

# Michael A Savageau

## List of Publications by Year in descending order

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102  
papers

7,081  
citations

61984

43  
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60623

81  
g-index

109  
all docs

109  
docs citations

109  
times ranked

3721  
citing authors

#	ARTICLE	IF	CITATIONS
1	Development of Genetic Circuitry Exhibiting Toggle Switch or Oscillatory Behavior in Escherichia coli. Cell, 2003, 113, 597-607.	28.9	643
2	Biochemical systems analysis. Journal of Theoretical Biology, 1969, 25, 365-369.	1.7	556
3	Biochemical systems analysis. Journal of Theoretical Biology, 1969, 25, 370-379.	1.7	423
4	Escherichia coli Habitats, Cell Types, and Molecular Mechanisms of Gene Control. American Naturalist, 1983, 122, 732-744.	2.1	271
5	Recasting nonlinear differential equations as S-systems: a canonical nonlinear form. Mathematical Biosciences, 1987, 87, 83-115.	1.9	248
6	Biochemical systems analysis. Journal of Theoretical Biology, 1970, 26, 215-226.	1.7	219
7	Parameter Sensitivity as a Criterion for Evaluating and Comparing the Performance of Biochemical Systems. Nature, 1971, 229, 542-544.	27.8	217
8	Design of gene circuits: lessons from bacteria. Nature Reviews Genetics, 2004, 5, 34-42.	16.3	206
9	Comparison of classical and autogenous systems of regulation in inducible operons. Nature, 1974, 252, 546-549.	27.8	203
10	Design principles for elementary gene circuits: Elements, methods, and examples. Chaos, 2001, 11, 142.	2.5	166
11	Michaelis-Menten mechanism reconsidered: implications of fractal kinetics. Journal of Theoretical Biology, 1995, 176, 115-124.	1.7	157
12	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
13	Concepts relating the behavior of biochemical systems to their underlying molecular properties. Archives of Biochemistry and Biophysics, 1971, 145, 612-621.	3.0	133
14	Accuracy of alternative representations for integrated biochemical systems. Biochemistry, 1987, 26, 6869-6880.	2.5	119
15	Biochemical systems theory and metabolic control theory: 1. fundamental similarities and differences. Mathematical Biosciences, 1987, 86, 127-145.	1.9	118
16	Rules for Coupled Expression of Regulator and Effector Genes in Inducible Circuits. Journal of Molecular Biology, 1996, 255, 121-139.	4.2	101
17	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
18	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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19	Development of fractal kinetic theory for enzyme-catalysed reactions and implications for the design of biochemical pathways. <i>BioSystems</i> , 1998, 47, 9-36.	2.0	90
20	Comparative analysis of prototype two-component systems with either bifunctional or monofunctional sensors: differences in molecular structure and physiological function. <i>Molecular Microbiology</i> , 2003, 48, 25-51.	2.5	85
21	Efficient Solution of Nonlinear Ordinary Differential Equations Expressed in S-system Canonical Form. <i>SIAM Journal on Numerical Analysis</i> , 1990, 27, 704-735.	2.3	84
22	Optimal design of feedback control by inhibition. <i>Journal of Molecular Evolution</i> , 1975, 5, 199-222.	1.8	83
23	A comparison of variant theories of intact biochemical systems. I. enzyme-enzyme interactions and biochemical systems theory. <i>Mathematical Biosciences</i> , 1989, 94, 161-193.	1.9	82
24	Relative Amino Acid Composition Signatures of Organisms and Environments. <i>PLoS ONE</i> , 2013, 8, e77319.	2.5	82
25	Growth equations: A general equation and a survey of special cases. <i>Mathematical Biosciences</i> , 1980, 48, 267-278.	1.9	80
26	Extending the method of mathematically controlled comparison to include numerical comparisons. <i>Bioinformatics</i> , 2000, 16, 786-798.	4.1	78
27	Strategies for representing metabolic pathways within biochemical systems theory: Reversible pathways. <i>Mathematical Biosciences</i> , 1989, 94, 239-269.	1.9	77
28	Phenotypes and tolerances in the design space of biochemical systems. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6435-6440.	7.1	77
29	Demand Theory of Gene Regulation. I. Quantitative Development of the Theory. <i>Genetics</i> , 1998, 149, 1665-1676.	2.9	71
30	A comparison of variant theories of intact biochemical systems. II. flux-oriented and metabolic control theories. <i>Mathematical Biosciences</i> , 1989, 94, 195-238.	1.9	70
31	Optimal design of feedback control by inhibition. <i>Journal of Molecular Evolution</i> , 1974, 4, 139-156.	1.8	68
32	Constraints among molecular and systemic properties: Implications for physiological genetics. <i>Journal of Theoretical Biology</i> , 1989, 141, 93-115.	1.7	65
33	Application of Biochemical Systems Theory to Metabolism in Human Red Blood Cells. <i>Journal of Biological Chemistry</i> , 1996, 271, 7927-7941.	3.4	65
34	Model Assessment and Refinement Using Strategies from Biochemical Systems Theory: Application to Metabolism in Human Red Blood Cells. <i>Journal of Theoretical Biology</i> , 1996, 179, 329-368.	1.7	63
35	Molecular Mechanisms Driving Switch Behavior in Xylem Cell Differentiation. <i>Cell Reports</i> , 2019, 28, 342-351.e4.	6.4	61
36	Hysteretic and graded responses in bacterial two-component signal transduction. <i>Molecular Microbiology</i> , 2008, 68, 1196-1215.	2.5	60

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37	Introduction to S-systems and the underlying power-law formalism. <i>Mathematical and Computer Modelling</i> , 1988, 11, 546-551.	2.0	59
38	Biochemical systems theory: Operational differences among variant representations and their significance. <i>Journal of Theoretical Biology</i> , 1991, 151, 509-530.	1.7	55
39	Effects of alternative connectivity on behavior of randomly constructed Boolean networks. <i>Physica D: Nonlinear Phenomena</i> , 2002, 170, 143-161.	2.8	55
40	Comparing systemic properties of ensembles of biological networks by graphical and statistical methods. <i>Bioinformatics</i> , 2000, 16, 527-533.	4.1	50
41	Design Principles for Regulator Gene Expression in a Repressible Gene Circuit. <i>Journal of Molecular Biology</i> , 2003, 332, 861-876.	4.2	50
42	Demand Theory of Gene Regulation. II. Quantitative Application to the Lactose and Maltose Operons of <i>Escherichia coli</i> . <i>Genetics</i> , 1998, 149, 1677-1691.	2.9	50
43	Effect of Overall Feedback Inhibition in Unbranched Biosynthetic Pathways. <i>Biophysical Journal</i> , 2000, 79, 2290-2304.	0.5	49
44	Equivalence between S-systems and Volterra systems. <i>Mathematical Biosciences</i> , 1986, 78, 47-55.	1.9	47
45	Proofreading systems of multiple stages for improved accuracy of biological discrimination. <i>Journal of Theoretical Biology</i> , 1980, 85, 99-123.	1.7	44
46	Distinctive Topologies of Partner-switching Signaling Networks Correlate with their Physiological Roles. <i>Journal of Molecular Biology</i> , 2007, 369, 1333-1352.	4.2	44
47	Energy cost of proofreading to increase fidelity of transfer ribonucleic acid aminoacylation. <i>Biochemistry</i> , 1979, 18, 3486-3493.	2.5	43
48	Quantitative evolutionary design of glucose 6-phosphate dehydrogenase expression in human erythrocytes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 14463-14468.	7.1	42
49	Signalling network with a bistable hysteretic switch controls developmental activation of the $\lambda$ transcription factor in <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2006, 61, 165-184.	2.5	42
50	Dominance according to metabolic control analysis: Major achievement or house of cards?. <i>Journal of Theoretical Biology</i> , 1992, 154, 131-136.	1.7	41
51	Alternative designs for a genetic switch: Analysis of switching times using the piecewise power-law representation. <i>Mathematical Biosciences</i> , 2002, 180, 237-253.	1.9	39
52	Subunit Structure of Regulator Proteins Influences the Design of Gene Circuitry: Analysis of Perfectly Coupled and Completely Uncoupled Circuits. <i>Journal of Molecular Biology</i> , 1995, 248, 739-755.	4.2	36
53	Regulation of Aerobic-to-Anaerobic Transitions by the FNR Cycle in <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2010, 397, 893-905.	4.2	36
54	Transport of Biosynthetic Intermediates: Regulation of Homoserine and Threonine Uptake in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 1974, 120, 114-120.	2.2	35

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55	Significance of autogenously regulated and constitutive synthesis of regulatory proteins in repressible biosynthetic systems. <i>Nature</i> , 1975, 258, 208-214.	27.8	34
56	Evidence of selection for low cognate amino acid bias in amino acid biosynthetic enzymes. <i>Molecular Microbiology</i> , 2005, 56, 1017-1034.	2.5	34
57	Analytical solutions to a generalized growth equation. <i>Journal of Mathematical Analysis and Applications</i> , 1984, 103, 380-386.	1.0	32
58	Transport of Biosynthetic Intermediates: Homoserine and Threonine Uptake in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 1974, 117, 1002-1009.	2.2	32
59	Completely uncoupled and perfectly coupled gene expression in repressible systems 1 Edited by K. Yamamoto. <i>Journal of Molecular Biology</i> , 1997, 266, 538-558.	4.2	31
60	Quantifying Global Tolerance of Biochemical Systems: Design Implications for Moiety-Transfer Cycles. <i>PLoS Computational Biology</i> , 2009, 5, e1000319.	3.2	31
61	Metabolic Regulation by Homoserine in <i>Escherichia coli</i> B/r. <i>Journal of Bacteriology</i> , 1973, 116, 663-672.	2.2	29
62	Qualitatively distinct phenotypes in the design space of biochemical systems. <i>FEBS Letters</i> , 2009, 583, 3914-3922.	2.8	28
63	Feedforward inhibition in biosynthetic pathways: inhibition of the aminoacyl-tRNA synthetase by intermediates of the pathway. <i>Journal of Theoretical Biology</i> , 1979, 77, 405-425.	1.7	26
64	Automated construction and analysis of the design space for biochemical systems. <i>Bioinformatics</i> , 2010, 26, 2601-2609.	4.1	26
65	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. <i>Biochemistry</i> , 1984, 23, 1701-1709.	2.5	25
66	Design of the lac gene circuit revisited. <i>Mathematical Biosciences</i> , 2011, 231, 19-38.	1.9	24
67	Phenotypic repertoire of the FNR regulatory network in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2011, 79, 149-165.	2.5	24
68	Strategy Revealing Phenotypic Differences among Synthetic Oscillator Designs. <i>ACS Synthetic Biology</i> , 2014, 3, 686-701.	3.8	23
69	Evolution of enzymes in a series is driven by dissimilar functional demands. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2226-2231.	7.1	22
70	Relating Mutant Genotype to Phenotype via Quantitative Behavior of the NADPH Redox Cycle in Human Erythrocytes. <i>PLoS ONE</i> , 2010, 5, e13031.	2.5	21
71	Optimization of kinetic proofreading: A general method for derivation of the constraint relations and an exploration of a specific case. <i>Journal of Theoretical Biology</i> , 1981, 93, 157-177.	1.7	20
72	Influence of fractal kinetics on molecular recognition. <i>Journal of Molecular Recognition</i> , 1993, 6, 149-157.	2.1	20

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73	Finding multiple roots of nonlinear algebraic equations using s-system methodology. Applied Mathematics and Computation, 1993, 55, 187-199.	2.2	20
74	Power-law formalism: A canonical nonlinear approach to modeling and analysis. , 1996, , 3323-3334.		20
75	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
76	A bistable hysteretic switch in an activatorâ€“repressor regulated restrictionâ€“modification system. Nucleic Acids Research, 2013, 41, 6045-6057.	14.5	19
77	Chapter 5 Enzyme kinetics in vitro and in vivo: Michaelis-Menten revisited. Principles of Medical Biology, 1995, , 93-146.	0.1	18
78	Irreversibility in Unbranched Pathways: Preferred Positions Based on Regulatory Considerations. Biophysical Journal, 2001, 80, 1174-1185.	0.5	17
79	Elucidating the genotypeâ€“phenotype map by automatic enumeration and analysis of the phenotypic repertoire. Npj Systems Biology and Applications, 2015, 1, .	3.0	17
80	Regulatory Design Governing Progression of Population Growth Phases in Bacteria. PLoS ONE, 2012, 7, e30654.	2.5	16
81	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
82	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
83	Phenotypic deconstruction of gene circuitry. Chaos, 2013, 23, 025108.	2.5	13
84	Unrelated toxinâ€“antitoxin systems cooperate to induce persistence. Journal of the Royal Society Interface, 2015, 12, 20150130.	3.4	12
85	Phenotype-centric modeling for elucidation of biological design principles. Journal of Theoretical Biology, 2018, 455, 281-292.	1.7	12
86	Accuracy of proofreading with zero energy cost. Journal of Theoretical Biology, 1981, 93, 179-195.	1.7	11
87	Autogenous and Classical Regulation of Gene Expression: A General Theory and Experimental Evidence. , 1979, , 57-108.		11
88	Biomedical Engineering Strategies in System Design Space. Annals of Biomedical Engineering, 2011, 39, 1278-1295.	2.5	10
89	Design principles of a conditional futile cycle exploited for regulation. Molecular BioSystems, 2015, 11, 1841-1849.	2.9	10
90	Rapid Discrimination Among Putative Mechanistic Models of Biochemical Systems. Scientific Reports, 2016, 6, 32375.	3.3	9

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91	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
92	Biochemical Systems Theory: Alternative Views of Metabolic Control. , 1990, , 69-87.		8
93	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
94	Models of Gene Function. ACS Symposium Series, 1983, , 3-25.	0.5	7
95	Phenotypes and Design Principles in System Design Space. , 2013, , 287-310.		7
96	Repression of the threonine synthetase system in Escherichia coli. Archives of Biochemistry and Biophysics, 1970, 137, 181-184.	3.0	5
97	Deconstructing Complex Nonlinear Models in System Design Space. Natural Computing Series, 2014, , 475-506.	2.2	3
98	TaxisPy: A Python-based software for the quantitative analysis of bacterial chemotaxis. Journal of Microbiological Methods, 2020, 175, 105918.	1.6	2
99	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
100	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
101	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
102	Phenotype-centric modeling for rational metabolic engineering. Metabolic Engineering, 2022, 72, 365-375.	7.0	0