

# Herbert M. Sauro

## List of Publications by Year in descending order

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118  
papers

7,412  
citations

81839

39  
h-index

60583

81  
g-index

153  
all docs

153  
docs citations

153  
times ranked

6547  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Systems Biology Graphical Notation. <i>Nature Biotechnology</i> , 2009, 27, 735-741.	9.4	828
2	BioModels Database: a free, centralized database of curated, published, quantitative kinetic models of biochemical and cellular systems. <i>Nucleic Acids Research</i> , 2006, 34, D689-D691.	6.5	661
3	Minimum information requested in the annotation of biochemical models (MIRIAM). <i>Nature Biotechnology</i> , 2005, 23, 1509-1515.	9.4	553
4	Metabolic control and its analysis. Additional relationships between elasticities and control coefficients. <i>FEBS Journal</i> , 1985, 148, 555-561.	0.2	273
5	Next Generation Simulation Tools: The Systems Biology Workbench and BioSPICE Integration. <i>OMICS A Journal of Integrative Biology</i> , 2003, 7, 355-372.	1.0	254
6	The Synthetic Biology Open Language (SBOL) provides a community standard for communicating designs in synthetic biology. <i>Nature Biotechnology</i> , 2014, 32, 545-550.	9.4	247
7	Transcriptional Dynamics of the Embryonic Stem Cell Switch. <i>PLoS Computational Biology</i> , 2006, 2, e123.	1.5	228
8	Quantitative analysis of signaling networks. <i>Progress in Biophysics and Molecular Biology</i> , 2004, 86, 5-43.	1.4	188
9	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	3.2	178
10	Designing and engineering evolutionary robust genetic circuits. <i>Journal of Biological Engineering</i> , 2010, 4, 12.	2.0	162
11	TinkerCell: modular CAD tool for synthetic biology. <i>Journal of Biological Engineering</i> , 2009, 3, 19.	2.0	161
12	Sensitivity analysis of stoichiometric networks: an extension of metabolic control analysis to non-steady state trajectories. <i>Journal of Theoretical Biology</i> , 2003, 222, 23-36.	0.8	135
13	Minimum Information About a Simulation Experiment (MIASE). <i>PLoS Computational Biology</i> , 2011, 7, e1001122.	1.5	133
14	In-Fusion BioBrick assembly and re-engineering. <i>Nucleic Acids Research</i> , 2010, 38, 2624-2636.	6.5	132
15	libRoadRunner: a high performance SBML simulation and analysis library. <i>Bioinformatics</i> , 2015, 31, 3315-3321.	1.8	130
16	It's an analog world. <i>Nature</i> , 2013, 497, 572-573.	13.7	124
17	COMBINE archive and OMEX format: one file to share all information to reproduce a modeling project. <i>BMC Bioinformatics</i> , 2014, 15, 369.	1.2	114
18	Antimony: a modular model definition language. <i>Bioinformatics</i> , 2009, 25, 2452-2454.	1.8	112

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19	Metabolic control and its analysis. Extensions to the theory and matrix method. FEBS Journal, 1987, 165, 215-221.	0.2	108
20	Tellurium: An extensible python-based modeling environment for systems and synthetic biology. BioSystems, 2018, 171, 74-79.	0.9	103
21	Computational tools for metabolic engineering. Metabolic Engineering, 2012, 14, 270-280.	3.6	93
22	Control analysis of time-dependent metabolic systems. Journal of Theoretical Biology, 1989, 137, 423-444.	0.8	89
23	Sharing Structure and Function in Biological Design with SBOL 2.0. ACS Synthetic Biology, 2016, 5, 498-506.	1.9	88
24	Visualization of Evolutionary Stability Dynamics and Competitive Fitness of Escherichia coli Engineered with Randomized Multigene Circuits. ACS Synthetic Biology, 2013, 2, 519-528.	1.9	85
25	Standard Biological Parts Knowledgebase. PLoS ONE, 2011, 6, e17005.	1.1	80
26	Enzyme-enzyme interactions and control analysis. 1. The case of non-additivity: monomer-oligomer associations. FEBS Journal, 1990, 187, 481-491.	0.2	77
27	Enzyme-enzyme interactions and control analysis. 2. The case of non-independence: heterologous associations. FEBS Journal, 1990, 187, 493-500.	0.2	74
28	Design and implementation of three incoherent feed-forward motif based biological concentration sensors. Systems and Synthetic Biology, 2007, 1, 119-128.	1.0	73
29	SBOL Visual: A Graphical Language for Genetic Designs. PLoS Biology, 2015, 13, e1002310.	2.6	73
30	Conservation analysis in biochemical networks: computational issues for software writers. Biophysical Chemistry, 2004, 109, 1-15.	1.5	72
31	Oscillatory dynamics arising from competitive inhibition and multisite phosphorylation. Journal of Theoretical Biology, 2007, 244, 68-76.	0.8	68
32	Conservation analysis of large biochemical networks. Bioinformatics, 2006, 22, 346-353.	1.8	65
33	Rationally designed bidirectional promoter improves the evolutionary stability of synthetic genetic circuits. Nucleic Acids Research, 2013, 41, e33-e33.	6.5	61
34	Reply to Intellectual property issues and synthetic biology standards. Nature Biotechnology, 2015, 33, 25-25.	9.4	54
35	Bifurcation discovery tool. Bioinformatics, 2005, 21, 3688-3690.	1.8	53
36	Preliminary Studies on the In Silico Evolution of Biochemical Networks. ChemBioChem, 2004, 5, 1423-1431.	1.3	52

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37	Harmonizing semantic annotations for computational models in biology. <i>Briefings in Bioinformatics</i> , 2019, 20, 540-550.	3.2	52
38	Mathematical modeling and synthetic biology. <i>Drug Discovery Today: Disease Models</i> , 2008, 5, 299-309.	1.2	48
39	Modularity defined. <i>Molecular Systems Biology</i> , 2008, 4, 166.	3.2	48
40	A Reappraisal of How to Build Modular, Reusable Models of Biological Systems. <i>PLoS Computational Biology</i> , 2014, 10, e1003849.	1.5	47
41	PyBioNetFit and the Biological Property Specification Language. <i>IScience</i> , 2019, 19, 1012-1036.	1.9	47
42	SCAMP: A metabolic simulator and control analysis program. <i>Mathematical and Computer Modelling</i> , 1991, 15, 15-28.	2.0	43
43	Metabolic control analysis. The effects of high enzyme concentrations. <i>FEBS Journal</i> , 1990, 192, 183-187.	0.2	41
44	Tellurium notebooks—An environment for reproducible dynamical modeling in systems biology. <i>PLoS Computational Biology</i> , 2018, 14, e1006220.	1.5	41
45	Essential information for synthetic DNA sequences. <i>Nature Biotechnology</i> , 2011, 29, 22-22.	9.4	40
46	Measuring Retroactivity from Noise in Gene Regulatory Networks. <i>Biophysical Journal</i> , 2011, 100, 1167-1177.	0.2	35
47	Control and regulation of pathways via negative feedback. <i>Journal of the Royal Society Interface</i> , 2017, 14, 20160848.	1.5	35
48	A Model for p53 Dynamics Triggered by DNA Damage. <i>SIAM Journal on Applied Dynamical Systems</i> , 2007, 6, 61-78.	0.7	31
49	Fan-out in gene regulatory networks. <i>Journal of Biological Engineering</i> , 2010, 4, 16.	2.0	31
50	Comparing simulation results of SBML capable simulators. <i>Bioinformatics</i> , 2008, 24, 1963-1965.	1.8	30
51	Computer-aided design of biological circuits using tinkercell. <i>Bioengineered Bugs</i> , 2010, 1, 276-283.	2.0	30
52	Communicating Structure and Function in Synthetic Biology Diagrams. <i>ACS Synthetic Biology</i> , 2019, 8, 1818-1825.	1.9	30
53	Synthetic biology: How best to build a cell. <i>Nature</i> , 2014, 509, 155-157.	13.7	30
54	Control by Enzymes, Coenzymes and Conserved Moieties. A Generalisation of the Connectivity Theorem of Metabolic Control Analysis. <i>FEBS Journal</i> , 1994, 225, 179-186.	0.2	29

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55	Synthetic Biology: Engineering Living Systems from Biophysical Principles. <i>Biophysical Journal</i> , 2017, 112, 1050-1058.	0.2	29
56	SBW - A Modular Framework for Systems Biology. , 2006, , .		25
57	Supporting the SBML layout extension. <i>Bioinformatics</i> , 2006, 22, 2966-2967.	1.8	25
58	Best Practices for Making Reproducible Biochemical Models. <i>Cell Systems</i> , 2020, 11, 109-120.	2.9	25
59	Standards and ontologies in computational systems biology. <i>Essays in Biochemistry</i> , 2008, 45, 211-222.	2.1	25
60	Randomized BioBrick Assembly: A Novel DNA Assembly Method for Randomizing and Optimizing Genetic Circuits and Metabolic Pathways. <i>ACS Synthetic Biology</i> , 2013, 2, 506-518.	1.9	24
61	Data Integration and Mining for Synthetic Biology Design. <i>ACS Synthetic Biology</i> , 2016, 5, 1086-1097.	1.9	23
62	Adjusting Phenotypes by Noise Control. <i>PLoS Computational Biology</i> , 2012, 8, e1002344.	1.5	23
63	Synthetic Biology Open Language (SBOL) Version 2.0.0. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 902-991.	1.0	22
64	Improving reproducibility in computational biology research. <i>PLoS Computational Biology</i> , 2020, 16, e1007881.	1.5	22
65	Moiety-conserved cycles and metabolic control analysis: problems in sequestration and metabolic channelling. <i>BioSystems</i> , 1994, 33, 55-67.	0.9	21
66	Synthetic Biology Open Language Visual (SBOL Visual) Version 2.0. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.0	21
67	Recent advances in biomedical simulations: a manifesto for model engineering. <i>F1000Research</i> , 2019, 8, 261.	0.8	21
68	Synthetic Biology Open Language (SBOL) Version 2.2.0. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.0	20
69	Proposed Data Model for the Next Version of the Synthetic Biology Open Language. <i>ACS Synthetic Biology</i> , 2015, 4, 57-71.	1.9	19
70	The Computational Versatility of Proteomic Signaling Networks. <i>Current Proteomics</i> , 2004, 1, 67-81.	0.1	18
71	Computational Tools for Modeling Protein Networks. <i>Current Proteomics</i> , 2006, 3, 181-197.	0.1	18
72	The first 10 years of the international coordination network for standards in systems and synthetic biology (COMBINE). <i>Journal of Integrative Bioinformatics</i> , 2020, 17, .	1.0	18

#	ARTICLE	IF	CITATIONS
73	Hierarchical Modeling for Synthetic Biology. ACS Synthetic Biology, 2012, 1, 353-364.	1.9	16
74	Synthetic Biology Open Language (SBOL) Version 2.3. Journal of Integrative Bioinformatics, 2019, 16, .	1.0	16
75	BioBrickâ„¢ Assembly Using the In-Fusion PCR Cloning Kit. Methods in Molecular Biology, 2013, 1073, 19-30.	0.4	15
76	Nonlinear biochemical signal processing via noise propagation. Journal of Chemical Physics, 2013, 139, 144108.	1.2	14
77	pySBOL: A Python Package for Genetic Design Automation and Standardization. ACS Synthetic Biology, 2019, 8, 1515-1518.	1.9	14
78	Challenges for Modeling and Simulation Methods in Systems Biology. , 2006, , .		13
79	Controlling E. coli Gene Expression Noise. IEEE Transactions on Biomedical Circuits and Systems, 2015, 9, 497-504.	2.7	12
80	phraSED-ML: A paraphrased, human-readable adaptation of SED-ML. Journal of Bioinformatics and Computational Biology, 2016, 14, 1650035.	0.3	12
81	The SBW-MATLAB interface. Bioinformatics, 2005, 21, 823-824.	1.8	11
82	Mechanistic and modular approaches to modeling and inference of cellular regulatory networks. , 0, , 143-159.		11
83	Computer-Aided Design for Synthetic Biology. , 2011, , 203-224.		11
84	Synthetic Biology Open Language (SBOL) Version 2.1.0. Journal of Integrative Bioinformatics, 2016, 13, .	1.0	11
85	BioSimulators: a central registry of simulation engines and services for recommending specific tools. Nucleic Acids Research, 2022, 50, W108-W114.	6.5	11
86	Sensitivity summation theorems for stochastic biochemical reaction systems. Mathematical Biosciences, 2010, 226, 109-119.	0.9	10
87	Regulatory Responses and Control Analysis: Assessment of the Relative Importance of Internal Effectors. , 1990, , 225-230.		10
88	Network Dynamics. Methods in Molecular Biology, 2009, 541, 269-309.	0.4	10
89	In search of noise-induced bimodality. BMC Biology, 2012, 10, 89.	1.7	9
90	libOmexMeta: enabling semantic annotation of models to support FAIR principles. Bioinformatics, 2021, 37, 4898-4900.	1.8	9

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91	Complexity Reduction of Biochemical Networks. , 2006, , .		8
92	Stochastic simulation GUI for biochemical networks. <i>Bioinformatics</i> , 2007, 23, 1859-1861.	1.8	8
93	The simulation experiment description markup language (SED-ML): language specification for level 1 version 4. <i>Journal of Integrative Bioinformatics</i> , 2021, 18, 20210021.	1.0	8
94	Software Tools for Systems Biology. , 2010, , 289-314.		7
95	SBML2TikZ: supporting the SBML render extension in LaTeX. <i>Bioinformatics</i> , 2010, 26, 2794-2795.	1.8	7
96	Non-equilibrium/equilibrium reactions: which controls?. <i>Biochemical Society Transactions</i> , 1986, 14, 624-625.	1.6	6
97	Synthetic Biology Open Language (SBOL) Version 2.1.0. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 291.	1.0	6
98	Application of Parameter Optimization to Search for Oscillatory Mass-Action Networks Using Python. <i>Processes</i> , 2019, 7, 163.	1.3	5
99	A compiler for biological networks on silicon chips. <i>PLoS Computational Biology</i> , 2020, 16, e1008063.	1.5	5
100	A portable structural analysis library for reaction networks. <i>BioSystems</i> , 2018, 169-170, 20-25.	0.9	4
101	Substrate cycles: do they really cause amplification?. <i>Biochemical Society Transactions</i> , 1985, 13, 762-763.	1.6	3
102	Publishing reproducible dynamic kinetic models. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	3
103	Practical resources for enhancing the reproducibility of mechanistic modeling in systems biology. <i>Current Opinion in Systems Biology</i> , 2021, 27, 100350.	1.3	3
104	PyBioNetFit and the Biological Property Specification Language. <i>SSRN Electronic Journal</i> , 0, , .	0.4	3
105	A Visual Language for Protein Design. <i>ACS Synthetic Biology</i> , 2017, 6, 1120-1123.	1.9	2
106	libsbmljsâ€”Enabling web-based SBML tools. <i>BioSystems</i> , 2020, 195, 104150.	0.9	2
107	Stochastic Modular Analysis for Gene Circuits: Interplay Among Retroactivity, Nonlinearity, and Stochasticity. <i>Methods in Molecular Biology</i> , 2015, 1244, 287-297.	0.4	2
108	Dynamics and Sensitivity of Signaling Pathways. <i>Current Pathobiology Reports</i> , 2022, 10, 11-22.	1.6	2

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109	In vitro control analysis of an enzyme system: Experimental and analytical developments. <i>Molecular and Cellular Biochemistry</i> , 1995, 145, 141-150.	1.4	1
110	Standards, Platforms, and Applications. , 2006, , 103-125.		1
111	Simulation of biochemical networks - Cellular networks as dynamic control systems. , 2006, 2006, 44-50.		1
112	Data Model Standardization for Synthetic Biomolecular Circuits and Systems. , 2011, , 281-293.		1
113	Measuring the degree of modularity in gene regulatory networks from the relaxation of finite perturbations. , 2012, , .		1
114	A brief note on the properties of linear pathways. <i>Biochemical Society Transactions</i> , 2020, 48, 1379-1395.	1.6	1
115	Innovation in Software for Systems Biology. Is There Any?. , 2006, , .		0
116	Introduction to the Special Issue on Computational Synthetic Biology. <i>ACM Journal on Emerging Technologies in Computing Systems</i> , 2014, 11, 1-5.	1.8	0
117	Standards, Platforms, and Applications. , 2014, , 133-167.		0
118	Status and Challenges of Reproducibility in Computational Systems and Synthetic Biology. , 2021, , 406-412.		0