

# Herbert M. Sauro

## List of Publications by Year in descending order

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Version: 2024-02-01

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	BioSimulators: a central registry of simulation engines and services for recommending specific tools. <i>Nucleic Acids Research</i> , 2022, 50, W108-W114.	6.5	11
2	Dynamics and Sensitivity of Signaling Pathways. <i>Current Pathobiology Reports</i> , 2022, 10, 11-22.	1.6	2
3	Status and Challenges of Reproducibility in Computational Systems and Synthetic Biology. , 2021, , 406-412.		0
4	Publishing reproducible dynamic kinetic models. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	3
5	libOmexMeta: enabling semantic annotation of models to support FAIR principles. <i>Bioinformatics</i> , 2021, 37, 4898-4900.	1.8	9
6	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
7	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
8	A compiler for biological networks on silicon chips. <i>PLoS Computational Biology</i> , 2020, 16, e1008063.	1.5	5
9	Best Practices for Making Reproducible Biochemical Models. <i>Cell Systems</i> , 2020, 11, 109-120.	2.9	25
10	Improving reproducibility in computational biology research. <i>PLoS Computational Biology</i> , 2020, 16, e1007881.	1.5	22
11	libsbmljs”Enabling web-based SBML tools. <i>BioSystems</i> , 2020, 195, 104150.	0.9	2
12	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
13	<sc>SBML</sc> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	3.2	178
14	A brief note on the properties of linear pathways. <i>Biochemical Society Transactions</i> , 2020, 48, 1379-1395.	1.6	1
15	Communicating Structure and Function in Synthetic Biology Diagrams. <i>ACS Synthetic Biology</i> , 2019, 8, 1818-1825.	1.9	30
16	PyBioNetFit and the Biological Property Specification Language. <i>IScience</i> , 2019, 19, 1012-1036.	1.9	47
17	Synthetic Biology Open Language (SBOL) Version 2.3. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.0	16
18	Application of Parameter Optimization to Search for Oscillatory Mass-Action Networks Using Python. <i>Processes</i> , 2019, 7, 163.	1.3	5

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19	Harmonizing semantic annotations for computational models in biology. <i>Briefings in Bioinformatics</i> , 2019, 20, 540-550.	3.2	52
20	pySBOL: A Python Package for Genetic Design Automation and Standardization. <i>ACS Synthetic Biology</i> , 2019, 8, 1515-1518.	1.9	14
21	Recent advances in biomedical simulations: a manifesto for model engineering. <i>F1000Research</i> , 2019, 8, 261.	0.8	21
22	Synthetic Biology Open Language (SBOL) Version 2.2.0. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.0	20
23	A portable structural analysis library for reaction networks. <i>BioSystems</i> , 2018, 169-170, 20-25.	0.9	4
24	Tellurium notebooks—An environment for reproducible dynamical modeling in systems biology. <i>PLoS Computational Biology</i> , 2018, 14, e1006220.	1.5	41
25	Tellurium: An extensible python-based modeling environment for systems and synthetic biology. <i>BioSystems</i> , 2018, 171, 74-79.	0.9	103
26	Synthetic Biology Open Language Visual (SBOL Visual) Version 2.0. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.0	21
27	Control and regulation of pathways via negative feedback. <i>Journal of the Royal Society Interface</i> , 2017, 14, 20160848.	1.5	35
28	A Visual Language for Protein Design. <i>ACS Synthetic Biology</i> , 2017, 6, 1120-1123.	1.9	2
29	Synthetic Biology: Engineering Living Systems from Biophysical Principles. <i>Biophysical Journal</i> , 2017, 112, 1050-1058.	0.2	29
30	Synthetic Biology Open Language (SBOL) Version 2.1.0. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, .	1.0	11
31	phraSED-ML: A paraphrased, human-readable adaptation of SED-ML. <i>Journal of Bioinformatics and Computational Biology</i> , 2016, 14, 1650035.	0.3	12
32	Sharing Structure and Function in Biological Design with SBOL 2.0. <i>ACS Synthetic Biology</i> , 2016, 5, 498-506.	1.9	88
33	Data Integration and Mining for Synthetic Biology Design. <i>ACS Synthetic Biology</i> , 2016, 5, 1086-1097.	1.9	23
34	Synthetic Biology Open Language (SBOL) Version 2.1.0. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 291.	1.0	6
35	Synthetic Biology Open Language (SBOL) Version 2.0.0. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 902-991.	1.0	22
36	Reply to Intellectual property issues and synthetic biology standards. <i>Nature Biotechnology</i> , 2015, 33, 25-25.	9.4	54

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37	libRoadRunner: a high performance SBML simulation and analysis library. <i>Bioinformatics</i> , 2015, 31, 3315-3321.	1.8	130
38	Controlling E. coli Gene Expression Noise. <i>IEEE Transactions on Biomedical Circuits and Systems</i> , 2015, 9, 497-504.	2.7	12
39	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
40	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
41	SBOL Visual: A Graphical Language for Genetic Designs. <i>PLoS Biology</i> , 2015, 13, e1002310.	2.6	73
42	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
43	A Reappraisal of How to Build Modular, Reusable Models of Biological Systems. <i>PLoS Computational Biology</i> , 2014, 10, e1003849.	1.5	47
44	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
45	Standards, Platforms, and Applications. , 2014, , 133-167.		0
46	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
47	Synthetic biology: How best to build a cell. <i>Nature</i> , 2014, 509, 155-157.	13.7	30
48	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
49	Visualization of Evolutionary Stability Dynamics and Competitive Fitness of Escherichia coli Engineered with Randomized Multigene Circuits. <i>ACS Synthetic Biology</i> , 2013, 2, 519-528.	1.9	85
50	Rationally designed bidirectional promoter improves the evolutionary stability of synthetic genetic circuits. <i>Nucleic Acids Research</i> , 2013, 41, e33-e33.	6.5	61
51	It's an analog world. <i>Nature</i> , 2013, 497, 572-573.	13.7	124
52	Nonlinear biochemical signal processing via noise propagation. <i>Journal of Chemical Physics</i> , 2013, 139, 144108.	1.2	14
53	BioBrickâ„¢ Assembly Using the In-Fusion PCR Cloning Kit. <i>Methods in Molecular Biology</i> , 2013, 1073, 19-30.	0.4	15
54	Measuring the degree of modularity in gene regulatory networks from the relaxation of finite perturbations. , 2012, , .		1

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55	In search of noise-induced bimodality. BMC Biology, 2012, 10, 89.	1.7	9
56	Hierarchical Modeling for Synthetic Biology. ACS Synthetic Biology, 2012, 1, 353-364.	1.9	16
57	Computational tools for metabolic engineering. Metabolic Engineering, 2012, 14, 270-280.	3.6	93
58	Adjusting Phenotypes by Noise Control. PLoS Computational Biology, 2012, 8, e1002344.	1.5	23
59	Measuring Retroactivity from Noise in Gene Regulatory Networks. Biophysical Journal, 2011, 100, 1167-1177.	0.2	35
60	Data Model Standardization for Synthetic Biomolecular Circuits and Systems. , 2011, , 281-293.		1
61	Computer-Aided Design for Synthetic Biology. , 2011, , 203-224.		11
62	Essential information for synthetic DNA sequences. Nature Biotechnology, 2011, 29, 22-22.	9.4	40
63	Minimum Information About a Simulation Experiment (MIASE). PLoS Computational Biology, 2011, 7, e1001122.	1.5	133
64	Standard Biological Parts Knowledgebase. PLoS ONE, 2011, 6, e17005.	1.1	80
65	Computer-aided design of biological circuits using tinkercell. Bioengineered Bugs, 2010, 1, 276-283.	2.0	30
66	Software Tools for Systems Biology. , 2010, , 289-314.		7
67	SBML2TikZ: supporting the SBML render extension in LaTeX. Bioinformatics, 2010, 26, 2794-2795.	1.8	7
68	In-Fusion BioBrick assembly and re-engineering. Nucleic Acids Research, 2010, 38, 2624-2636.	6.5	132
69	Sensitivity summation theorems for stochastic biochemical reaction systems. Mathematical Biosciences, 2010, 226, 109-119.	0.9	10
70	Fan-out in gene regulatory networks. Journal of Biological Engineering, 2010, 4, 16.	2.0	31
71	Designing and engineering evolutionary robust genetic circuits. Journal of Biological Engineering, 2010, 4, 12.	2.0	162
72	Antimony: a modular model definition language. Bioinformatics, 2009, 25, 2452-2454.	1.8	112

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73	The Systems Biology Graphical Notation. Nature Biotechnology, 2009, 27, 735-741.	9.4	828
74	TinkerCell: modular CAD tool for synthetic biology. Journal of Biological Engineering, 2009, 3, 19.	2.0	161
75	Network Dynamics. Methods in Molecular Biology, 2009, 541, 269-309.	0.4	10
76	Mathematical modeling and synthetic biology. Drug Discovery Today: Disease Models, 2008, 5, 299-309.	1.2	48
77	Comparing simulation results of SBML capable simulators. Bioinformatics, 2008, 24, 1963-1965.	1.8	30
78	Modularity defined. Molecular Systems Biology, 2008, 4, 166.	3.2	48
79	Standards and ontologies in computational systems biology. Essays in Biochemistry, 2008, 45, 211-222.	2.1	25
80	Stochastic simulation GUI for biochemical networks. Bioinformatics, 2007, 23, 1859-1861.	1.8	8
81	A Model for p53 Dynamics Triggered by DNA Damage. SIAM Journal on Applied Dynamical Systems, 2007, 6, 61-78.	0.7	31
82	Oscillatory dynamics arising from competitive inhibition and multisite phosphorylation. Journal of Theoretical Biology, 2007, 244, 68-76.	0.8	68
83	Design and implementation of three incoherent feed-forward motif based biological concentration sensors. Systems and Synthetic Biology, 2007, 1, 119-128.	1.0	73
84	Standards, Platforms, and Applications. , 2006, , 103-125.		1
85	Complexity Reduction of Biochemical Networks. , 2006, , .		8
86	Simulation of biochemical networks - Cellular networks as dynamic control systems. , 2006, 2006, 44-50.		1
87	Conservation analysis of large biochemical networks. Bioinformatics, 2006, 22, 346-353.	1.8	65
88	Transcriptional Dynamics of the Embryonic Stem Cell Switch. PLoS Computational Biology, 2006, 2, e123.	1.5	228
89	Computational Tools for Modeling Protein Networks. Current Proteomics, 2006, 3, 181-197.	0.1	18
90	SBW - A Modular Framework for Systems Biology. , 2006, , .		25

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91	Innovation in Software for Systems Biology. Is There Any?. , 2006, , .		0
92	BioModels Database: a free, centralized database of curated, published, quantitative kinetic models of biochemical and cellular systems. Nucleic Acids Research, 2006, 34, D689-D691.	6.5	661
93	Challenges for Modeling and Simulation Methods in Systems Biology. , 2006, , .		13
94	Supporting the SBML layout extension. Bioinformatics, 2006, 22, 2966-2967.	1.8	25
95	Minimum information requested in the annotation of biochemical models (MIRIAM). Nature Biotechnology, 2005, 23, 1509-1515.	9.4	553
96	The SBW-MATLAB interface. Bioinformatics, 2005, 21, 823-824.	1.8	11
97	Bifurcation discovery tool. Bioinformatics, 2005, 21, 3688-3690.	1.8	53
98	Quantitative analysis of signaling networks. Progress in Biophysics and Molecular Biology, 2004, 86, 5-43.	1.4	188
99	Preliminary Studies on the In Silico Evolution of Biochemical Networks. ChemBioChem, 2004, 5, 1423-1431.	1.3	52
100	Conservation analysis in biochemical networks: computational issues for software writers. Biophysical Chemistry, 2004, 109, 1-15.	1.5	72
101	The Computational Versatility of Proteomic Signaling Networks. Current Proteomics, 2004, 1, 67-81.	0.1	18
102	Sensitivity analysis of stoichiometric networks: an extension of metabolic control analysis to non-steady state trajectories. Journal of Theoretical Biology, 2003, 222, 23-36.	0.8	135
103	Next Generation Simulation Tools: The Systems Biology Workbench and BioSPICE Integration. OMICS A Journal of Integrative Biology, 2003, 7, 355-372.	1.0	254
104	In vitro control analysis of an enzyme system: Experimental and analytical developments. Molecular and Cellular Biochemistry, 1995, 145, 141-150.	1.4	1
105	Moiety-conserved cycles and metabolic control analysis: problems in sequestration and metabolic channelling. BioSystems, 1994, 33, 55-67.	0.9	21
106	Control by Enzymes, Coenzymes and Conserved Moieties. A Generalisation of the Connectivity Theorem of Metabolic Control Analysis. FEBS Journal, 1994, 225, 179-186.	0.2	29
107	SCAMP: A metabolic simulator and control analysis program. Mathematical and Computer Modelling, 1991, 15, 15-28.	2.0	43
108	Enzyme-enzyme interactions and control analysis. 1. The case of non-additivity: monomer-oligomer associations. FEBS Journal, 1990, 187, 481-491.	0.2	77

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109	Enzyme-enzyme interactions and control analysis. 2. The case of non-independence: heterologous associations. FEBS Journal, 1990, 187, 493-500.	0.2	74
110	Metabolic control analysis. The effects of high enzyme concentrations. FEBS Journal, 1990, 192, 183-187.	0.2	41
111	Regulatory Responses and Control Analysis: Assessment of the Relative Importance of Internal Effectors. , 1990, , 225-230.		10
112	Control analysis of time-dependent metabolic systems. Journal of Theoretical Biology, 1989, 137, 423-444.	0.8	89
113	Metabolic control and its analysis. Extensions to the theory and matrix method. FEBS Journal, 1987, 165, 215-221.	0.2	108
114	Non-equilibrium/equilibrium reactions: which controls?. Biochemical Society Transactions, 1986, 14, 624-625.	1.6	6
115	Substrate cycles: do they really cause amplification?. Biochemical Society Transactions, 1985, 13, 762-763.	1.6	3
116	Metabolic control and its analysis. Additional relationships between elasticities and control coefficients. FEBS Journal, 1985, 148, 555-561.	0.2	273
117	Mechanistic and modular approaches to modeling and inference of cellular regulatory networks. , 0, , 143-159.		11
118	PyBioNetFit and the Biological Property Specification Language. SSRN Electronic Journal, 0, , .	0.4	3