

Vassily Hatzimanikatis

List of Publications by Citations

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156
papers

7,564
citations

48
h-index

84
g-index

180
ext. papers

8,892
ext. citations

7.3
avg, IF

6.29
L-index

#	Paper	IF	Citations
156	A genome-scale metabolic reconstruction for Escherichia coli K-12 MG1655 that accounts for 1260 ORFs and thermodynamic information. <i>Molecular Systems Biology</i> , 2007 , 3, 121	12.2	1044
155	Thermodynamics-based metabolic flux analysis. <i>Biophysical Journal</i> , 2007 , 92, 1792-805	2.9	456
154	Group contribution method for thermodynamic analysis of complex metabolic networks. <i>Biophysical Journal</i> , 2008 , 95, 1487-99	2.9	294
153	Exploring the diversity of complex metabolic networks. <i>Bioinformatics</i> , 2005 , 21, 1603-9	7.2	273
152	Metabolic fluxes in riboflavin-producing <i>Bacillus subtilis</i> . <i>Nature Biotechnology</i> , 1997 , 15, 448-52	44.5	221
151	Metabolic flux analysis of hybridoma cells in different culture media using mass balances. <i>Biotechnology and Bioengineering</i> , 1996 , 50, 299-318	4.9	200
150	Kinetic models in industrial biotechnology - Improving cell factory performance. <i>Metabolic Engineering</i> , 2014 , 24, 38-60	9.7	183
149	Genome-scale thermodynamic analysis of Escherichia coli metabolism. <i>Biophysical Journal</i> , 2006 , 90, 1453-61	5.1	176
148	Analysis and design of metabolic reaction networks via mixed-integer linear optimization. <i>AIChE Journal</i> , 1996 , 42, 1277-1292	3.6	134
147	Discovery and analysis of novel metabolic pathways for the biosynthesis of industrial chemicals: 3-hydroxypropanoate. <i>Biotechnology and Bioengineering</i> , 2010 , 106, 462-73	4.9	125
146	Metabolic control analysis under uncertainty: framework development and case studies. <i>Biophysical Journal</i> , 2004 , 87, 3750-63	2.9	125
145	Inverse metabolic engineering: A strategy for directed genetic engineering of useful phenotypes. <i>Biotechnology and Bioengineering</i> , 1996 , 52, 109-21	4.9	122
144	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020 , 38, 272-276	16.5	121
143	Towards kinetic modeling of genome-scale metabolic networks without sacrificing stoichiometric, thermodynamic and physiological constraints. <i>Biotechnology Journal</i> , 2013 , 8, 1043-57	5.6	114
142	Manipulating redox and ATP balancing for improved production of succinate in <i>E. coli</i> . <i>Metabolic Engineering</i> , 2011 , 13, 76-81	9.7	104
141	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	5.7	97
140	Insights into the relation between mRNA and protein expression patterns: I. Theoretical considerations. <i>Biotechnology and Bioengineering</i> , 2003 , 84, 822-33	4.9	91

139	Inverse metabolic engineering: a strategy for directed genetic engineering of useful phenotypes. <i>Biotechnology and Bioengineering</i> , 2002 , 79, 568-79	4.9	84
138	Effect of <i>Vitreoscilla</i> hemoglobin dosage on microaerobic <i>Escherichia coli</i> carbon and energy metabolism. <i>Biotechnology and Bioengineering</i> , 1996 , 49, 139-50	4.9	83
137	Design of computational retrobiosynthesis tools for the design of de novo synthetic pathways. <i>Current Opinion in Chemical Biology</i> , 2015 , 28, 99-104	9.7	82
136	MCA has more to say. <i>Journal of Theoretical Biology</i> , 1996 , 182, 233-42	2.3	78
135	Computational framework for predictive biodegradation. <i>Biotechnology and Bioengineering</i> , 2009 , 104, 1086-97	4.9	77
134	Production of biofuels and biochemicals: in need of an ORACLE. <i>Trends in Biotechnology</i> , 2010 , 28, 391-7	15.1	74
133	Dynamical analysis of gene networks requires both mRNA and protein expression information. <i>Metabolic Engineering</i> , 1999 , 1, 275-81	9.7	74
132	Mathematical modeling of the eukaryotic heat-shock response: dynamics of the hsp70 promoter. <i>Biophysical Journal</i> , 2005 , 88, 1646-58	2.9	73
131	Proteomics: theoretical and experimental considerations. <i>Biotechnology Progress</i> , 1999 , 15, 312-8	2.8	73
130	Metabolic Needs and Capabilities of <i>Toxoplasma gondii</i> through Combined Computational and Experimental Analysis. <i>PLoS Computational Biology</i> , 2015 , 11, e1004261	5	71
129	Metabolic networks: enzyme function and metabolite structure. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 300-6	8.1	69
128	Heading in the right direction: thermodynamics-based network analysis and pathway engineering. <i>Current Opinion in Biotechnology</i> , 2015 , 36, 176-82	11.4	67
127	Computational discovery of biochemical routes to specialty chemicals. <i>Chemical Engineering Science</i> , 2004 , 59, 5051-5060	4.4	67
126	Insights into the relation between mRNA and protein expression patterns: II. Experimental observations in <i>Escherichia coli</i> . <i>Biotechnology and Bioengineering</i> , 2003 , 84, 834-41	4.9	67
125	Sustainability assessment of succinic acid production technologies from biomass using metabolic engineering. <i>Energy and Environmental Science</i> , 2016 , 9, 2794-2805	35.4	67
124	Optimization of regulatory architectures in metabolic reaction networks. <i>Biotechnology and Bioengineering</i> , 1996 , 52, 485-500	4.9	64
123	Network thermodynamics in the post-genomic era. <i>Current Opinion in Microbiology</i> , 2010 , 13, 350-7	7.9	61
122	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, 476-82	4.9	61

121	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, 129-43	3.1	60
120	In silico feasibility of novel biodegradation pathways for 1,2,4-trichlorobenzene. <i>BMC Systems Biology</i> , 2010 , 4, 7	3.5	58
119	Modeling of uncertainties in biochemical reactions. <i>Biotechnology and Bioengineering</i> , 2011 , 108, 413-23	4.9	57
118	Identification of metabolic engineering targets for the enhancement of 1,4-butanediol production in recombinant E. coli using large-scale kinetic models. <i>Metabolic Engineering</i> , 2016 , 35, 148-159	9.7	56
117	Metabolic engineering under uncertainty. I: framework development. <i>Metabolic Engineering</i> , 2006 , 8, 133-41	9.7	56
116	A mathematical description of regulation of the G1-S transition of the mammalian cell cycle. <i>Biotechnology and Bioengineering</i> , 1999 , 65, 631-7	4.9	55
115	Effects of spatiotemporal variations on metabolic control: approximate analysis using (log)linear kinetic models. <i>Biotechnology and Bioengineering</i> , 1997 , 54, 91-104	4.9	54
114	Application of mathematical tools for metabolic design of microbial ethanol production. <i>Biotechnology and Bioengineering</i> , 1998 , 58, 154-61	4.9	54
113	Theoretical considerations and computational analysis of the complexity in polyketide synthesis pathways. <i>Journal of the American Chemical Society</i> , 2005 , 127, 9930-8	16.4	54
112	Metabolic engineering under uncertainty--II: analysis of yeast metabolism. <i>Metabolic Engineering</i> , 2006 , 8, 142-59	9.7	54
111	Identification and dynamics of the human ZDHHC16-ZDHHC6 palmitoylation cascade. <i>ELife</i> , 2017 , 6,	8.9	53
110	Antihypertensive drugs metabolism: an update to pharmacokinetic profiles and computational approaches. <i>Current Pharmaceutical Design</i> , 2015 , 21, 806-22	3.3	50
109	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	9.7	49
108	A model for protein translation: polysome self-organization leads to maximum protein synthesis rates. <i>Biophysical Journal</i> , 2007 , 92, 717-30	2.9	45
107	Functional and Computational Genomics Reveal Unprecedented Flexibility in Stage-Specific Toxoplasma Metabolism. <i>Cell Host and Microbe</i> , 2020 , 27, 290-306.e11	23.4	44
106	The ETFL formulation allows multi-omics integration in thermodynamics-compliant metabolism and expression models. <i>Nature Communications</i> , 2020 , 11, 30	17.4	41
105	The SIB Swiss Institute of Bioinformatics Resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016 , 44, D27-37	20.1	41
104	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	9.4	41

103	Genome-Scale Identification of Essential Metabolic Processes for Targeting the Plasmodium Liver Stage. <i>Cell</i> , 2019 , 179, 1112-1128.e26	56.2	41
102	Do genome-scale models need exact solvers or clearer standards?. <i>Molecular Systems Biology</i> , 2015 , 11, 831	12.2	41
101	Effects of codon distributions and tRNA competition on protein translation. <i>Biophysical Journal</i> , 2008 , 95, 1018-33	2.9	41
100	DREAMS of metabolism. <i>Trends in Biotechnology</i> , 2010 , 28, 501-8	15.1	40
99	Thermodynamic analysis of biodegradation pathways. <i>Biotechnology and Bioengineering</i> , 2009 , 103, 532-41	4.9	39
98	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	5	38
97	The origins of time-delay in template biopolymerization processes. <i>PLoS Computational Biology</i> , 2010 , 6, e1000726	5	38
96	An algorithmic framework for genome-wide modeling and analysis of translation networks. <i>Biophysical Journal</i> , 2006 , 90, 1136-46	2.9	37
95	Bioenergetics-based modeling of Plasmodium falciparum metabolism reveals its essential genes, nutritional requirements, and thermodynamic bottlenecks. <i>PLoS Computational Biology</i> , 2017 , 13, e1005397	5.9	36
94	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	11.5	35
93	Enhanced flux prediction by integrating relative expression and relative metabolite abundance into thermodynamically consistent metabolic models. <i>PLoS Computational Biology</i> , 2019 , 15, e1007036	5	34
92	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	20.1	34
91	Metabolic consequences of phosphotransferase (PTS) mutation in a phenylalanine-producing recombinant Escherichia coli. <i>Biotechnology Progress</i> , 1997 , 13, 768-75	2.8	32
90	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	3.7	31
89	Constraining the flux space using thermodynamics and integration of metabolomics data. <i>Methods in Molecular Biology</i> , 2014 , 1191, 49-63	1.4	31
88	Integrating computational methods to retrofit enzymes to synthetic pathways. <i>Biotechnology and Bioengineering</i> , 2012 , 109, 572-82	4.9	30
87	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	9.7	29
86	Rites of passage: requirements and standards for building kinetic models of metabolic phenotypes. <i>Current Opinion in Biotechnology</i> , 2015 , 36, 146-53	11.4	27

85	pyTFA and matTFA: a Python package and a Matlab toolbox for Thermodynamics-based Flux Analysis. <i>Bioinformatics</i> , 2019 , 35, 167-169	7.2	26
84	A model-based optimization framework for the inference on gene regulatory networks from DNA array data. <i>Bioinformatics</i> , 2004 , 20, 3221-35	7.2	26
83	Memote: A community driven effort towards a standardized genome-scale metabolic model test suite		26
82	lumpGEM: Systematic generation of subnetworks and elementally balanced lumped reactions for the biosynthesis of target metabolites. <i>PLoS Computational Biology</i> , 2017 , 13, e1005513	5	25
81	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	3.6	25
80	Bistability explains threshold phenomena in protein aggregation both in vitro and in vivo. <i>Biophysical Journal</i> , 2006 , 90, 886-95	2.9	24
79	Model-Driven Understanding of Palmitoylation Dynamics: Regulated Acylation of the Endoplasmic Reticulum Chaperone Calnexin. <i>PLoS Computational Biology</i> , 2016 , 12, e1004774	5	24
78	Tunable reporter signal production in feedback-uncoupled arsenic bioreporters. <i>Microbial Biotechnology</i> , 2013 , 6, 503-14	6.3	23
77	Thermodynamic calculations for biochemical transport and reaction processes in metabolic networks. <i>Biophysical Journal</i> , 2010 , 99, 3139-44	2.9	23
76	A design-build-test cycle using modeling and experiments reveals interdependencies between upper glycolysis and xylose uptake in recombinant and improves predictive capabilities of large-scale kinetic models. <i>Biotechnology for Biofuels</i> , 2017 , 10, 166	7.8	22
75	Modeling metabolic networks of individual bacterial agents in heterogeneous and dynamic soil habitats (IndiMeSH). <i>PLoS Computational Biology</i> , 2019 , 15, e1007127	5	21
74	A genome-scale integration and analysis of <i>Lactococcus lactis</i> translation data. <i>PLoS Computational Biology</i> , 2013 , 9, e1003240	5	21
73	A computational framework for the design of optimal protein synthesis. <i>Biotechnology and Bioengineering</i> , 2012 , 109, 2127-33	4.9	20
72	Nonlinear metabolic control analysis. <i>Metabolic Engineering</i> , 1999 , 1, 75-87	9.7	20
71	Kinetic models of metabolism that consider alternative steady-state solutions of intracellular fluxes and concentrations. <i>Metabolic Engineering</i> , 2019 , 52, 29-41	9.7	20
70	Discovery and Evaluation of Biosynthetic Pathways for the Production of Five Methyl Ethyl Ketone Precursors. <i>ACS Synthetic Biology</i> , 2018 , 7, 1858-1873	5.7	19
69	Analysis of the maximum theoretical yield for the synthesis of erythromycin precursors in <i>Escherichia coli</i> . <i>Biotechnology and Bioengineering</i> , 2006 , 95, 638-44	4.9	19
68	Exploring biochemical pathways for mono-ethylene glycol (MEG) synthesis from synthesis gas. <i>Metabolic Engineering</i> , 2017 , 41, 173-181	9.7	18

67	Quantification of Cooperativity in Heterodimer-DNA Binding Improves the Accuracy of Binding Specificity Models. <i>Journal of Biological Chemistry</i> , 2016 , 291, 10293-306	5.4	18
66	Impact of iron reduction on the metabolism of <i>Clostridium acetobutylicum</i> . <i>Environmental Microbiology</i> , 2019 , 21, 3548-3563	5.2	17
65	Large-scale kinetic metabolic models of KT2440 for consistent design of metabolic engineering strategies. <i>Biotechnology for Biofuels</i> , 2020 , 13, 33	7.8	17
64	Thermodynamics-based Metabolite Sensitivity Analysis in metabolic networks. <i>Metabolic Engineering</i> , 2017 , 39, 117-127	9.7	17
63	Studies on glycolysis II. Multiple steady states in bacterial glycolysis. <i>Chemical Engineering Science</i> , 1997 , 52, 2579-2588	4.4	17
62	Redefining solubility parameters: Bulk and surface properties from unified molecular descriptors. <i>Journal of Chemical Thermodynamics</i> , 2017 , 111, 207-220	2.9	16
61	Updated ATLAS of Biochemistry with New Metabolites and Improved Enzyme Prediction Power. <i>ACS Synthetic Biology</i> , 2020 , 9, 1479-1482	5.7	16
60	A mathematical model for the G1/S transition of the mammalian cell cycle. <i>Biotechnology Letters</i> , 1995 , 17, 669-674	3	15
59	A computational framework for integration of lipidomics data into metabolic pathways. <i>Metabolic Engineering</i> , 2014 , 23, 1-8	9.7	14
58	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, 462-70		14
57	Solvation quantities from a COSMO-RS equation of state. <i>Journal of Chemical Thermodynamics</i> , 2015 , 90, 294-309	2.9	13
56	Molecular thermodynamics of metabolism: quantum thermochemical calculations for key metabolites. <i>Physical Chemistry Chemical Physics</i> , 2015 , 17, 10438-53	3.6	13
55	Molecular thermodynamics of metabolism: hydration quantities and the equation-of-state approach. <i>Physical Chemistry Chemical Physics</i> , 2016 , 18, 32570-32592	3.6	13
54	Particle-Based Simulation Reveals Macromolecular Crowding Effects on the Michaelis-Menten Mechanism. <i>Biophysical Journal</i> , 2019 , 117, 355-368	2.9	13
53	Toward a Simple Predictive Molecular Thermodynamic Model for Bulk Phases and Interfaces. <i>Industrial & Engineering Chemistry Research</i> , 2017 , 56, 10900-10910	3.9	13
52	Functional genomics of <i>Plasmodium falciparum</i> using metabolic modelling and analysis. <i>Briefings in Functional Genomics</i> , 2013 , 12, 316-27	4.9	13
51	Mechanistic Modeling of Genetic Circuits for ArsR Arsenic Regulation. <i>ACS Synthetic Biology</i> , 2017 , 6, 862-874	5.7	12
50	A method for pulsed periodic optimization of chemical reaction systems. <i>Chemical Engineering Science</i> , 1993 , 48, 789-797	4.4	12

49	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	3.2	11
48	A computational workflow for the expansion of heterologous biosynthetic pathways to natural product derivatives. <i>Nature Communications</i> , 2021 , 12, 1760	17.4	11
47	Statistical inference in ensemble modeling of cellular metabolism. <i>PLoS Computational Biology</i> , 2019 , 15, e1007536	5	11
46	On Lewis acidity/basicity and hydrogen bonding in the equation-of-state approach. <i>Journal of Chemical Thermodynamics</i> , 2017 , 110, 3-15	2.9	10
45	Reconstruction of biological pathways and metabolic networks from in silico labeled metabolites. <i>Biotechnology Journal</i> , 2017 , 12, 1600464	5.6	10
44	Control Theory Concepts for Modeling Uncertainty in Enzyme Kinetics of Biochemical Networks. <i>Industrial & Engineering Chemistry Research</i> , 2019 , 58, 13544-13554	3.9	9
43	Analysis of human metabolism by reducing the complexity of the genome-scale models using redHUMAN. <i>Nature Communications</i> , 2020 , 11, 2821	17.4	8
42	Analysis of Translation Elongation Dynamics in the Context of an Escherichia coli Cell. <i>Biophysical Journal</i> , 2016 , 110, 2120-31	2.9	8
41	A genome-scale metabolic model of <i>Saccharomyces cerevisiae</i> that integrates expression constraints and reaction thermodynamics. <i>Nature Communications</i> , 2021 , 12, 4790	17.4	8
40	110th Anniversary: From Solubility Parameters to Predictive Equation-of-State Modeling. <i>Industrial & Engineering Chemistry Research</i> , 2019 , 58, 12787-12800	3.9	7
39	Uncertainty reduction in biochemical kinetic models: Enforcing desired model properties. <i>PLoS Computational Biology</i> , 2019 , 15, e1007242	5	6
38	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	5	5
37	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,	11.5	5
36	Noise analysis of genome-scale protein synthesis using a discrete computational model of translation. <i>Journal of Chemical Physics</i> , 2015 , 143, 044109	3.9	4
35	TEX-FBA: A constraint-based method for integrating gene expression, thermodynamics, and metabolomics data into genome-scale metabolic models		4
34	NICEdrug.ch, a workflow for rational drug design and systems-level analysis of drug metabolism. <i>ELife</i> , 2021 , 10,	8.9	4
33	Exploration of trade-offs between steady-state and dynamic properties in signaling cycles. <i>Physical Biology</i> , 2012 , 9, 045010	3	3
32	Emergence of diauxie as an optimal growth strategy under resource allocation constraints in cellular metabolism		3

31	Finding metabolic pathways in large networks through atom-conserving substrate-product pairs		3
30	Finding metabolic pathways in large networks through atom-conserving substrate-product pairs. <i>Bioinformatics</i> , 2021 ,	7.2	3
29	The solubility parameters of carbon dioxide and ionic liquids: Are they an enigma?. <i>Fluid Phase Equilibria</i> , 2021 , 527, 112828	2.5	3
28	Dynamic Radiolabeling of S-Palmitoylated Proteins. <i>Methods in Molecular Biology</i> , 2019 , 2009, 111-127	1.4	2
27	A memorial review of Jay Bailey's contribution in prokaryotic metabolic engineering. <i>Biotechnology and Bioengineering</i> , 2002 , 79, 504-8	4.9	2
26	The architecture of the endoplasmic reticulum is regulated by the reversible lipid modification of the shaping protein CLIMP-63		2
25	Enhanced flux prediction by integrating relative expression and relative metabolite abundance into thermodynamically consistent metabolic models		2
24	ETFL: A formulation for flux balance models accounting for expression, thermodynamics, and resource allocation constraints		2
23	Constraint-based metabolic control analysis for rational strain engineering. <i>Metabolic Engineering</i> , 2021 , 66, 191-203	9.7	2
22	ATLASx: a computational map for the exploration of biochemical space		2
21	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	3.6	2
20	Mechanistically consistent reduced models of synthetic gene networks. <i>Biophysical Journal</i> , 2013 , 104, 2098-109	2.9	1
19	Symbolic Kinetic Models in Python (SKiMpy): Intuitive modeling of large-scale biological kinetic models		1
18	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		1
17	Particle-based simulation reveals macromolecular crowding effects on the Michaelis-Menten mechanism		1
16	Assigning enzyme sequences to orphan and novel reactions using knowledge of substrate reactive sites		1
15	Large-scale kinetic metabolic models of <i>Pseudomonas putida</i> for a consistent design of metabolic engineering strategies		1
14	The effects of model complexity and size on metabolic flux distribution and control. Case study in <i>E. coli</i>		1

13	PhenoMapping: a protocol to map cellular phenotypes to metabolic bottlenecks, identify conditional essentiality, and curate metabolic models. <i>STAR Protocols</i> , 2021 , 2, 100280	1.4	1
12	Pathway Design 2021 , 237-257		1
11	The influence of the crowding assumptions in biofilm simulations. <i>PLoS Computational Biology</i> , 2021 , 17, e1009158	5	1
10	ARBRE: Computational resource to predict pathways towards industrially important aromatic compounds.. <i>Metabolic Engineering</i> , 2022 ,	9.7	1
9	Jay Bailey as mentor--the studentsSperspective. <i>Biotechnology and Bioengineering</i> , 2002 , 79, 484-9	4.9	0
8	Quantitative modeling of human metabolism: A call for a community effort. <i>Current Opinion in Systems Biology</i> , 2021 , 26, 109-115	3.2	0
7	Spatio-temporal modeling of the crowding conditions and metabolic variability in microbial communities. <i>PLoS Computational Biology</i> , 2021 , 17, e1009140	5	0
6	Expanding biochemical knowledge and illuminating metabolic dark matter with ATLASx.. <i>Nature Communications</i> , 2022 , 13, 1560	17.4	0
5	Computational tools and resources for designing new pathways to small molecules.. <i>Current Opinion in Biotechnology</i> , 2022 , 76, 102722	11.4	0
4	The systems engineering of cellular processes. <i>Computer Aided Chemical Engineering</i> , 2006 , 71-80	0.6	
3	Modelling molecular mechanisms within their cellular environment. <i>Journal of Biotechnology</i> , 1999 , 71, 263-265	3.7	
2	Discovery of Novel Routes for the Production of Fuels and Chemicals 2009 , 141-148		
1	Thermodynamics of Metabolic Pathways 2021 , 213-235		