

Attila Csikasz-Nagy

List of Publications by Year in descending order

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Version: 2024-02-01

85
papers

3,538
citations

218381

26
h-index

149479

56
g-index

93
all docs

93
docs citations

93
times ranked

3312
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Integrative Analysis of Cell Cycle Control in Budding Yeast. <i>Molecular Biology of the Cell</i> , 2004, 15, 3841-3862. | 0.9 | 584 |
| 2 | 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 |
| 3 | The dynamics of cell cycle regulation. <i>BioEssays</i> , 2002, 24, 1095-1109. | 1.2 | 277 |
| 4 | Analysis of a Generic Model of Eukaryotic Cell-Cycle Regulation. <i>Biophysical Journal</i> , 2006, 90, 4361-4379. | 0.2 | 226 |
| 5 | Irreversible cell-cycle transitions are due to systems-level feedback. <i>Nature Cell Biology</i> , 2007, 9, 724-728. | 4.6 | 178 |
| 6 | The critical size is set at a single-cell level by growth rate to attain homeostasis and adaptation. <i>Nature Communications</i> , 2012, 3, 1012. | 5.8 | 170 |
| 7 | 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 |
| 8 | 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 |
| 9 | The Cell Cycle Switch Computes Approximate Majority. <i>Scientific Reports</i> , 2012, 2, 656. | 1.6 | 92 |
| 10 | An Insulin-to-Insulin Regulatory Network Orchestrates Phenotypic Specificity in Development and Physiology. <i>PLoS Genetics</i> , 2014, 10, e1004225. | 1.5 | 90 |
| 11 | Computational systems biology of the cell cycle. <i>Briefings in Bioinformatics</i> , 2009, 10, 424-434. | 3.2 | 70 |
| 12 | Stochastic Petri Net extension of a yeast cell cycle model. <i>Journal of Theoretical Biology</i> , 2008, 254, 850-860. | 0.8 | 63 |
| 13 | Circadian rhythms synchronize mitosis in <i>Neurospora crassa</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1397-1402. | 3.3 | 63 |
| 14 | Spatial segregation of polarity factors into distinct cortical clusters is required for cell polarity control. <i>Nature Communications</i> , 2013, 4, 1834. | 5.8 | 52 |
| 15 | Finishing the Cell Cycle. <i>Journal of Theoretical Biology</i> , 1999, 199, 223-233. | 0.8 | 50 |
| 16 | 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 |
| 17 | Prosperity is associated with instability in dynamical networks. <i>Journal of Theoretical Biology</i> , 2012, 299, 126-138. | 0.8 | 49 |
| 18 | Computing with biological switches and clocks. <i>Natural Computing</i> , 2018, 17, 761-779. | 1.8 | 45 |

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|----|--|-----|-----------|
| 19 | Cell cycle regulation by feedâ€forward loops coupling transcription and phosphorylation. <i>Molecular Systems Biology</i> , 2009, 5, 236. | 3.2 | 44 |
| 20 | Restriction point control of the mammalian cell cycle via the cyclin E/Cdk2:p27 complex. <i>FEBS Journal</i> , 2010, 277, 357-367. | 2.2 | 44 |
| 21 | Response dynamics of phosphorelays suggest their potential utility in cell signalling. <i>Journal of the Royal Society Interface</i> , 2011, 8, 480-488. | 1.5 | 42 |
| 22 | Time scale and dimension analysis of a budding yeast cell cycle model. <i>BMC Bioinformatics</i> , 2006, 7, 494. | 1.2 | 34 |
| 23 | 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 |
| 24 | Noise Reduction in Complex Biological Switches. <i>Scientific Reports</i> , 2016, 6, 20214. | 1.6 | 33 |
| 25 | Spatial controls for growth zone formation during the fission yeast cell cycle. <i>Yeast</i> , 2008, 25, 59-69. | 0.8 | 31 |
| 26 | Models of Breast Morphogenesis Based on Localization of Stem Cells in the Developing Mammary Lobule. <i>Stem Cell Reports</i> , 2015, 4, 699-711. | 2.3 | 29 |
| 27 | 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 |
| 28 | Proteostasis collapse, a hallmark of aging, hinders the chaperone-Start network and arrests cells in G1. <i>ELife</i> , 2019, 8, . | 2.8 | 28 |
| 29 | Modeling the septation initiation network (SIN) in fission yeast cells. <i>Current Genetics</i> , 2007, 51, 245-255. | 0.8 | 27 |
| 30 | Module-based construction of plasmids for chromosomal integration of the fission yeast <i>Schizosaccharomyces pombe</i> . <i>Open Biology</i> , 2015, 5, 150054. | 1.5 | 23 |
| 31 | Molecular Filters for Noise Reduction. <i>Biophysical Journal</i> , 2018, 114, 3000-3011. | 0.2 | 22 |
| 32 | <i>Hsp12p</i> and <i>PAU</i> genes are involved in ecological interactions between natural yeast strains. <i>Environmental Microbiology</i> , 2015, 17, 3069-3081. | 1.8 | 21 |
| 33 | Qualitative and Quantitative Protein Complex Prediction Through Proteome-Wide Simulations. <i>PLoS Computational Biology</i> , 2015, 11, e1004424. | 1.5 | 21 |
| 34 | Cooperation and competition in the dynamics of tissue architecture during homeostasis and tumorigenesis. <i>Seminars in Cancer Biology</i> , 2013, 23, 293-298. | 4.3 | 20 |
| 35 | Microsimulation based quantitative analysis of COVID-19 management strategies. <i>PLoS Computational Biology</i> , 2022, 18, e1009693. | 1.5 | 19 |
| 36 | <i>Neurospora crassa</i> as a model organism to explore the interconnected network of the cell cycle and the circadian clock. <i>Fungal Genetics and Biology</i> , 2014, 71, 52-57. | 0.9 | 18 |

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|----|---|-----|-----------|
| 37 | Analysis of a budding yeast cell cycle model using the shapes of local sensitivity functions. <i>International Journal of Chemical Kinetics</i> , 2008, 40, 710-720. | 1.0 | 17 |
| 38 | Adaptive dynamics with a single two-state protein. <i>Journal of the Royal Society Interface</i> , 2008, 5, S41-7. | 1.5 | 16 |
| 39 | Interpretation of morphogen gradients by a synthetic bistable circuit. <i>Nature Communications</i> , 2020, 11, 5545. | 5.8 | 16 |
| 40 | Transcriptional Regulation Is a Major Controller of Cell Cycle Transition Dynamics. <i>PLoS ONE</i> , 2012, 7, e29716. | 1.1 | 15 |
| 41 | Reverse Engineering Models of Cell Cycle Regulation. <i>Advances in Experimental Medicine and Biology</i> , 2008, 641, 88-97. | 0.8 | 15 |
| 42 | Minimum Criteria for DNA Damage-Induced Phase Advances in Circadian Rhythms. <i>PLoS Computational Biology</i> , 2009, 5, e1000384. | 1.5 | 14 |
| 43 | Overexpression limits of fission yeast cell cycle regulators <i>in vivo</i> and <i>in silico</i> . <i>Molecular Systems Biology</i> , 2011, 7, 556. | 3.2 | 14 |
| 44 | Linkers of Cell Polarity and Cell Cycle Regulation in the Fission Yeast Protein Interaction Network. <i>PLoS Computational Biology</i> , 2012, 8, e1002732. | 1.5 | 14 |
| 45 | Regulating the total level of a signaling protein can vary its dynamics in a range from switch like ultrasensitivity to adaptive responses. <i>FEBS Journal</i> , 2009, 276, 3290-3298. | 2.2 | 13 |
| 46 | 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 |
| 47 | Studying Irreversible Transitions in a Model of Cell Cycle Regulation. <i>Electronic Notes in Theoretical Computer Science</i> , 2009, 232, 39-53. | 0.9 | 12 |
| 48 | Molecular Network Dynamics of Cell Cycle Control: Transitions to Start and Finish. <i>Methods in Molecular Biology</i> , 2011, 761, 277-291. | 0.4 | 11 |
| 49 | Efficient Switches in Biology and Computer Science. <i>PLoS Computational Biology</i> , 2017, 13, e1005100. | 1.5 | 11 |
| 50 | Dynamics of SIN Asymmetry Establishment. <i>PLoS Computational Biology</i> , 2013, 9, e1003147. | 1.5 | 10 |
| 51 | Single molecules can operate as primitive biological sensors, switches and oscillators. <i>BMC Systems Biology</i> , 2018, 12, 70. | 3.0 | 9 |
| 52 | In vivo and in silico analysis of PCNA ubiquitylation in the activation of the Post Replication Repair pathway in <i>S. cerevisiae</i> . <i>BMC Systems Biology</i> , 2013, 7, 24. | 3.0 | 7 |
| 53 | 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 |
| 54 | Synthetic Physical Interactions with the Yeast Centrosome. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2183-2194. | 0.8 | 7 |

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|----|---|-----|-----------|
| 55 | A network approach to mixing delegates at meetings. <i>ELife</i> , 2014, 3, e02273. | 2.8 | 5 |
| 56 | Unifying the mechanism of mitotic exit control in a spatiotemporal logical model. <i>PLoS Biology</i> , 2020, 18, e3000917. | 2.6 | 5 |
| 57 | Role of mRNA Gestation and Senescence in Noise Reduction during the Cell Cycle. <i>In Silico Biology</i> , 2010, 10, 81-88. | 0.4 | 4 |
| 58 | Information Cascades and the Collapse of Cooperation. <i>Scientific Reports</i> , 2020, 10, 8004. | 1.6 | 4 |
| 59 | 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 |
| 60 | Combining Game Theory and Graph Theory to Model Interactions between Cells in the Tumor Microenvironment. <i>SIMA Springer Series</i> , 2012, , 3-18. | 0.4 | 3 |
| 61 | Combining data integration and molecular dynamics for target identification in $\hat{\pm}$ -Synuclein-aggregating neurodegenerative diseases: Structural insights on Synaptojanin-1 (Synj1). <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1032-1042. | 1.9 | 3 |
| 62 | 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 |
| 63 | Systematic analysis of noise reduction properties of coupled and isolated feed-forward loops. <i>PLoS Computational Biology</i> , 2021, 17, e1009622. | 1.5 | 3 |
| 64 | Diversity of synaptic protein complexes as a function of the abundance of their constituent proteins: A modeling approach. <i>PLoS Computational Biology</i> , 2022, 18, e1009758. | 1.5 | 3 |
| 65 | Time-keeping and decision-making in living cells: Part I. <i>Interface Focus</i> , 2022, 12, . | 1.5 | 3 |
| 66 | Projecting cell polarity into the next decade. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20130001. | 1.8 | 2 |
| 67 | Role of Computational Modeling in Understanding Cell Cycle Oscillators. <i>Methods in Molecular Biology</i> , 2016, 1342, 59-70. | 0.4 | 2 |
| 68 | Toward Large-Scale Computational Prediction of Protein Complexes. <i>Methods in Molecular Biology</i> , 2018, 1819, 271-295. | 0.4 | 2 |
| 69 | Context-dependent prediction of protein complexes by SiComPre. <i>Npj Systems Biology and Applications</i> , 2018, 4, 37. | 1.4 | 2 |
| 70 | Morphogenetic checkpoint in fission yeast? Yes!. <i>Microbiology (United Kingdom)</i> , 2002, 148, 2270-2271. | 0.7 | 2 |
| 71 | Time-keeping and decision-making in living cells: Part II. <i>Interface Focus</i> , 2022, 12, . | 1.5 | 2 |
| 72 | Comparative analysis of the intracellular responses to disease-related aggregation-prone proteins. <i>Journal of Proteomics</i> , 2020, 225, 103862. | 1.2 | 1 |

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|----|--|-----|-----------|
| 73 | Coupled membrane transporters reduce noise. Physical Review E, 2020, 101, 012414. | 0.8 | 1 |
| 74 | Evolution of opposing regulatory interactions underlies the emergence of eukaryotic cell cycle checkpoints. Scientific Reports, 2021, 11, 11122. | 1.6 | 1 |
| 75 | 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 |
| 76 | âœKeystone Speciesâœof Molecular Interaction Networks. Developments in Environmental Modelling, 2012, 25, 73-88. | 0.3 | 0 |
| 77 | Computational Models of Cell Cycle Transitions. Methods in Molecular Biology, 2018, 1819, 297-316. | 0.4 | 0 |
| 78 | Cell Cycle. , 2013, , 220-231. | | 0 |
| 79 | A polarizÃjt sejtnevekedÃs s sejtciklus kapcsolata. Magyar TudomÃjny, 0, , . | 0.0 | 0 |
| 80 | Unifying the mechanism of mitotic exit control in a spatiotemporal logical model. , 2020, 18, e3000917. | | 0 |
| 81 | Unifying the mechanism of mitotic exit control in a spatiotemporal logical model. , 2020, 18, e3000917. | | 0 |
| 82 | Unifying the mechanism of mitotic exit control in a spatiotemporal logical model. , 2020, 18, e3000917. | | 0 |
| 83 | Unifying the mechanism of mitotic exit control in a spatiotemporal logical model. , 2020, 18, e3000917. | | 0 |
| 84 | Unifying the mechanism of mitotic exit control in a spatiotemporal logical model. , 2020, 18, e3000917. | | 0 |
| 85 | Unifying the mechanism of mitotic exit control in a spatiotemporal logical model. , 2020, 18, e3000917. | | 0 |