 472-476.	27.8	167
22	Different Mechanisms Confer Gradual Control and Memory at Nutrient- and Stress-Regulated Genes in Yeast. Molecular and Cellular Biology, 2015, 35, 3669-3683.	2.3	16
23	Measuring fast gene dynamics in single cells with time-lapse luminescence microscopy. Molecular Biology of the Cell, 2014, 25, 3699-3708.	2.1	23
24	Multicolor Timelapse Luminescence Microscopy: Optimizing Luciferases to Track Fast Gene Dynamics in Single Yeast Cells. Biophysical Journal, 2014, 106, 372a-373a.	0.5	0
25	Programming stress–induced altruistic death in engineered bacteria. Molecular Systems Biology, 2012, 8, 626.	7.2	55
26	Chromatin: Bind at Your Own RSC. Current Biology, 2011, 21, R223-R225.	3.9	2
27	Evolution of networks and sequences in eukaryotic cell cycle control. Philosophical Transactions of the Royal Society B: Biological Sciences, 2011, 366, 3532-3544.	4.0	121
28	Protein sequestration generates a flexible ultrasensitive response in a genetic network. Molecular Systems Biology, 2009, 5, 272.	7.2	209
29	Molecular Titration and Ultrasensitivity in Regulatory Networks. Journal of Molecular Biology, 2008, 384, 1106-1119.	4.2	248
30	Designing sequential transcription logic: a simple genetic circuit for conditional memory. Systems and Synthetic Biology, 2007, 1, 89-98.	1.0	30
31	Two-Faced Cyclins with Eyes on the Targets. Cell Cycle, 2005, 4, 125-130.	2.6	36
32	Nonlinear protein degradation and the function of genetic circuits. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 9559-9564.	7.1	157
33	Transcriptional regulation by the numbers: applications. Current Opinion in Genetics and Development, 2005, 15, 125-135.	3.3	343
34	Transcriptional regulation by the numbers: models. Current Opinion in Genetics and Development, 2005, 15, 116-124.	3.3	660
35	On schemes of combinatorial transcription logic. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5136-5141.	7.1	586
36	Surveying determinants of protein structure designability across different energy models and amino-acid alphabets: A consensus. Journal of Chemical Physics, 2000, 112, 2533-2547.	3.0	35

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37	Universal correlation between energy gap and foldability for the random energy model and lattice proteins. Journal of Chemical Physics, 1999, 111, 6599-6609.	3.0	19
38	Effect of alphabet size and foldability requirements on protein structure designability. Proteins: Structure, Function and Bioinformatics, 1999, 34, 113-124.	2.6	56
39	Protein Heteronuclear NMR Assignments Using Mean-Field Simulated Annealing. Journal of Magnetic Resonance, 1997, 125, 34-42.	2.1	55