

# Vassily Hatzimanikatis

## List of Publications by Year in descending order

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143  
papers

9,870  
citations

36303

51  
h-index

48315

88  
g-index

180  
all docs

180  
docs citations

180  
times ranked

7670  
citing authors

#	ARTICLE	IF	CITATIONS
1	A genome-scale metabolic reconstruction for Escherichia coli K12 MG1655 that accounts for 1260 ORFs and thermodynamic information. <i>Molecular Systems Biology</i> , 2007, 3, 121.	7.2	1,234
2	Thermodynamics-Based Metabolic Flux Analysis. <i>Biophysical Journal</i> , 2007, 92, 1792-1805.	0.5	560
3	Group Contribution Method for Thermodynamic Analysis of Complex Metabolic Networks. <i>Biophysical Journal</i> , 2008, 95, 1487-1499.	0.5	345
4	Exploring the diversity of complex metabolic networks. <i>Bioinformatics</i> , 2005, 21, 1603-1609.	4.1	322
5	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	17.5	314
6	Metabolic fluxes in riboflavin-producing <i>Bacillus subtilis</i> . <i>Nature Biotechnology</i> , 1997, 15, 448-452.	17.5	241
7	Kinetic models in industrial biotechnology – Improving cell factory performance. <i>Metabolic Engineering</i> , 2014, 24, 38-60.	7.0	238
8	Metabolic flux analysis of hybridoma cells in different culture media using mass balances. , 1996, 50, 299-318.		226
9	Genome-Scale Thermodynamic Analysis of Escherichia coli Metabolism. <i>Biophysical Journal</i> , 2006, 90, 1453-1461.	0.5	195
10	Analysis and design of metabolic reaction networks via mixed-integer linear optimization. <i>AIChE Journal</i> , 1996, 42, 1277-1292.	3.6	160
11	Metabolic Control Analysis under Uncertainty: Framework Development and Case Studies. <i>Biophysical Journal</i> , 2004, 87, 3750-3763.	0.5	153
12	Discovery and analysis of novel metabolic pathways for the biosynthesis of industrial chemicals: 3-hydroxypropanoate. <i>Biotechnology and Bioengineering</i> , 2010, 106, 462-473.	3.3	146
13	Towards kinetic modeling of genome-scale metabolic networks without sacrificing stoichiometric, thermodynamic and physiological constraints. <i>Biotechnology Journal</i> , 2013, 8, 1043-1057.	3.5	141
14	Inverse metabolic engineering: A strategy for directed genetic engineering of useful phenotypes. , 1996, 52, 109-121.		136
15	ATLAS of Biochemistry: A Repository of All Possible Biochemical Reactions for Synthetic Biology and Metabolic Engineering Studies. <i>ACS Synthetic Biology</i> , 2016, 5, 1155-1166.	3.8	132
16	Manipulating redox and ATP balancing for improved production of succinate in <i>E. coli</i> . <i>Metabolic Engineering</i> , 2011, 13, 76-81.	7.0	113
17	Design of computational retrobiosynthesis tools for the design of de novo synthetic pathways. <i>Current Opinion in Chemical Biology</i> , 2015, 28, 99-104.	6.1	113
18	Insights into the relation between mRNA and protein expression patterns: I. theoretical considerations. <i>Biotechnology and Bioengineering</i> , 2003, 84, 822-833.	3.3	106

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19	Production of biofuels and biochemicals: in need of an ORACLE. Trends in Biotechnology, 2010, 28, 391-397.	9.3	100
20	Computational framework for predictive biodegradation. Biotechnology and Bioengineering, 2009, 104, 1086-1097.	3.3	96
21	Proteomics: Theoretical and Experimental Considerations. Biotechnology Progress, 1999, 15, 312-318.	2.6	93
22	Sustainability assessment of succinic acid production technologies from biomass using metabolic engineering. Energy and Environmental Science, 2016, 9, 2794-2805.	30.8	93
23	MCA Has More to Say. Journal of Theoretical Biology, 1996, 182, 233-242.	1.7	92
24	Metabolic Needs and Capabilities of Toxoplasma gondii through Combined Computational and Experimental Analysis. PLoS Computational Biology, 2015, 11, e1004261.	3.2	92
25	Genome-Scale Identification of Essential Metabolic Processes for Targeting the Plasmodium Liver Stage. Cell, 2019, 179, 1112-1128.e26.	28.9	92
26	Identification and dynamics of the human ZDHHC16-ZDHHC6 palmitoylation cascade. ELife, 2017, 6, .	6.0	89
27	Inverse metabolic engineering: A strategy for directed genetic engineering of useful phenotypes. Biotechnology and Bioengineering, 2002, 79, 568-579.	3.3	88
28	Effect of Vitreoscilla hemoglobin dosage on microaerobic Escherichia coli carbon and energy metabolism. Biotechnology and Bioengineering, 1996, 49, 139-150.	3.3	87
29	Heading in the right direction: thermodynamics-based network analysis and pathway engineering. Current Opinion in Biotechnology, 2015, 36, 176-182.	6.6	86
30	Dynamical Analysis of Gene Networks Requires Both mRNA and Protein Expression Information. Metabolic Engineering, 1999, 1, 275-281.	7.0	85
31	Mathematical Modeling of the Eukaryotic Heat-Shock Response: Dynamics of the hsp70 Promoter. Biophysical Journal, 2005, 88, 1646-1658.	0.5	83
32	Metabolic networks: enzyme function and metabolite structure. Current Opinion in Structural Biology, 2004, 14, 300-306.	5.7	81
33	Functional and Computational Genomics Reveal Unprecedented Flexibility in Stage-Specific Toxoplasma Metabolism. Cell Host and Microbe, 2020, 27, 290-306.e11.	11.0	81
34	Identification of metabolic engineering targets for the enhancement of 1,4-butanediol production in recombinant E. coli using large-scale kinetic models. Metabolic Engineering, 2016, 35, 148-159.	7.0	78
35	Optimization of regulatory architectures in metabolic reaction networks. , 1996, 52, 485-500.		77
36	Insights into the relation between mrna and protein expression patterns: ii. Experimental observations in Escherichia coli. Biotechnology and Bioengineering, 2003, 84, 834-841.	3.3	77

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37	pyTFA and matTFA: a Python package and a Matlab toolbox for Thermodynamics-based Flux Analysis. <i>Bioinformatics</i> , 2019, 35, 167-169.	4.1	75
38	In silico feasibility of novel biodegradation pathways for 1,2,4-trichlorobenzene. <i>BMC Systems Biology</i> , 2010, 4, 7.	3.0	74
39	Computational discovery of biochemical routes to specialty chemicals. <i>Chemical Engineering Science</i> , 2004, 59, 5051-5060.	3.8	73
40	Network thermodynamics in the post-genomic era. <i>Current Opinion in Microbiology</i> , 2010, 13, 350-357.	5.1	73
41	Modeling of uncertainties in biochemical reactions. <i>Biotechnology and Bioengineering</i> , 2011, 108, 413-423.	3.3	73
42	iSCHRUNK – In Silico Approach to Characterization and Reduction of Uncertainty in the Kinetic Models of Genome-scale Metabolic Networks. <i>Metabolic Engineering</i> , 2016, 33, 158-168.	7.0	72
43	The ETFL formulation allows multi-omics integration in thermodynamics-compliant metabolism and expression models. <i>Nature Communications</i> , 2020, 11, 30.	12.8	71
44	From network models to network responses: integration of thermodynamic and kinetic properties of yeast genome-scale metabolic networks. <i>FEMS Yeast Research</i> , 2012, 12, 129-143.	2.3	70
45	Effects of spatiotemporal variations on metabolic control: Approximate analysis using (log)linear kinetic models. , 1997, 54, 91-104.		68
46	Metabolic engineering under uncertainty. I: Framework development. <i>Metabolic Engineering</i> , 2006, 8, 133-141.	7.0	68
47	Antihypertensive Drugs Metabolism: An Update to Pharmacokinetic Profiles and Computational Approaches. <i>Current Pharmaceutical Design</i> , 2014, 21, 806-822.	1.9	68
48	Do genome-scale models need exact solvers or clearer standards?. <i>Molecular Systems Biology</i> , 2015, 11, 831.	7.2	68
49	Recombinant cyclin E expression activates proliferation and obviates surface attachment of chinese hamster ovary (CHO) cells in protein-free medium. <i>Biotechnology and Bioengineering</i> , 1995, 47, 476-482.	3.3	67
50	A mathematical description of regulation of the G1-S transition of the mammalian cell cycle. <i>Biotechnology and Bioengineering</i> , 1999, 65, 631-637.	3.3	67
51	Enzyme annotation for orphan and novel reactions using knowledge of substrate reactive sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7298-7307.	7.1	65
52	Metabolic engineering under uncertainty – II: Analysis of yeast metabolism. <i>Metabolic Engineering</i> , 2006, 8, 142-159.	7.0	64
53	The SIB Swiss Institute of Bioinformatics –™ resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016, 44, D27-D37.	14.5	64
54	Application of mathematical tools for metabolic design of microbial ethanol production. , 1998, 58, 154-161.		62

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55	Enhanced flux prediction by integrating relative expression and relative metabolite abundance into thermodynamically consistent metabolic models. <i>PLoS Computational Biology</i> , 2019, 15, e1007036.	3.2	62
56	redGEM: Systematic reduction and analysis of genome-scale metabolic reconstructions for development of consistent core metabolic models. <i>PLoS Computational Biology</i> , 2017, 13, e1005444.	3.2	61
57	Theoretical Considerations and Computational Analysis of the Complexity in Polyketide Synthesis Pathways. <i>Journal of the American Chemical Society</i> , 2005, 127, 9930-9938.	13.7	60
58	Efficient cleavage of aryl ether C–O linkages by Rh–Ni and Ru–Ni nanoscale catalysts operating in water. <i>Chemical Science</i> , 2018, 9, 5530-5535.	7.4	57
59	A Model for Protein Translation: Polysome Self-Organization Leads to Maximum Protein Synthesis Rates. <i>Biophysical Journal</i> , 2007, 92, 717-730.	0.5	50
60	The Origins of Time-Delay in Template Biopolymerization Processes. <i>PLoS Computational Biology</i> , 2010, 6, e1000726.	3.2	49
61	Single-molecule kinetic analysis of HP1-chromatin binding reveals a dynamic network of histone modification and DNA interactions. <i>Nucleic Acids Research</i> , 2017, 45, 10504-10517.	14.5	49
62	A genome-scale metabolic model of <i>Saccharomyces cerevisiae</i> that integrates expression constraints and reaction thermodynamics. <i>Nature Communications</i> , 2021, 12, 4790.	12.8	48
63	Constraining the Flux Space Using Thermodynamics and Integration of Metabolomics Data. <i>Methods in Molecular Biology</i> , 2014, 1191, 49-63.	0.9	47
64	Effects of Codon Distributions and tRNA Competition on Protein Translation. <i>Biophysical Journal</i> , 2008, 95, 1018-1033.	0.5	45
65	Thermodynamic analysis of biodegradation pathways. <i>Biotechnology and Bioengineering</i> , 2009, 103, 532-541.	3.3	45
66	Modeling metabolic networks of individual bacterial agents in heterogeneous and dynamic soil habitats (IndiMeSH). <i>PLoS Computational Biology</i> , 2019, 15, e1007127.	3.2	45
67	DREAMS of metabolism. <i>Trends in Biotechnology</i> , 2010, 28, 501-508.	9.3	44
68	A method for analysis and design of metabolism using metabolomics data and kinetic models: Application on lipidomics using a novel kinetic model of sphingolipid metabolism. <i>Metabolic Engineering</i> , 2016, 37, 46-62.	7.0	44
69	Bioenergetics-based modeling of <i>Plasmodium falciparum</i> metabolism reveals its essential genes, nutritional requirements, and thermodynamic bottlenecks. <i>PLoS Computational Biology</i> , 2017, 13, e1005397.	3.2	44
70	A Novel Pulse-Chase SILAC Strategy Measures Changes in Protein Decay and Synthesis Rates Induced by Perturbation of Proteostasis with an Hsp90 Inhibitor. <i>PLoS ONE</i> , 2013, 8, e80423.	2.5	42
71	An Algorithmic Framework for Genome-Wide Modeling and Analysis of Translation Networks. <i>Biophysical Journal</i> , 2006, 90, 1136-1146.	0.5	41
72	A computational workflow for the expansion of heterologous biosynthetic pathways to natural product derivatives. <i>Nature Communications</i> , 2021, 12, 1760.	12.8	40

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73	lumpGEM: Systematic generation of subnetworks and elementally balanced lumped reactions for the biosynthesis of target metabolites. <i>PLoS Computational Biology</i> , 2017, 13, e1005513.	3.2	39
74	Metabolic Consequences of Phosphotransferase (PTS) Mutation in a Phenylalanine-Producing Recombinant <i>Escherichia coli</i> . <i>Biotechnology Progress</i> , 1997, 13, 768-775.	2.6	38
75	Rites of passage: requirements and standards for building kinetic models of metabolic phenotypes. <i>Current Opinion in Biotechnology</i> , 2015, 36, 146-153.	6.6	38
76	Impact of iron reduction on the metabolism of <i>Clostridium acetobutylicum</i> . <i>Environmental Microbiology</i> , 2019, 21, 3548-3563.	3.8	38
77	Model-Driven Understanding of Palmitoylation Dynamics: Regulated Acylation of the Endoplasmic Reticulum Chaperone Calnexin. <i>PLoS Computational Biology</i> , 2016, 12, e1004774.	3.2	37
78	A design-build-test cycle using modeling and experiments reveals interdependencies between upper glycolysis and xylose uptake in recombinant <i>S. cerevisiae</i> and improves predictive capabilities of large-scale kinetic models. <i>Biotechnology for Biofuels</i> , 2017, 10, 166.	6.2	37
79	Kinetic models of metabolism that consider alternative steady-state solutions of intracellular fluxes and concentrations. <i>Metabolic Engineering</i> , 2019, 52, 29-41.	7.0	36
80	Updated ATLAS of Biochemistry with New Metabolites and Improved Enzyme Prediction Power. <i>ACS Synthetic Biology</i> , 2020, 9, 1479-1482.	3.8	34
81	Large-scale kinetic metabolic models of <i>Pseudomonas putida</i> KT2440 for consistent design of metabolic engineering strategies. <i>Biotechnology for Biofuels</i> , 2020, 13, 33.	6.2	34
82	Integrating computational methods to retrofit enzymes to synthetic pathways. <i>Biotechnology and Bioengineering</i> , 2012, 109, 572-582.	3.3	32
83	A model-based optimization framework for the inference on gene regulatory networks from DNA array data. <i>Bioinformatics</i> , 2004, 20, 3221-3235.	4.1	31
84	Thermodynamic Calculations for Biochemical Transport and Reaction Processes in Metabolic Networks. <i>Biophysical Journal</i> , 2010, 99, 3139-3144.	0.5	30
85	A model-based optimization framework for the inference of regulatory interactions using time-course DNA microarray expression data. <i>BMC Bioinformatics</i> , 2007, 8, 228.	2.6	29
86	Discovery and Evaluation of Biosynthetic Pathways for the Production of Five Methyl Ethyl Ketone Precursors. <i>ACS Synthetic Biology</i> , 2018, 7, 1858-1873.	3.8	29
87	Bistability Explains Threshold Phenomena in Protein Aggregation both In Vitro and In Vivo. <i>Biophysical Journal</i> , 2006, 90, 886-895.	0.5	28
88	Thermodynamics-based Metabolite Sensitivity Analysis in metabolic networks. <i>Metabolic Engineering</i> , 2017, 39, 117-127.	7.0	27
89	Exploring biochemical pathways for mono-ethylene glycol (MEG) synthesis from synthesis gas. <i>Metabolic Engineering</i> , 2017, 41, 173-181.	7.0	26
90	Tunable reporter signal production in feedback-uncoupled arsenic bioreporters. <i>Microbial Biotechnology</i> , 2013, 6, 503-514.	4.2	25

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91	Particle-Based Simulation Reveals Macromolecular Crowding Effects on the Michaelis-Menten Mechanism. <i>Biophysical Journal</i> , 2019, 117, 355-368.	0.5	24
92	A computational framework for the design of optimal protein synthesis. <i>Biotechnology and Bioengineering</i> , 2012, 109, 2127-2133.	3.3	23
93	Emergence of diauxie as an optimal growth strategy under resource allocation constraints in cellular metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	23
94	A Genome-Scale Integration and Analysis of <i>Lactococcus lactis</i> Translation Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003240.	3.2	22
95	Solvation quantities from a COSMO-RS equation of state. <i>Journal of Chemical Thermodynamics</i> , 2015, 90, 294-309.	2.0	21
96	Nonlinear Metabolic Control Analysis. <i>Metabolic Engineering</i> , 1999, 1, 75-87.	7.0	20
97	Uncertainty reduction in biochemical kinetic models: Enforcing desired model properties. <i>PLoS Computational Biology</i> , 2019, 15, e1007242.	3.2	20
98	Analysis of the maximum theoretical yield for the synthesis of erythromycin precursors in <i>Escherichia coli</i> . <i>Biotechnology and Bioengineering</i> , 2006, 95, 638-644.	3.3	19
99	Analysis of human metabolism by reducing the complexity of the genome-scale models using redHUMAN. <i>Nature Communications</i> , 2020, 11, 2821.	12.8	19
100	Expanding biochemical knowledge and illuminating metabolic dark matter with ATLASx. <i>Nature Communications</i> , 2022, 13, 1560.	12.8	19
101	A mathematical model for the G1/S transition of the mammalian cell cycle. <i>Biotechnology Letters</i> , 1995, 17, 669-674.	2.2	18
102	Studies on glycolysis â€” I. Multiple steady states in bacterial glycolysis. <i>Chemical Engineering Science</i> , 1997, 52, 2579-2588.	3.8	18
103	Molecular thermodynamics of metabolism: hydration quantities and the equation-of-state approach. <i>Physical Chemistry Chemical Physics</i> , 2016, 18, 32570-32592.	2.8	18
104	Quantification of Cooperativity in Heterodimer-DNA Binding Improves the Accuracy of Binding Specificity Models. <i>Journal of Biological Chemistry</i> , 2016, 291, 10293-10306.	3.4	18
105	Mechanistic Modeling of Genetic Circuits for ArsR Arsenic Regulation. <i>ACS Synthetic Biology</i> , 2017, 6, 862-874.	3.8	18
106	Toward a Simple Predictive Molecular Thermodynamic Model for Bulk Phases and Interfaces. <i>Industrial &amp; Engineering Chemistry Research</i> , 2017, 56, 10900-10910.	3.7	18
107	The AlkB Monooxygenase of <i>Pseudomonas oleovorans</i> . Synthesis, Stability and Level in Recombinant <i>Escherichia coli</i> and the Native Host. <i>FEBS Journal</i> , 1997, 244, 462-470.	0.2	17
108	A computational framework for integration of lipidomics data into metabolic pathways. <i>Metabolic Engineering</i> , 2014, 23, 1-8.	7.0	17

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109	Redefining solubility parameters: Bulk and surface properties from unified molecular descriptors. <i>Journal of Chemical Thermodynamics</i> , 2017, 111, 207-220.	2.0	17
110	Control Theory Concepts for Modeling Uncertainty in Enzyme Kinetics of Biochemical Networks. <i>Industrial &amp; Engineering Chemistry Research</i> , 2019, 58, 13544-13554.	3.7	17
111	Functional genomics of <i>Plasmodium falciparum</i> using metabolic modelling and analysis. <i>Briefings in Functional Genomics</i> , 2013, 12, 316-327.	2.7	16
112	Molecular thermodynamics of metabolism: quantum thermochemical calculations for key metabolites. <i>Physical Chemistry Chemical Physics</i> , 2015, 17, 10438-10453.	2.8	16
113	Analysis of Translation Elongation Dynamics in the Context of an <i>Escherichia coli</i> Cell. <i>Biophysical Journal</i> , 2016, 110, 2120-2131.	0.5	15
114	A method for pulsed periodic optimization of chemical reaction systems. <i>Chemical Engineering Science</i> , 1993, 48, 789-797.	3.8	14
115	Reconstruction of biological pathways and metabolic networks from in silico labeled metabolites. <i>Biotechnology Journal</i> , 2017, 12, 1600464.	3.5	14
116	Statistical inference in ensemble modeling of cellular metabolism. <i>PLoS Computational Biology</i> , 2019, 15, e1007536.	3.2	14
117	Integration of metabolic, regulatory and signaling networks towards analysis of perturbation and dynamic responses. <i>Current Opinion in Systems Biology</i> , 2017, 2, 59-66.	2.6	13
118	On Lewis acidity/basicity and hydrogen bonding in the equation-of-state approach. <i>Journal of Chemical Thermodynamics</i> , 2017, 110, 3-15.	2.0	13
119	Constraint-based metabolic control analysis for rational strain engineering. <i>Metabolic Engineering</i> , 2021, 66, 191-203.	7.0	12
120	Spatio-temporal modeling of the crowding conditions and metabolic variability in microbial communities. <i>PLoS Computational Biology</i> , 2021, 17, e1009140.	3.2	12
121	Computational tools and resources for designing new pathways to small molecules. <i>Current Opinion in Biotechnology</i> , 2022, 76, 102722.	6.6	12
122	NICEpath: Finding metabolic pathways in large networks through atom-conserving substrate–product pairs. <i>Bioinformatics</i> , 2021, 37, 3560-3568.	4.1	10
123	<i>110th Anniversary</i>: From Solubility Parameters to Predictive Equation-of-State Modeling. <i>Industrial &amp; Engineering Chemistry Research</i> , 2019, 58, 12787-12800.	3.7	9
124	The solubility parameters of carbon dioxide and ionic liquids: Are they an enigma?. <i>Fluid Phase Equilibria</i> , 2021, 527, 112828.	2.5	8
125	NICEdrug.ch, a workflow for rational drug design and systems-level analysis of drug metabolism. <i>ELife</i> , 2021, 10, .	6.0	8
126	Noise analysis of genome-scale protein synthesis using a discrete computational model of translation. <i>Journal of Chemical Physics</i> , 2015, 143, 044109.	3.0	7



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127	Investigating the deregulation of metabolic tasks via Minimum Network Enrichment Analysis (MiNEA) as applied to nonalcoholic fatty liver disease using mouse and human omics data. <i>PLoS Computational Biology</i> , 2019, 15, e1006760.	3.2	6
128	Exploration of trade-offs between steady-state and dynamic properties in signaling cycles. <i>Physical Biology</i> , 2012, 9, 045010.	1.8	4
129	Integrative approaches for signalling and metabolic networks. <i>Integrative Biology (United Kingdom)</i> , 2015, 7, 844-845.	1.3	4
130	The effects of model complexity and size on metabolic flux distribution and control: case study in <i>Escherichia coli</i> . <i>BMC Bioinformatics</i> , 2021, 22, 134.	2.6	4
131	Dynamic Radiolabeling of S-Palmitoylated Proteins. <i>Methods in Molecular Biology</i> , 2019, 2009, 111-127.	0.9	3
132	Quantitative modeling of human metabolism: A call for a community effort. <i>Current Opinion in Systems Biology</i> , 2021, 26, 109-115.	2.6	3
133	The influence of the crowding assumptions in biofilm simulations. <i>PLoS Computational Biology</i> , 2021, 17, e1009158.	3.2	3
134	ARBRE: Computational resource to predict pathways towards industrially important aromatic compounds. <i>Metabolic Engineering</i> , 2022, 72, 259-274.	7.0	3
135	A memorial review of Jay Bailey's contribution in prokaryotic metabolic engineering. <i>Biotechnology and Bioengineering</i> , 2002, 79, 504-508.	3.3	2
136	Jay Bailey as mentor?The students' perspective. <i>Biotechnology and Bioengineering</i> , 2002, 79, 484-489.	3.3	1
137	The systems engineering of cellular processes. <i>Computer Aided Chemical Engineering</i> , 2006, , 71-80.	0.5	1
138	Systems biology. <i>Current Opinion in Biotechnology</i> , 2011, 22, 538-540.	6.6	1
139	Mechanistically Consistent Reduced Models of Synthetic Gene Networks. <i>Biophysical Journal</i> , 2013, 104, 2098-2109.	0.5	1
140	Editorial: Metabolic modeling in biotechnology and medical research. <i>Biotechnology Journal</i> , 2013, 8, 962-963.	3.5	1
141	PhenoMapping: A protocol to map cellular phenotypes to metabolic bottlenecks, identify conditional essentiality, and curate metabolic models. <i>STAR Protocols</i> , 2021, 2, 100280.	1.2	1
142	Modelling molecular mechanisms within their cellular environment. <i>Journal of Biotechnology</i> , 1999, 71, 263-265.	3.8	0
143	Discovery of Novel Routes for the Production of Fuels and Chemicals. , 2009, , 141-148.		0