John J Tyson

List of Publications by Year
in descending order

251 papers	17,444 citations	19636 61 h-index	17090 122 g-index
273 all docs	273 docs citations	273 times ranked	11937 citing authors

#	Article	IF	Citations
1	Understanding virtual patients efficiently and rigorously by combining machine learning with dynamical modelling. Journal of Pharmacokinetics and Pharmacodynamics, 2022, , 1.	0.8	1
2	From the Belousovâ€"Zhabotinsky reaction to biochemical clocks, traveling waves and cell cycle regulation. Biochemical Journal, 2022, 479, 185-206.	1.7	5
3	Mathematical analysis of robustness of oscillations in models of the mammalian circadian clock. PLoS Computational Biology, 2022, 18, e1008340.	1.5	4
4	Time-keeping and decision-making in living cells: Part I. Interface Focus, 2022, 12, .	1.5	3
5	Mitotic kinase oscillation governs the latching of cell cycle switches. Current Biology, 2022, 32, 2780-2785.e2.	1.8	5
6	Time-keeping and decision-making in living cells: Part II. Interface Focus, 2022, 12, .	1.5	2
7	Time-keeping and decision-making inÂtheÂcell cycle. Interface Focus, 2022, 12, .	1.5	10
8	Mechanisms of signalling-memory governing progression through the eukaryotic cell cycle. Current Opinion in Cell Biology, 2021, 69, 7-16.	2.6	21
9	Computational modeling of chromosome re-replication in mutant strains of fission yeast. Molecular Biology of the Cell, 2021, 32, 830-841.	0.9	0
10	Natural antisense transcript of *Period2, Per2AS,* regulates the amplitude of the mouse circadian clock. Genes and Development, 2021, 35, 899-913.	2.7	13
11	Modeling and analysis of the macronutrient signaling network in budding yeast. Molecular Biology of the Cell, 2021, 32, ar20.	0.9	4
12	Cell Cycle Regulation. Bifurcation Theory. , 2021, , 41-57.		1
13	Mitotic Cycle Regulation. II. Traveling Waves. , 2021, , 19-40.		0
14	Mitotic Cycle Regulation. I. Oscillations and Bistability. , 2021, , 1-17.		0
15	Computational modeling of unphosphorylated CtrA:Cori binding in the Caulobacter cell cycle. IScience, 2021, 24, 103413.	1.9	2
16	A Single Light-Responsive Sizer Can Control Multiple-Fission Cycles in Chlamydomonas. Current Biology, 2020, 30, 634-644.e7.	1.8	16
17	A stochastic model for error correction of kinetochore-microtubule attachments in budding yeast. PLoS ONE, 2020, 15, e0236293.	1.1	0
18	Genetic interactions derived from high-throughput phenotyping of 6589 yeast cell cycle mutants. Npj Systems Biology and Applications, 2020, 6, 11.	1.4	3

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19	A Dynamical Paradigm for Molecular Cell Biology. Trends in Cell Biology, 2020, 30, 504-515.	3.6	53
20	A hybrid stochastic model of the budding yeast cell cycle. Npj Systems Biology and Applications, 2020, 6, 7.	1.4	5
21	Cell cycle control and environmental response by second messengers in Caulobacter crescentus. BMC Bioinformatics, 2020, 21, 408.	1.2	9
22	Misuse of the Michaelis–Menten rate law for protein interaction networks and its remedy. PLoS Computational Biology, 2020, 16, e1008258.	1.5	45
23	A stochastic model of size control in the budding yeast cell cycle. BMC Bioinformatics, 2019, 20, 322.	1.2	6
24	Efficiently Encoding Complex Biochemical Models with the Multistate Model Builder (MSMB). Methods in Molecular Biology, 2019, 1945, 119-139.	0.4	1
25	Ectopic Activation of the Spindle Assembly Checkpoint Signaling Cascade Reveals Its Biochemical Design. Current Biology, 2019, 29, 104-119.e10.	1.8	23
26	Modeling the dynamic behavior of biochemical regulatory networks. Journal of Theoretical Biology, 2019, 462, 514-527.	0.8	35
27	Quasi-Newton Stochastic Optimization Algorithm for Parameter Estimation of a Stochastic Model of the Budding Yeast Cell Cycle. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 301-311.	1.9	6
28	Systems biology: perspectives on multiscale modeling in research on endocrine-related cancers. Endocrine-Related Cancer, 2019, 26, R345-R368.	1.6	14
29	Genome stability during cell proliferation: A systems analysis of the molecular mechanisms controlling progression through the eukaryotic cell cycle. Current Opinion in Systems Biology, 2018, 9, 22-31.	1.3	13
30	CrossPlan: systematic planning of genetic crosses to validate mathematical models. Bioinformatics, 2018, 34, 2237-2244.	1.8	3
31	JigCell Model Connector: building large molecular network models from components. Simulation, 2018, 94, 993-1008.	1.1	2
32	Deciphering the Dynamics of Interlocked Feedback Loops in a Model of the Mammalian Circadian Clock. Biophysical Journal, 2018, 115, 2055-2066.	0.2	7
33	Dilution and titration of cell-cycle regulators may control cell size in budding yeast. PLoS Computational Biology, 2018, 14, e1006548.	1.5	45
34	Mathematical Analysis of Cytokine-Induced Differentiation of Granulocyte-Monocyte Progenitor Cells. Frontiers in Immunology, 2018, 9, 2048.	2.2	17
35	Modeling the interactions of sense and antisense Period transcripts in the mammalian circadian clock network. PLoS Computational Biology, 2018, 14, e1005957.	1.5	10
36	CrossPlan. , 2018, , .		1

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37	A Stochastic Model of Size Control in the Budding Yeast Cell Cycle. , 2018, , .		0
38	Predicting network modules of cell cycle regulators using relative protein abundance statistics. BMC Systems Biology, 2017, 11, 30.	3.0	9
39	Spatiotemporal Models of the Asymmetric Division Cycle of Caulobacter crescentus. Results and Problems in Cell Differentiation, 2017, 61, 23-48.	0.2	5
40	GraphSpace: stimulating interdisciplinary collaborations in network biology. Bioinformatics, 2017, 33, 3134-3136.	1.8	23
41	Cell-cycle transitions: a common role for stoichiometric inhibitors. Molecular Biology of the Cell, 2017, 28, 3437-3446.	0.9	16
42	Hybrid ODE/SSA Model of the Budding Yeast Cell Cycle Control Mechanism with Mutant Case Study. , 2017, , .		2
43	A Stochastic Model of the Yeast Cell Cycle Reveals Roles for Feedback Regulation in Limiting Cellular Variability. PLoS Computational Biology, 2016, 12, e1005230.	1.5	42
44	A Bistable Switch Mechanism for Stem Cell Domain Nucleation in the Shoot Apical Meristem. Frontiers in Plant Science, 2016, 7, 674.	1.7	5
45	Model-driven experimental approach reveals the complex regulatory distribution of p53 by the circadian factor Period 2. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13516-13521.	3.3	81
46	Cell Division: Flipping the Mitotic Switches. Current Biology, 2016, 26, R1272-R1274.	1.8	5
47	A Hybrid Stochastic Model of the Budding Yeast Cell Cycle Control Mechanism. , 2016, , .		3
48	A stochastic spatiotemporal model of a response-regulator network in the <i>Caulobacter crescentus</i> cell cycle. Physical Biology, 2016, 13, 035007.	0.8	6
49	The <i>Physarum polycephalum</i> Genome Reveals Extensive Use of Prokaryotic Two-Component and Metazoan-Type Tyrosine Kinase Signaling. Genome Biology and Evolution, 2016, 8, 109-125.	1.1	87
50	A Model of Yeast Cell-Cycle Regulation Based on a Standard Component Modeling Strategy for Protein Regulatory Networks. PLoS ONE, 2016, 11, e0153738.	1.1	25
51	Dynamic Modeling of the Interaction Between Autophagy and Apoptosis in Mammalian Cells. CPT: Pharmacometrics and Systems Pharmacology, 2015, 4, 263-272.	1.3	67
52	From START to FINISH: computational analysis of cell cycle control in budding yeast. Npj Systems Biology and Applications, 2015, 1, 15016.	1.4	66
53	JigCell Run Manager (JC-RM): a tool for managing large sets of biochemical model parametrizations. BMC Systems Biology, 2015, 9, 95.	3.0	3
54	Dynamical Localization of DivL and PleC in the Asymmetric Division Cycle of Caulobacter crescentus: A Theoretical Investigation of Alternative Models. PLoS Computational Biology, 2015, 11, e1004348.	1.5	15

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55	Experimental testing of a new integrated model of the budding yeast START transition. Molecular Biology of the Cell, 2015, 26, 3966-3984.	0.9	25
56	Bistability, Oscillations, and Traveling Waves in Frog Egg Extracts. Bulletin of Mathematical Biology, 2015, 77, 796-816.	0.9	7
57	Cell Cycle Control by a Minimal Cdk Network. PLoS Computational Biology, 2015, 11, e1004056.	1.5	49
58	A Mathematical Framework for Understanding Four-Dimensional Heterogeneous Differentiation of $\hbox{CD4}^{+}$ CD4 + T Cells. Bulletin of Mathematical Biology, 2015, 77, 1046-1064.	0.9	21
59	Models in biology: lessons from modeling regulation of the eukaryotic cell cycle. BMC Biology, 2015, 13, 46.	1.7	61
60	Endocrine resistance in breast cancer â€" An overview and update. Molecular and Cellular Endocrinology, 2015, 418, 220-234.	1.6	280
61	A Stochastic Model Correctly Predicts Changes in Budding Yeast Cell Cycle Dynamics upon Periodic Expression of CLN2. PLoS ONE, 2014, 9, e96726.	1.1	9
62	Multistate Model Builder (MSMB): a flexible editor for compact biochemical models. BMC Systems Biology, 2014, 8, 42.	3.0	10
63	Control of cell growth, division and death: information processing in living cells. Interface Focus, 2014, 4, 20130070.	1.5	31
64	Mathematical models of the transitions between endocrine therapy responsive and resistant states in breast cancer. Journal of the Royal Society Interface, 2014, 11, 20140206.	1.5	30
65	Optimization and model reduction in the high dimensional parameter space of a budding yeast cell cycle model. BMC Systems Biology, 2013, 7, 53.	3.0	23
66	Minimal Models for Cell-Cycle Control Based on Competitive Inhibition andÂMultisite Phosphorylations of Cdk Substrates. Biophysical Journal, 2013, 104, 1367-1379.	0.2	13
67	Role for regulated phosphatase activity in generating mitotic oscillations in *Xenopus* cell-free extracts. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20539-20544.	3.3	7
68	Modelling the effect of GRP78 on anti-oestrogen sensitivity and resistance in breast cancer. Interface Focus, 2013, 3, 20130012.	1.5	26
69	Modeling the estrogen receptor to growth factor receptor signaling switch in human breast cancer cells. FEBS Letters, 2013, 587, 3327-3334.	1.3	24
70	Irreversible Transitions, Bistability and Checkpoint Controls in the Eukaryotic Cell Cycle. , 2013, , 265-285.		13
71	Molecular mechanisms creating bistable switches at cell cycle transitions. Open Biology, 2013, 3, 120179.	1.5	62
72	Measurement and modeling of transcriptional noise in the cell cycle regulatory network. Cell Cycle, 2013, 12, 3392-3407.	1.3	18

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73	Potential Role of a Bistable Histidine Kinase Switch in the Asymmetric Division Cycle of Caulobacter crescentus. PLoS Computational Biology, 2013, 9, e1003221.	1.5	16
74	Top-Down Network Analysis to Drive Bottom-Up Modeling of Physiological Processes. Journal of Computational Biology, 2013, 20, 409-418.	0.8	14
75	Cell Cycle Dynamics, Bistability and Oscillations. , 2013, , 263-270.		1
76	Mammalian Cell Cycle Regulation. , 2013, , 1-24.		3
77	Cell Cycle Model Analysis, Bifurcation Theory. , 2013, , 274-278.		1
78	Cell Cycle Modeling, Differential Equation. , 2013, , 282-286.		0
79	Cell Cycle Dynamics, Irreversibility. , 2013, , 270-273.		0
80	Cell Cycle, Budding Yeast. , 2013, , 337-341.		2
81	Network Topologies and Dynamics Leading to Endotoxin Tolerance and Priming in Innate Immune Cells. PLoS Computational Biology, 2012, 8, e1002526.	1.5	51
82	A simple theoretical framework for understanding heterogeneous differentiation of CD4+ T cells. BMC Systems Biology, 2012, 6, 66.	3.0	49
83	Hybrid modeling and simulation of stochastic effects on progression through the eukaryotic cell cycle. Journal of Chemical Physics, 2012, 136, 034105.	1.2	31
84	Network Topologies and Dynamics Leading to Endotoxin Tolerance and Priming in Innate Immune Cells. Biophysical Journal, 2012, 102, 730a.	0.2	0
85	A Mathematical Model of Mitotic Exit in Budding Yeast: The Role of Polo Kinase. PLoS ONE, 2012, 7, e30810.	1.1	12
86	Endoplasmic Reticulum Stress, the Unfolded Protein Response, Autophagy, and the Integrated Regulation of Breast Cancer Cell Fate. Cancer Research, 2012, 72, 1321-1331.	0.4	183
87	Oscillatory Dynamics of Cell Cycle Proteins in Single Yeast Cells Analyzed by Imaging Cytometry. PLoS ONE, 2011, 6, e26272.	1.1	23
88	Dynamic modelling of oestrogen signalling and cell fate in breast cancer cells. Nature Reviews Cancer, 2011, 11, 523-532.	12.8	179
89	Cell Cycle: Who Turns the Crank?. Current Biology, 2011, 21, R185-R187.	1.8	9
90	Endoplasmic reticulum stress, the unfolded protein response, and gene network modeling in antiestrogen resistant breast cancer. Hormone Molecular Biology and Clinical Investigation, 2011, 5, 35-44.	0.3	49

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91	System-level feedbacks make the anaphase switch irreversible. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 10016-10021.	3.3	55
92	Stochastic exit from mitosis in budding yeast. Cell Cycle, 2011, 10, 999-1009.	1.3	26
93	A Mathematical Model for the Reciprocal Differentiation of T Helper 17 Cells and Induced Regulatory T Cells. PLoS Computational Biology, 2011, 7, e1002122.	1.5	76
94	A Hybrid Model of Mammalian Cell Cycle Regulation. PLoS Computational Biology, 2011, 7, e1001077.	1.5	83
95	Regulated protein kinases and phosphatases in cell cycle decisions. Current Opinion in Cell Biology, 2010, 22, 801-808.	2.6	54
96	Model Composition for Macromolecular Regulatory Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 278-287.	1.9	14
97	A model of yeast cell–cycle regulation based on multisite phosphorylation. Molecular Systems Biology, 2010, 6, 405.	3.2	97
98	Functional Motifs in Biochemical Reaction Networks. Annual Review of Physical Chemistry, 2010, 61, 219-240.	4.8	257
99	Exploring the roles of noise in the eukaryotic cell cycle. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6471-6476.	3.3	140
100	Cell cycle regulation by feed–forward loops coupling transcription and phosphorylation. Molecular Systems Biology, 2009, 5, 236.	3.2	44
101	Model aggregation: a building-block approach to creating large macromolecular regulatory networks. Bioinformatics, 2009, 25, 3289-3295.	1.8	13
102	The Interleukin-1 Receptor-Associated Kinase M Selectively Inhibits the Alternative, Instead of the Classical NFκB Pathway. Journal of Innate Immunity, 2009, 1, 164-174.	1.8	28
103	Temporal Controls of the Asymmetric Cell Division Cycle in Caulobacter crescentus. PLoS Computational Biology, 2009, 5, e1000463.	1.5	30
104	Bistability by multiple phosphorylation of regulatory proteins. Progress in Biophysics and Molecular Biology, 2009, 100, 47-56.	1.4	74
105	Computing with Proteins. Computer, 2009, 42, 47-56.	1.2	16
106	System–level feedbacks control cell cycle progression. FEBS Letters, 2009, 583, 3992-3998.	1.3	38
107	A quantitative model of the effect of unreplicated DNA on cell cycle progression in frog egg extracts. Journal of Theoretical Biology, 2009, 260, 110-120.	0.8	8
108	Computational Analysis of Dynamical Responses to the Intrinsic Pathway of Programmed Cell Death. Biophysical Journal, 2009, 97, 415-434.	0.2	86

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109	Modeling Molecular Regulatory Networks with JigCell and PET. Methods in Molecular Biology, 2009, 500, 81-111.	0.4	7
110	Deterministic parallel global parameter estimation for a model of the budding yeast cell cycle. Journal of Global Optimization, 2008, 40, 719-738.	1.1	25
111	Spatial controls for growth zone formation during the fission yeast cell cycle. Yeast, 2008, 25, 59-69.	0.8	31
112	Antagonism and bistability in protein interaction networks. Journal of Theoretical Biology, 2008, 250, 209-218.	0.8	66
113	Design principles of biochemical oscillators. Nature Reviews Molecular Cell Biology, 2008, 9, 981-991.	16.1	970
114	Temporal Organization of the Cell Cycle. Current Biology, 2008, 18, R759-R768.	1.8	165
115	Stochastic Simulation of Enzyme-Catalyzed Reactions with Disparate Timescales. Biophysical Journal, 2008, 95, 3563-3574.	0.2	53
116	Biological switches and clocks. Journal of the Royal Society Interface, 2008, 5, S1-8.	1.5	101
117	A Quantitative Study of the Division Cycle of Caulobacter crescentus Stalked Cells. PLoS Computational Biology, 2008, 4, e9.	1.5	51
118	Reverse Engineering Models of Cell Cycle Regulation. Advances in Experimental Medicine and Biology, 2008, 641, 88-97.	0.8	15
119	A proposal for robust temperature compensation of circadian rhythms. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1195-1200.	3.3	57
120	Computational Model of the Division Cycle of Caulobacter crescentus. AIP Conference Proceedings, 2007, , .	0.3	0
121	Modeling Networks of Coupled Enzymatic Reactions Using the Total Quasi-Steady State Approximation. PLoS Computational Biology, 2007, 3, e45.	1.5	147
122	Exploring Mechanisms of the DNA-Damage Response: p53 Pulses and their Possible Relevance to Apoptosis. Cell Cycle, 2007, 6, 85-94.	1.3	121
123	A Mathematical Programming Formulation for the Budding Yeast Cell Cycle. Simulation, 2007, 83, 497-514.	1.1	3
124	Dynamical modeling of syncytial mitotic cycles in <i>Drosophila</i> embryos. Molecular Systems Biology, 2007, 3, 131.	3.2	41
125	Mathematical modeling as a tool for investigating cell cycle control networks. Methods, 2007, 41, 238-247.	1.9	77
126	Bringing cartoons to life. Nature, 2007, 445, 823-823.	13.7	45

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127	Irreversible cell-cycle transitions are due to systems-level feedback. Nature Cell Biology, 2007, 9, 724-728.	4.6	178
128	Modeling the septation initiation network (SIN) in fission yeast cells. Current Genetics, 2007, 51, 245-255.	0.8	27
129	The JigCell Model Builder: A Spreadsheet Interface for Creating Biochemical Reaction Network Models. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006, 3, 155-164.	1.9	21
130	Analysis of a Generic Model of Eukaryotic Cell-Cycle Regulation. Biophysical Journal, 2006, 90, 4361-4379.	0.2	226
131	Cell Cycle Control in Bacteria and Yeast: A Case of Convergent Evolution?. Cell Cycle, 2006, 5, 522-529.	1.3	26
132	Another turn for p53. Molecular Systems Biology, 2006, 2, 2006.0032.	3.2	43
133	Computer evaluation of network dynamics models with application to cell cycle control in budding yeast. IET Systems Biology, 2006, 153, 13.	2.0	10
134	The Role of Composition and Aggregation in Modeling Macromolecular Regulatory Networks. , 2006, , .		4
135	Periodic forcing of a mathematical model of the eukaryotic cell cycle. Physical Review E, 2006, 73, 011910.	0.8	10
136	Synchronization of Eukaryotic Cells by Periodic Forcing. Physical Review Letters, 2006, 96, 148102.	2.9	23
137	Challenges for Modeling and Simulation Methods in Systems Biology. , 2006, , .		13
138	Steady States and Oscillations in the p53/Mdm2 Network. Cell Cycle, 2005, 4, 488-493.	1.3	221
139	Parameter Estimation for a Mathematical Model of the Cell Cycle in Frog Eggs. Journal of Computational Biology, 2005, 12, 48-63.	0.8	38
140	A Quantitative Study of the Division Cycle of Caulobacter crescentus Stalked Cells. PLoS Computational Biology, 2005, preprint, e9.	1.5	0
141	Rewiring the exit from mitosis. Cell Cycle, 2005, 4, 1107-12.	1.3	8
142	Modelling the fission yeast cell cycle. Briefings in Functional Genomics & Proteomics, 2004, 2, 298-307.	3.8	36
143	Integrative Analysis of Cell Cycle Control in Budding Yeast. Molecular Biology of the Cell, 2004, 15, 3841-3862.	0.9	584
144	The JigCell Model Builder and Run Manager. Bioinformatics, 2004, 20, 3680-3681.	1.8	33

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145	Cycling without the Cyclosome: Modeling a Yeast Strain Lacking the APC. Cell Cycle, 2004, 3, 627-631.	1.3	21
146	Monitoring p53's pulse. Nature Genetics, 2004, 36, 113-114.	9.4	37
147	A precarious balance. Current Biology, 2004, 14, R262-R263.	1.8	7
148	Finding all steady state solutions of chemical kinetic models. Nonlinear Analysis: Real World Applications, 2004, 5, 801-814.	0.9	11
149	A model for restriction point control of the mammalian cell cycle. Journal of Theoretical Biology, 2004, 230, 563-579.	0.8	272
150	Turbulence near cyclic fold bifurcations in birhythmic media. Physical Review E, 2004, 70, 026212.	0.8	11
151	Bifurcation analysis of a model of the budding yeast cell cycle. Chaos, 2004, 14, 653-661.	1.0	54
152	Cycling without the cyclosome: modeling a yeast strain lacking the APC. Cell Cycle, 2004, 3, 629-33.	1.3	10
153	Sniffers, buzzers, toggles and blinkers: dynamics of regulatory and signaling pathways in the cell. Current Opinion in Cell Biology, 2003, 15, 221-231.	2.6	1,423
154	A kinetic model of the cyclin E/Cdk2 developmental timer in Xenopus laevis embryos. Biophysical Chemistry, 2003, 104, 573-589.	1.5	25
155	Mathematical model of the morphogenesis checkpoint in budding yeast. Journal of Cell Biology, 2003, 163, 1243-1254.	2.3	78
156	Modeling Regulatory Networks at Virginia Tech. OMICS A Journal of Integrative Biology, 2003, 7, 285-299.	1.0	14
157	Hysteresis drives cell-cycle transitions in Xenopus laevis egg extracts. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 975-980.	3.3	506
158	Modelling the controls of the eukaryotic cell cycle. Biochemical Society Transactions, 2003, 31, 1526-1529.	1.6	65
159	The dynamics of cell cycle regulation. BioEssays, 2002, 24, 1095-1109.	1.2	277
160	Mathematical model of the cell division cycle of fission yeast. Chaos, 2001, 11, 277.	1.0	144
161	A stochastic, molecular model of the fission yeast cell cycle: role of the nucleocytoplasmic ratio in cycle time regulation. Biophysical Chemistry, 2001, 92, 1-15.	1.5	56
162	Regulation of the Eukaryotic Cell Cycle: Molecular Antagonism, Hysteresis, and Irreversible Transitions. Journal of Theoretical Biology, 2001, 210, 249-263.	0.8	328

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163	Network dynamics and cell physiology. Nature Reviews Molecular Cell Biology, 2001, 2, 908-916.	16.1	481
164	Molecular, metabolic, and genetic control: An introduction. Chaos, 2001, 11, 81.	1.0	12
165	Mathematical Model for Early Development of the Sea Urchin Embryo. Bulletin of Mathematical Biology, 2000, 62, 37-59.	0.9	23
166	Kinetic Analysis of a Molecular Model of the Budding Yeast Cell Cycle. Molecular Biology of the Cell, 2000, 11, 369-391.	0.9	437
167	Modeling the fission yeast cell cycle: Quantized cycle times in wee1- cdc25Delta mutant cells. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 7865-7870.	3.3	117
168	On Traveling Wave Solutions of Fisher's Equation in Two Spatial Dimensions. SIAM Journal on Applied Mathematics, 2000, 60, 371-391.	0.8	53
169	Travelling waves and static structures in a two-dimensional exactly solvable reaction-diffusion system. Journal of Physics A, 1999, 32, 8033-8044.	1.6	8
170	Velocity-curvature dependence for chemical waves in the Belousov-Zhabotinsky reaction: Theoretical explanation of experimental observations. Physical Review E, 1999, 59, 3920-3925.	0.8	10
171	Finishing the Cell Cycle. Journal of Theoretical Biology, 1999, 199, 223-233.	0.8	50
172	Models of cell cycle control in eukaryotes. Journal of Biotechnology, 1999, 71, 239-244.	1.9	28
173	A Simple Model of Circadian Rhythms Based on Dimerization and Proteolysis of PER and TIM. Biophysical Journal, 1999, 77, 2411-2417.	0.2	168
174	Bifurcation Analysis of a Model of Mitotic Control in Frog Eggs. Journal of Theoretical Biology, 1998, 195, 69-85.	0.8	122
175	Modeling M-phase control in Xenopus oocyte extracts: the surveillance mechanism for unreplicated DNA. Biophysical Chemistry, 1998, 72, 169-184.	1.5	57
176	Mathematical model of the fission yeast cell cycle with checkpoint controls at the G1/S, G2/M and metaphase/anaphase transitions. Biophysical Chemistry, 1998, 72, 185-200.	1.5	121
177	Modeling the control of DNA replication in fission yeast. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 9147-9152.	3.3	165
178	A Proposal for Temperature Compensation of the Orcadian Rhythm in Drosophila Based on Dimerization of the Per Protein. Chronobiology International, 1997, 14, 521-529.	0.9	31
179	Steady-state autowave patterns in a two-dimensional excitable medium with a band of different excitability. Physica D: Nonlinear Phenomena, 1997, 102, 300-312.	1.3	6
180	Cellular automaton model of three-dimensional excitable media. Journal of the Chemical Society, Faraday Transactions, 1996, 92, 2883.	1.7	10

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181	Chemical kinetic theory: understanding cell-cycle regulation. Trends in Biochemical Sciences, 1996, 21, 89-96.	3.7	92
182	Nonspiral excitation waves beyond the eikonal approximation. Physical Review E, 1996, 54, 4338-4346.	0.8	10
183	Propagation of waves through a line of discontinuity in two-dimensional excitable media: Refraction and reflection of autowaves. Physical Review E, 1996, 54, 1958-1968.	0.8	16
184	Quantitative analysis of a molecular model of mitotic control in fission yeast. Journal of Theoretical Biology, 1995, 173, 283-305.	0.8	93
185	Checkpoints in the cell cycle from a modeler's perspective. , 1995, 1, 1-8.		29
186	A Theory of Rotating Scroll Waves in Excitable Media. , 1995, , 93-118.		2
187	What Everyone Should Know About the Belousov-Zhabotinsky Reaction. Lecture Notes in Biomathematics, 1994, , 569-587.	0.3	35
188	Modeling the Cell Division Cycle: M-phase Trigger, Oscillations, and Size Control. Journal of Theoretical Biology, 1993, 165, 101-134.	0.8	142
189	The Dynamics of Scroll Waves in Excitable Media. SIAM Review, 1992, 34, 1-39.	4.2	147
190	Law of mass action. Nature, 1992, 357, 106-106.	13.7	3
191	Diffusion and wave propagation in cellular automaton models of excitable media. Physica D: Nonlinear Phenomena, 1992, 55, 309-327.	1.3	63
192	Third generation cellular automaton for modeling excitable media. Physica D: Nonlinear Phenomena, 1992, 55, 328-339.	1.3	31
193	A cellular automaton model of excitable media IV. Untwisted scroll rings. Physica D: Nonlinear Phenomena, 1991, 50, 189-206.	1.3	15
194	The dynamics of helical scroll waves in excitable media. Physica D: Nonlinear Phenomena, 1991, 53, 151-161.	1.3	15
195	Modeling the cell division cycle: cdc2 and cyclin interactions.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 7328-7332.	3.3	397
196	THE DIFFERENTIAL GEOMETRY OF SCROLL WAVES. International Journal of Bifurcation and Chaos in Applied Sciences and Engineering, 1991, 01, 723-744.	0.7	31
197	Experimental study of spiral waves in the cerium-catalyzed Belousov-Zhabotinskii reaction. The Journal of Physical Chemistry, 1990, 94, 8677-8682.	2.9	15
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200	A cellular automaton model of excitable media. Physica D: Nonlinear Phenomena, 1990, 46, 392-415.	1.3	118
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