Michael A Savageau

List of Publications by Year
in descending order

102 papers	7,081 citations	61984 43 h-index	60623 81 g-index
109 all docs	109 docs citations	109 times ranked	3721 citing authors

#	Article	IF	Citations
1	Phenotype-centric modeling for rational metabolic engineering. Metabolic Engineering, 2022, 72, 365-375.	7.0	0
2	Mechanistic Modeling of Biochemical Systems without A Priori Parameter Values Using the Design Space Toolbox v.3.0. IScience, 2020, 23, 101200.	4.1	8
3	TaxisPy: A Python-based software for the quantitative analysis of bacterial chemotaxis. Journal of Microbiological Methods, 2020, 175, 105918.	1.6	2
4	Molecular Mechanisms Driving Switch Behavior in Xylem Cell Differentiation. Cell Reports, 2019, 28, 342-351.e4.	6.4	61
5	Phenotype-centric modeling for elucidation of biological design principles. Journal of Theoretical Biology, 2018, 455, 281-292.	1.7	12
6	Design Space Toolbox V2: Automated Software Enabling a Novel Phenotype-Centric Modeling Strategy for Natural and Synthetic Biological Systems. Frontiers in Genetics, 2016, 7, 118.	2.3	16
7	Rapid Discrimination Among Putative Mechanistic Models of Biochemical Systems. Scientific Reports, 2016, 6, 32375.	3.3	9
8	Elucidating the genotype–phenotype map by automatic enumeration and analysis of the phenotypic repertoire. Npj Systems Biology and Applications, 2015, 1, .	3.0	17
9	Unrelated toxin–antitoxin systems cooperate to induce persistence. Journal of the Royal Society Interface, 2015, 12, 20150130.	3.4	12
10	Design principles of a conditional futile cycle exploited for regulation. Molecular BioSystems, 2015, 11, 1841-1849.	2.9	10
11	Evolution of a Genome-Encoded Bias in Amino Acid Biosynthetic Pathways Is a Potential Indicator of Amino Acid Dynamics in the Environment. Molecular Biology and Evolution, 2014, 31, 2865-2878.	8.9	1
12	Strategy Revealing Phenotypic Differences among Synthetic Oscillator Designs. ACS Synthetic Biology, 2014, 3, 686-701.	3.8	23
13	Deconstructing Complex Nonlinear Models in System Design Space. Natural Computing Series, 2014, , 475-506.	2.2	3
14	Molecular mechanisms of multiple toxin–antitoxin systems are coordinated to govern the persister phenotype. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2528-37.	7.1	101
15	Phenotypes and Design Principles in System Design Space. , 2013, , 287-310.		7
16	A bistable hysteretic switch in an activator–repressor regulated restriction–modification system. Nucleic Acids Research, 2013, 41, 6045-6057.	14.5	19
17	Phenotypic deconstruction of gene circuitry. Chaos, 2013, 23, 025108.	2.5	13
18	Relative Amino Acid Composition Signatures of Organisms and Environments. PLoS ONE, 2013, 8, e77319.	2.5	82

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19	Regulatory Design Governing Progression of Population Growth Phases in Bacteria. PLoS ONE, 2012, 7, e30654.	2.5	16
20	Design of the lac gene circuit revisited. Mathematical Biosciences, 2011, 231, 19-38.	1.9	24
21	Phenotypic repertoire of the FNR regulatory network in *Escherichia coli*. Molecular Microbiology, 2011, 79, 149-165.	2.5	24
22	Biomedical Engineering Strategies in System Design Space. Annals of Biomedical Engineering, 2011, 39, 1278-1295.	2.5	10
23	Automated construction and analysis of the design space for biochemical systems. Bioinformatics, 2010, 26, 2601-2609.	4.1	26
24	Regulation of Aerobic-to-Anaerobic Transitions by the FNR Cycle in Escherichia coli. Journal of Molecular Biology, 2010, 397, 893-905.	4.2	36
25	Relating Mutant Genotype to Phenotype via Quantitative Behavior of the NADPH Redox Cycle in Human Erythrocytes. PLoS ONE, 2010, 5, e13031.	2.5	21
26	Phenotypes and tolerances in the design space of biochemical systems. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6435-6440.	7.1	77
27	Quantifying Global Tolerance of Biochemical Systems: Design Implications for Moiety-Transfer Cycles. PLoS Computational Biology, 2009, 5, e1000319.	3.2	31
28	Qualitatively distinct phenotypes in the design space of biochemical systems. FEBS Letters, 2009, 583, 3914-3922.	2.8	28
29	Hysteretic and graded responses in bacterial two-component signal transduction. Molecular Microbiology, 2008, 68, 1196-1215.	2.5	60
30	Stabilizing and Destabilizing Effects of Embedding 3-Node Subgraphs on the State Space of Boolean Networks. Lecture Notes in Computer Science, 2008, , 100-107.	1.3	1
31	Distinctive Topologies of Partner-switching Signaling Networks Correlate with their Physiological Roles. Journal of Molecular Biology, 2007, 369, 1333-1352.	4.2	44
32	Signalling network with a bistable hysteretic switch controls developmental activation of the σF transcription factor inBacillus subtilis. Molecular Microbiology, 2006, 61, 165-184.	2.5	42
33	Evolution of enzymes in a series is driven by dissimilar functional demands. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 2226-2231.	7.1	22
34	Evidence of selection for low cognate amino acid bias in amino acid biosynthetic enzymes. Molecular Microbiology, 2005, 56, 1017-1034.	2.5	34
35	Design of gene circuits: lessons from bacteria. Nature Reviews Genetics, 2004, 5, 34-42.	16.3	206
36	Comparative analysis of prototype two-component systems with either bifunctional or monofunctional sensors: differences in molecular structure and physiological function. Molecular Microbiology, 2003, 48, 25-51.	2.5	85

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37	Design Principles for Regulator Gene Expression in a Repressible Gene Circuit. Journal of Molecular Biology, 2003, 332, 861-876.	4.2	50
38	Development of Genetic Circuitry Exhibiting Toggle Switch or Oscillatory Behavior in Escherichia coli. Cell, 2003, 113, 597-607.	28.9	643
39	Quantitative evolutionary design of glucose 6-phosphate dehydrogenase expression in human erythrocytes. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 14463-14468.	7.1	42
40	Alternative designs for a genetic switch: Analysis of switching times using the piecewise power-law representation. Mathematical Biosciences, 2002, 180, 237-253.	1.9	39
41	Effects of alternative connectivity on behavior of randomly constructed Boolean networks. Physica D: Nonlinear Phenomena, 2002, 170, 143-161.	2.8	55
42	Irreversibility in Unbranched Pathways: Preferred Positions Based on Regulatory Considerations. Biophysical Journal, 2001, 80, 1174-1185.	0.5	17
43	Design principles for elementary gene circuits: Elements, methods, and examples. Chaos, 2001, 11, 142.	2.5	166
44	Comparing systemic properties of ensembles of biological networks by graphical and statistical methods. Bioinformatics, 2000, 16, 527-533.	4.1	50
45	Extending the method of mathematically controlled comparison to include numerical comparisons. Bioinformatics, 2000, 16, 786-798.	4.1	78
46	Effect of Overall Feedback Inhibition in Unbranched Biosynthetic Pathways. Biophysical Journal, 2000, 79, 2290-2304.	0.5	49
47	Development of fractal kinetic theory for enzyme-catalysed reactions and implications for the design of biochemical pathways. BioSystems, 1998, 47, 9-36.	2.0	90
48	Demand Theory of Gene Regulation. I. Quantitative Development of the Theory. Genetics, 1998, 149, 1665-1676.	2.9	71
49	Demand Theory of Gene Regulation. II. Quantitative Application to the Lactose and Maltose Operons of Escherichia coli. Genetics, 1998, 149, 1677-1691.	2.9	50
50	Completely uncoupled and perfectly coupled gene expression in repressible systems 1 1Edited by K. Yamamoto. Journal of Molecular Biology, 1997, 266, 538-558.	4.2	31
51	Rules for Coupled Expression of Regulator and Effector Genes in Inducible Circuits. Journal of Molecular Biology, 1996, 255, 121-139.	4.2	101
52	Power-law formalism: A canonical nonlinear approach to modeling and analysis. , 1996, , 3323-3334.		20
53	Model Assessment and Refinement Using Strategies from Biochemical Systems Theory: Application to Metabolism in Human Red Blood Cells. Journal of Theoretical Biology, 1996, 179, 329-368.	1.7	63
54	Application of Biochemical Systems Theory to Metabolism in Human Red Blood Cells. Journal of Biological Chemistry, 1996, 271, 7927-7941.	3.4	65

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55	Michaelis-Menten mechanism reconsidered: implications of fractal kinetics. Journal of Theoretical Biology, 1995, 176, 115-124.	1.7	157
56	Chapter 5 Enzyme kinetics in vitro and in vivo: Michaelis-Menten revisited. Principles of Medical Biology, 1995, , 93-146.	0.1	18
57	Subunit Structure of Regulator Proteins Influences the Design of Gene Circuitry: Analysis of Perfectly Coupled and Completely Uncoupled Circuits. Journal of Molecular Biology, 1995, 248, 739-755.	4.2	36
58	Analysis of systems influencing renal hemodynamics and sodium excretion. I. Biochemical systems theory. Integrative Psychological and Behavioral Science, 1994, 29, 55-73.	0.3	1
59	Influence of fractal kinetics on molecular recognition. Journal of Molecular Recognition, 1993, 6, 149-157.	2.1	20
60	Finding multiple roots of nonlinear algebraic equations using s-system methodology. Applied Mathematics and Computation, 1993, 55, 187-199.	2.2	20
61	Dominance according to metabolic control analysis: Major achievement or house of cards?. Journal of Theoretical Biology, 1992, 154, 131-136.	1.7	41
62	Biochemical systems theory: Operational differences among variant representations and their significance. Journal of Theoretical Biology, 1991, 151, 509-530.	1.7	55
63	Metabolite channeling: Implications for regulation of metabolism and for quantitative description of reactions in vivo. Journal of Theoretical Biology, 1991, 152, 85-92.	1.7	13
64	Efficient Solution of Nonlinear Ordinary Differential Equations Expressed in S-system Canonical Form. SIAM Journal on Numerical Analysis, 1990, 27, 704-735.	2.3	84
65	Biochemical Systems Theory: Alternative Views of Metabolic Control. , 1990, , 69-87.		8
66	Constraints among molecular and systemic properties: Implications for physiological genetics. Journal of Theoretical Biology, 1989, 141, 93-115.	1.7	65
67	A comparison of variant theories of intact biochemical systems. I. enzyme-enzyme interactions and biochemical systems theory. Mathematical Biosciences, 1989, 94, 161-193.	1.9	82
68	A comparison of variant theories of intact biochemical systems. II. flux-oriented and metabolic control theories. Mathematical Biosciences, 1989, 94, 195-238.	1.9	70
69	Strategies for representing metabolic pathways within biochemical systems theory: Reversible pathways. Mathematical Biosciences, 1989, 94, 239-269.	1.9	77
70	Introduction to S-systems and the underlying power-law formalism. Mathematical and Computer Modelling, 1988, 11, 546-551.	2.0	59
71	Biochemical systems theory and metabolic control theory: 1. fundamental similarities and differences. Mathematical Biosciences, 1987, 86, 127-145.	1.9	118
72	Biochemical systems theory and metabolic control theory: 2. the role of summation and connectivity relationships. Mathematical Biosciences, 1987, 86, 147-169.	1.9	94

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73	Recasting nonlinear differential equations as S-systems: a canonical nonlinear form. Mathematical Biosciences, 1987, 87, 83-115.	1.9	248
74	Accuracy of alternative representations for integrated biochemical systems. Biochemistry, 1987, 26, 6869-6880.	2.5	119
75	Equivalence between S-systems and Volterra systems. Mathematical Biosciences, 1986, 78, 47-55.	1.9	47
76	Analytical solutions to a generalized growth equation. Journal of Mathematical Analysis and Applications, 1984, 103, 380-386.	1.0	32
77	Integrated function of a kinetic proofreading mechanism: steady-state analysis testing internal consistency of data obtained in vivo and in vitro and predicting parameter values. Biochemistry, 1984, 23, 1701-1709.	2.5	25
78	Models of Gene Function. ACS Symposium Series, 1983, , 3-25.	0.5	7
79	Escherichia coli Habitats, Cell Types, and Molecular Mechanisms of Gene Control. American Naturalist, 1983, 122, 732-744.	2.1	271
80	Optimization of kinetic proofreading: A general method for derivation of the constraint relations and an exploration of a specific case. Journal of Theoretical Biology, 1981, 93, 157-177.	1.7	20
81	Accuracy of proofreading with zero energy cost. Journal of Theoretical Biology, 1981, 93, 179-195.	1.7	11
82	Proofreading systems of multiple stages for improved accuracy of biological discrimination. Journal of Theoretical Biology, 1980, 85, 99-123.	1.7	44
83	Growth equations: A general equation and a survey of special cases. Mathematical Biosciences, 1980, 48, 267-278.	1.9	80
84	Feedforward inhibition in biosynthetic pathways: inhibition of the aminoacyl-tRNA synthetase by the penultimate product. Journal of Theoretical Biology, 1979, 77, 385-404.	1.7	7
85	Feedforward inhibition in biosynthetic pathways: inhibition of the aminoacyl-tRNA synthetase by intermediates of the pathway. Journal of Theoretical Biology, 1979, 77, 405-425.	1.7	26
86	Energy cost of proofreading to increase fidelity of transfer ribonucleic acid aminoacylation. Biochemistry, 1979, 18, 3486-3493.	2.5	43
87	Autogenous and Classical Regulation of Gene Expression: A General Theory and Experimental Evidence. , 1979, , 57-108.		11
88	Optimal design of feedback control by inhibition. Journal of Molecular Evolution, 1975, 5, 199-222.	1.8	83
89	Significance of autogenously regulated and constitutive synthesis of regulatory proteins in repressible biosynthetic systems. Nature, 1975, 258, 208-214.	27.8	34
90	Optimal design of feedback control by inhibition. Journal of Molecular Evolution, 1974, 4, 139-156.	1.8	68

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91	Comparison of classical and autogenous systems of regulation in inducible operons. Nature, 1974, 252, 546-549.	27.8	203
92	Transport of Biosynthetic Intermediates: Homoserine and Threonine Uptake in *Escherichia coli*. Journal of Bacteriology, 1974, 117, 1002-1009.	2.2	32
93	Transport of Biosynthetic Intermediates: Regulation of Homoserine and Threonine Uptake in *Escherichia coli*. Journal of Bacteriology, 1974, 120, 114-120.	2.2	35
94	Metabolic Regulation by Homoserine in *Escherichia coli* B/r. Journal of Bacteriology, 1973, 116, 663-672.	2.2	29
95	A possible role in the regulation of primary amination for a complex of glutamine: Î±-Ketoglutarate amidotransferase and glutamate dehydrogenase in Escherichia coli. Biochemical and Biophysical Research Communications, 1972, 48, 41-47.	2.1	19
96	The Behavior of Intact Biochemical Control Systems* *This will not be an exhaustive review of the different methods for analyzing biochemical systems, but rather a selective treatment of one particular approach. Reviews covering alternative approaches to these problems have recently been presented (28, 33).. Current Topics in Cellular Regulation, 1972, 6, 63-130.	9.6	142
97	Concepts relating the behavior of biochemical systems to their underlying molecular properties. Archives of Biochemistry and Biophysics, 1971, 145, 612-621.	3.0	133
98	Parameter Sensitivity as a Criterion for Evaluating and Comparing the Performance of Biochemical Systems. Nature, 1971, 229, 542-544.	27.8	217
99	Biochemical systems analysis. Journal of Theoretical Biology, 1970, 26, 215-226.	1.7	219
100	Repression of the threonine synthetase system in Escherichia coli. Archives of Biochemistry and Biophysics, 1970, 137, 181-184.	3.0	5
101	Biochemical systems analysis. Journal of Theoretical Biology, 1969, 25, 365-369.	1.7	556
102	Biochemical systems analysis. Journal of Theoretical Biology, 1969, 25, 370-379.	1.7	423