

Attila Csikasz-Nagy

List of Publications by Year in descending order

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85
papers

3,538
citations

218592

26
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149623

56
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93
all docs

93
docs citations

93
times ranked

3312
citing authors

#	ARTICLE	IF	CITATIONS
1	Microsimulation based quantitative analysis of COVID-19 management strategies. PLoS Computational Biology, 2022, 18, e1009693.	1.5	19
2	Diversity of synaptic protein complexes as a function of the abundance of their constituent proteins: A modeling approach. PLoS Computational Biology, 2022, 18, e1009758.	1.5	3
3	Time-keeping and decision-making in living cells: Part I. Interface Focus, 2022, 12, .	1.5	3
4	Time-keeping and decision-making in living cells: Part II. Interface Focus, 2022, 12, .	1.5	2
5	Evolution of opposing regulatory interactions underlies the emergence of eukaryotic cell cycle checkpoints. Scientific Reports, 2021, 11, 11122.	1.6	1
6	Systematic analysis of noise reduction properties of coupled and isolated feed-forward loops. PLoS Computational Biology, 2021, 17, e1009622.	1.5	3
7	Interpretation of morphogen gradients by a synthetic bistable circuit. Nature Communications, 2020, 11, 5545.	5.8	16
8	Information Cascades and the Collapse of Cooperation. Scientific Reports, 2020, 10, 8004.	1.6	4
9	Comparative analysis of the intracellular responses to disease-related aggregation-prone proteins. Journal of Proteomics, 2020, 225, 103862.	1.2	1
10	Coupled membrane transporters reduce noise. Physical Review E, 2020, 101, 012414.	0.8	1
11	Combining data integration and molecular dynamics for target identification in α -Synuclein-aggregating neurodegenerative diseases: Structural insights on Synptojanin-1 (Synj1). Computational and Structural Biotechnology Journal, 2020, 18, 1032-1042.	1.9	3
12	Unifying the mechanism of mitotic exit control in a spatiotemporal logical model. PLoS Biology, 2020, 18, e3000917.	2.6	5
13	Unifying the mechanism of mitotic exit control in a spatiotemporal logical model. , 2020, 18, e3000917.		0
14	Unifying the mechanism of mitotic exit control in a spatiotemporal logical model. , 2020, 18, e3000917.		0
15	Unifying the mechanism of mitotic exit control in a spatiotemporal logical model. , 2020, 18, e3000917.		0
16	Unifying the mechanism of mitotic exit control in a spatiotemporal logical model. , 2020, 18, e3000917.		0
17	Unifying the mechanism of mitotic exit control in a spatiotemporal logical model. , 2020, 18, e3000917.		0
18	Unifying the mechanism of mitotic exit control in a spatiotemporal logical model. , 2020, 18, e3000917.		0

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19	Synthetic Physical Interactions with the Yeast Centrosome. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2183-2194.	0.8	7
20	Competition in the chaperone-client network subordinates cell-cycle entry to growth and stress. <i>Life Science Alliance</i> , 2019, 2, e201800277.	1.3	13
21	Proteostasis collapse, a hallmark of aging, hinders the chaperone-Start network and arrests cells in G1. <i>ELife</i> , 2019, 8, .	2.8	28
22	Computational Models of Cell Cycle Transitions. <i>Methods in Molecular Biology</i> , 2018, 1819, 297-316.	0.4	0
23	Toward Large-Scale Computational Prediction of Protein Complexes. <i>Methods in Molecular Biology</i> , 2018, 1819, 271-295.	0.4	2
24	Context-dependent prediction of protein complexes by SiComPre. <i>Npj Systems Biology and Applications</i> , 2018, 4, 37.	1.4	2
25	Molecular Filters for Noise Reduction. <i>Biophysical Journal</i> , 2018, 114, 3000-3011.	0.2	22
26	Single molecules can operate as primitive biological sensors, switches and oscillators. <i>BMC Systems Biology</i> , 2018, 12, 70.	3.0	9
27	Computing with biological switches and clocks. <i>Natural Computing</i> , 2018, 17, 761-779.	1.8	45
28	Adaptive Mistranslation Accelerates the Evolution of Fluconazole Resistance and Induces Major Genomic and Gene Expression Alterations in <i>Candida albicans</i> . <i>MSphere</i> , 2017, 2, .	1.3	29
29	Molecular Network Dynamics of Cell Cycle Control: Periodicity of Start and Finish. <i>Methods in Molecular Biology</i> , 2017, 1524, 331-349.	0.4	7
30	Growth Rate as a Direct Regulator of the Start Network to Set Cell Size. <i>Frontiers in Cell and Developmental Biology</i> , 2017, 5, 57.	1.8	34
31	Efficient Switches in Biology and Computer Science. <i>PLoS Computational Biology</i> , 2017, 13, e1005100.	1.5	11
32	Noise Reduction in Complex Biological Switches. <i>Scientific Reports</i> , 2016, 6, 20214.	1.6	33
33	Role of Computational Modeling in Understanding Cell Cycle Oscillators. <i>Methods in Molecular Biology</i> , 2016, 1342, 59-70.	0.4	2
34	The effects of an editor serving as one of the reviewers during the peer-review process. <i>F1000Research</i> , 2016, 5, 683.	0.8	3
35	The effects of an editor serving as one of the reviewers during the peer-review process. <i>F1000Research</i> , 2016, 5, 683.	0.8	4
36	<sc>Hsp12p</sc> and <sc>i>PAU</i> genes are involved in ecological interactions between natural yeast strains. <i>Environmental Microbiology</i> , 2015, 17, 3069-3081.	1.8	21

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37	Module-based construction of plasmids for chromosomal integration of the fission yeast <i>Schizosaccharomyces pombe</i> . Open Biology, 2015, 5, 150054.	1.5	23
38	Qualitative and Quantitative Protein Complex Prediction Through Proteome-Wide Simulations. PLoS Computational Biology, 2015, 11, e1004424.	1.5	21
39	Models of Breast Morphogenesis Based on Localization of Stem Cells in the Developing Mammary Lobule. Stem Cell Reports, 2015, 4, 699-711.	2.3	29
40	Circadian rhythms synchronize mitosis in <i>Neurospora crassa</i> . Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 1397-1402.	3.3	63
41	An Insulin-to-Insulin Regulatory Network Orchestrates Phenotypic Specificity in Development and Physiology. PLoS Genetics, 2014, 10, e1004225.	1.5	90
42	<i>Neurospora crassa</i> as a model organism to explore the interconnected network of the cell cycle and the circadian clock. Fungal Genetics and Biology, 2014, 71, 52-57.	0.9	18
43	A network approach to mixing delegates at meetings. ELife, 2014, 3, e02273.	2.8	5
44	In vivo and in silico analysis of PCNA ubiquitylation in the activation of the Post Replication Repair pathway in <i>S. cerevisiae</i> . BMC Systems Biology, 2013, 7, 24.	3.0	7
45	Cooperation and competition in the dynamics of tissue architecture during homeostasis and tumorigenesis. Seminars in Cancer Biology, 2013, 23, 293-298.	4.3	20
46	Spatial segregation of polarity factors into distinct cortical clusters is required for cell polarity control. Nature Communications, 2013, 4, 1834.	5.8	52
47	Dynamics of SIN Asymmetry Establishment. PLoS Computational Biology, 2013, 9, e1003147.	1.5	10
48	Projecting cell polarity into the next decade. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20130001.	1.8	2
49	Cell Cycle. , 2013, , 220-231.		0
50	Linkers of Cell Polarity and Cell Cycle Regulation in the Fission Yeast Protein Interaction Network. PLoS Computational Biology, 2012, 8, e1002732.	1.5	14
51	Combining Game Theory and Graph Theory to Model Interactions between Cells in the Tumor Microenvironment. SIMAI Springer Series, 2012, , 3-18.	0.4	3
52	The Cell Cycle Switch Computes Approximate Majority. Scientific Reports, 2012, 2, 656.	1.6	92
53	The critical size is set at a single-cell level by growth rate to attain homeostasis and adaptation. Nature Communications, 2012, 3, 1012.	5.8	170
54	Keystone Species of Molecular Interaction Networks. Developments in Environmental Modelling, 2012, 25, 73-88.	0.3	0

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55	Transcriptional Regulation Is a Major Controller of Cell Cycle Transition Dynamics. PLoS ONE, 2012, 7, e29716.	1.1	15
56	Prosperity is associated with instability in dynamical networks. Journal of Theoretical Biology, 2012, 299, 126-138.	0.8	49
57	1SA-06 Feedback and feed-forward controls of cell cycle transitions(1SA Dynamics and Robustness in) Tj ETQq1 1 0.784314 rgBT /Ov 2011, 51, S1-S2.	0.0	0
58	Overexpression limits of fission yeast cell cycle regulators <i>in vivo</i> and <i>in silico</i> . Molecular Systems Biology, 2011, 7, 556.	3.2	14
59	Response dynamics of phosphorelays suggest their potential utility in cell signalling. Journal of the Royal Society Interface, 2011, 8, 480-488.	1.5	42
60	Molecular Network Dynamics of Cell Cycle Control: Transitions to Start and Finish. Methods in Molecular Biology, 2011, 761, 277-291.	0.4	11
61	Restriction point control of the mammalian cell cycle via the cyclin E/Cdk2:p27 complex. FEBS Journal, 2010, 277, 357-367.	2.2	44
62	Role of mRNA Gestation and Senescence in Noise Reduction during the Cell Cycle. In Silico Biology, 2010, 10, 81-88.	0.4	4
63	Cell cycle regulation by feed-forward loops coupling transcription and phosphorylation. Molecular Systems Biology, 2009, 5, 236.	3.2	44
64	Computational systems biology of the cell cycle. Briefings in Bioinformatics, 2009, 10, 424-434.	3.2	70
65	Minimum Criteria for DNA Damage-Induced Phase Advances in Circadian Rhythms. PLoS Computational Biology, 2009, 5, e1000384.	1.5	14
66	Regulating the total level of a signaling protein can vary its dynamics in a range from switch like ultrasensitivity to adaptive responses. FEBS Journal, 2009, 276, 3290-3298.	2.2	13
67	Studying Irreversible Transitions in a Model of Cell Cycle Regulation. Electronic Notes in Theoretical Computer Science, 2009, 232, 39-53.	0.9	12
68	Stochastic Petri Net extension of a yeast cell cycle model. Journal of Theoretical Biology, 2008, 254, 850-860.	0.8	63
69	Spatial controls for growth zone formation during the fission yeast cell cycle. Yeast, 2008, 25, 59-69.	0.8	31
70	Analysis of a budding yeast cell cycle model using the shapes of local sensitivity functions. International Journal of Chemical Kinetics, 2008, 40, 710-720.	1.0	17
71	Adaptive dynamics with a single two-state protein. Journal of the Royal Society Interface, 2008, 5, S41-7.	1.5	16
72	Reverse Engineering Models of Cell Cycle Regulation. Advances in Experimental Medicine and Biology, 2008, 641, 88-97.	0.8	15

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73	Computational Analysis of Mammalian Cell Division Gated by a Circadian Clock: Quantized Cell Cycles and Cell Size Control. <i>Journal of Biological Rhythms</i> , 2007, 22, 542-553.	1.4	50
74	Irreversible cell-cycle transitions are due to systems-level feedback. <i>Nature Cell Biology</i> , 2007, 9, 724-728.	4.6	178
75	Modeling the septation initiation network (SIN) in fission yeast cells. <i>Current Genetics</i> , 2007, 51, 245-255.	0.8	27
76	Analysis of a Generic Model of Eukaryotic Cell-Cycle Regulation. <i>Biophysical Journal</i> , 2006, 90, 4361-4379.	0.2	226
77	Time scale and dimension analysis of a budding yeast cell cycle model. <i>BMC Bioinformatics</i> , 2006, 7, 494.	1.2	34
78	Integrative Analysis of Cell Cycle Control in Budding Yeast. <i>Molecular Biology of the Cell</i> , 2004, 15, 3841-3862.	0.9	584
79	The dynamics of cell cycle regulation. <i>BioEssays</i> , 2002, 24, 1095-1109.	1.2	277
80	Morphogenetic checkpoint in fission yeast? Yes!. <i>Microbiology (United Kingdom)</i> , 2002, 148, 2270-2271.	0.7	2
81	Kinetic Analysis of a Molecular Model of the Budding Yeast Cell Cycle. <i>Molecular Biology of the Cell</i> , 2000, 11, 369-391.	0.9	437
82	Modeling the fission yeast cell cycle: Quantized cycle times in <i>wee1- cdc25Delta</i> mutant cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 7865-7870.	3.3	117
83	Finishing the Cell Cycle. <i>Journal of Theoretical Biology</i> , 1999, 199, 223-233.	0.8	50
84	Mathematical model of the fission yeast cell cycle with checkpoint controls at the G1/S, G2/M and metaphase/anaphase transitions. <i>Biophysical Chemistry</i> , 1998, 72, 185-200.	1.5	121
85	A polarizÁlt sejtnÁrvekedÁs Ás a sejtciklus kapcsolata. <i>Magyar TudomÁny</i> , 0, , .	0.0	0