Matteo Barberis

List of Publications by Year
in descending order

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49 papers	878 citations	471477 17 h-index	526264 27 g-index
55 all docs	55 docs citations	55 times ranked	964 citing authors

#	Article	IF	Citations
1	Cell Size at S Phase Initiation: An Emergent Property of the G1/S Network. PLoS Computational Biology, 2007, 3, e64.	3.2	96
2	The yeast cyclin-dependent kinase inhibitor Sic1 and mammalian p27Kip1 are functional homologues with a structurally conserved inhibitory domain. Biochemical Journal, 2005, 387, 639-647.	3.7	66
3	ROS networks: designs, aging, Parkinsonâ€™s disease and precision therapies. Npj Systems Biology and Applications, 2020, 6, 34.	3.0	50
4	A Mechanistic Computational Model Reveals That Plasticity of CD4+ T Cell Differentiation Is a Function of Cytokine Composition and Dosage. Frontiers in Physiology, 2018, 9, 878.	2.8	46
5	Simulation of Stimulation: Cytokine Dosage and Cell Cycle Crosstalk Driving Timing-Dependent T Cell Differentiation. Frontiers in Physiology, 2018, 9, 879.	2.8	44
6	Systems Pharmacology: An opinion on how to turn the impossible into grand challenges. Drug Discovery Today: Technologies, 2015, 15, 23-31.	4.0	40
7	Conserved forkhead dimerization motif controls DNA replication timing and spatial organization of chromosomes in <i>S. cerevisiae</i>. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2411-E2419.	7.1	40
8	Towards a systems biology approach to mammalian cell cycle: modeling the entrance into S phase of quiescent fibroblasts after serum stimulation. BMC Bioinformatics, 2009, 10, S16.	2.6	37
9	A Clb/Cdk1-mediated regulation of Fkh2 synchronizes CLB expression in the budding yeast cell cycle. Npj Systems Biology and Applications, 2017, 3, 7.	3.0	32
10	Sic1 plays a role in timing and oscillatory behaviour of B-type cyclins. Biotechnology Advances, 2012, 30, 108-130.	11.7	29
11	Fkh1 and Fkh2 associate with Sir2 to control CLB2 transcription under normal and oxidative stress conditions. Frontiers in Physiology, 2013, 4, 173.	2.8	27
12	A model for the spatiotemporal organization of DNA replication in Saccharomyces cerevisiae. Molecular Genetics and Genomics, 2009, 282, 25-35.	2.1	26
13	Predictable Irreversible Switching Between Acute and Chronic Inflammation. Frontiers in Immunology, 2018, 9, 1596.	4.8	26
14	Computer-Aided Whole-Cell Design: Taking a Holistic Approach by Integrating Synthetic With Systems Biology. Frontiers in Bioengineering and Biotechnology, 2020, 8, 942.	4.1	25
15	Sic1 as a timer of Clb cyclin waves in the yeast cell cycleâ€ƒâ€“â€ƒdesign principle of not just an inhibitor. FEBS Journal, 2012, 279, 3386-3410.	4.7	22
16	Advances and challenges in logical modeling of cell cycle regulation: perspective for multi-scale, integrative yeast cell models. FEMS Yeast Research, 2017, 17, fow103.	2.3	21
17	Sirtuins-Mediated System-Level Regulation of Mammalian Tissues at the Interface between Metabolism and Cell Cycle: A Systematic Review. Biology, 2021, 10, 194.	2.8	21
18	Integrative computational approach identifies drug targets in CD4+ T-cell-mediated immune disorders. Npj Systems Biology and Applications, 2021, 7, 4.	3.0	18

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19	Replication Origins and Timing of Temporal Replication in Budding Yeast: How to Solve the Conundrum?. Current Genomics, 2010, 11, 199-211.	1.6	17
20	CK2 regulates in vitro the activity of the yeast cyclin-dependent kinase inhibitor Sic1. Biochemical and Biophysical Research Communications, 2005, 336, 1040-1048.	2.1	15
21	Unraveling interactions of cell cycleâ€regulating proteins Sic1 and Bâ€type cyclins in living yeast cells: a FLIMâ€FRET approach. FASEB Journal, 2012, 26, 546-554.	0.5	14
22	Quantitative Systems Biology to decipher design principles of a dynamic cell cycle network: the â€œMaximum Allowable mammalian Tradeâ€"Offâ€"Weightâ€• (MAmTOW). Npj Systems Biology and Applications, 2017, 3, 26.	3.0	14
23	A multi-approach and multi-scale platform to model CD4+ T cells responding to infections. PLoS Computational Biology, 2021, 17, e1009209.	3.2	12
24	System-Level Scenarios for the Elucidation of T Cell-Mediated Germinal Center B Cell Differentiation. Frontiers in Immunology, 2021, 12, 734282.	4.8	12
25	ChIP-exo analysis highlights Fkh1 and Fkh2 transcription factors as hubs that integrate multi-scale networks in budding yeast. Nucleic Acids Research, 2019, 47, 7825-7841.	14.5	11
26	Synthetic designs regulating cellular transitions: Fine-tuning of switches and oscillators. Current Opinion in Systems Biology, 2021, 25, 11-26.	2.6	10
27	A low number of SIC1 mRNA molecules ensures a low noise level in cell cycle progression of budding yeast. Molecular BioSystems, 2011, 7, 2804.	2.9	9
28	Clb3-centered regulations are recurrent across distinct parameter regions in minimal autonomous cell cycle oscillator designs. Npj Systems Biology and Applications, 2020, 6, 8.	3.0	9
29	Understanding Principles of the Dynamic Biochemical Networks of Life Through Systems Biology. , 2014, , 21-44.		7
30	Learning to read and write in evolution: from static pseudoenzymes and pseudosignalers to dynamic gear shifters. Biochemical Society Transactions, 2017, 45, 635-652.	3.4	7
31	The Peculiar Glycolytic Pathway in Hyperthermophylic Archaea: Understanding Its Whims by Experimentation In Silico. International Journal of Molecular Sciences, 2017, 18, 876.	4.1	7
32	INSIGHTS INTO THE NETWORK CONTROLLING THE G₁/S TRANSITION IN BUDDING YEAST. , 2007, , .		7
33	GEMMER: GEnome-wide tool for Multi-scale Modeling data Extraction and Representation for <i>Saccharomyces cerevisiae</i>. Bioinformatics, 2018, 34, 2147-2149.	4.1	6
34	SysMod: the ISCB community for data-driven computational modelling and multi-scale analysis of biological systems. Bioinformatics, 2021, 37, 3702-3706.	4.1	6
35	What Influences DNA Replication Rate in Budding Yeast?. PLoS ONE, 2010, 5, e10203.	2.5	5
36	Maps for when the living gets tough: Maneuvering through a hostile energy landscape. IFAC-PapersOnLine, 2016, 49, 364-370.	0.9	5

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37	Quantitative model of eukaryotic Cdk control through the Forkhead CONTROLLER. Npj Systems Biology and Applications, 2021, 7, 28.	3.0	5
38	Advanced Modeling of Cellular Proliferation: Toward a Multi-scale Framework Coupling Cell Cycle to Metabolism by Integrating Logical and Constraint-Based Models. Methods in Molecular Biology, 2019, 2049, 365-385.	0.9	5
39	Insights into the network controlling the G1/S transition in budding yeast. Genome Informatics, 2007, 18, 85-99.	0.4	5
40	KINETIC MODELLING OF DNA REPLICATION INITIATION IN BUDDING YEAST. , 2010, , .		4
41	Molecular Systems Biology of Sic1 in Yeast Cell Cycle Regulation Through Multiscale Modeling. Advances in Experimental Medicine and Biology, 2012, 736, 135-167.	1.6	4
42	Cyclin/Forkhead-mediated coordination of cyclin waves: an autonomous oscillator rationalizing the quantitative model of Cdk control for budding yeast. Npj Systems Biology and Applications, 2021, 7, 48.	3.0	4
43	A variable fork rate affects timing of origin firing and S phase dynamics in Saccharomyces cerevisiae. Journal of Biotechnology, 2013, 168, 174-184.	3.8	2
44	Complex Stability and an Irrevertible Transition Reverted by Peptide and Fibroblasts in a Dynamic Model of Innate Immunity. Frontiers in Immunology, 2020, 10, 3091.	4.8	2
45	Unveiling Forkhead-mediated regulation of yeast cell cycle and metabolic networks. Computational and Structural Biotechnology Journal, 2022, 20, 1743-1751.	4.1	2
46	Coupling Cell Division to Metabolic Pathways Through Transcription. , 2019, , 74-93.		1
47	Kinetic modelling of DNA replication initiation in budding yeast. Genome Informatics, 2010, 24, 1-20.	0.4	1
48	Experimental and Stochastic Model Analysis of the Influence of SIC1, CLN2 and CLB5 Transcriptional Noise on the Timing Regulation of G1/S Transition in S. Cerevisiae Cell-Cycle. Biophysical Journal, 2012, 102, 228a.	0.5	0
49	Stigma/Style Cell-Cycle Inhibitor 1, a Regulator of Cell Proliferation, Interacts With a Specific 14-3-3 Protein and Is Degraded During Cell Division. Frontiers in Plant Science, 2022, 13, 857745.	3.6	0