Jacky L Snoep

List of Publications by Year
in descending order

137 papers	8,280 citations	87888 38 h-index	49909 87 g-index
154 all docs	154 docs citations	154 times ranked	8116 citing authors

#	Article	IF	Citations
1	The Systems Biology Graphical Notation. Nature Biotechnology, 2009, 27, 735-741.	17.5	828
2	BioModels Database: a free, centralized database of curated, published, quantitative kinetic models of biochemical and cellular systems. Nucleic Acids Research, 2006, 34, D689-D691.	14.5	661
3	Can yeast glycolysis be understood in terms of in vitro kinetics of the constituent enzymes? Testing biochemistry. FEBS Journal, 2000, 267, 5313-5329.	0.2	587
4	Minimum information requested in the annotation of biochemical models (MIRIAM). Nature Biotechnology, 2005, 23, 1509-1515.	17.5	553
5	BioModels Database: An enhanced, curated and annotated resource for published quantitative kinetic models. BMC Systems Biology, 2010, 4, 92.	3.0	467
6	The Glycolytic Flux in <i>Escherichia coli</i> Is Controlled by the Demand for ATP. Journal of Bacteriology, 2002, 184, 3909-3916.	2.2	315
7	The Steady-State Internal Redox State (NADH/NAD) Reflects the External Redox State and Is Correlated with Catabolic Adaptation in <i>Escherichia coli</i>. Journal of Bacteriology, 1999, 181, 2351-2357.	2.2	300
8	Web-based kinetic modelling using JWS Online. Bioinformatics, 2004, 20, 2143-2144.	4.1	295
9	Reproducible computational biology experiments with SED-ML - The Simulation Experiment Description Markup Language. BMC Systems Biology, 2011, 5, 198.	3.0	211
10	Metabolic engineering of lactic acid bacteria, the combined approach: kinetic modelling, metabolic control and experimental analysis The GenBank accession number for the sequence reported in this paper is AY046926.. Microbiology (United Kingdom), 2002, 148, 1003-1013.	1.8	196
11	Isolation, characterization, and physiological role of the pyruvate dehydrogenase complex and alpha-acetolactate synthase of Lactococcus lactis subsp. lactis bv. diacetylactis. Journal of Bacteriology, 1992, 174, 4838-4841.	2.2	149
12	Minimum Information About a Simulation Experiment (MIASE). PLoS Computational Biology, 2011, 7, e1001122.	3.2	133
13	Transduction of Intracellular and Intercellular Dynamics in Yeast Glycolytic Oscillations. Biophysical Journal, 2000, 78, 1145-1153.	0.5	116
14	DNA supercoiling depends on the phosphorylation potential in Escherichia coli. Molecular Microbiology, 1996, 20, 351-360.	2.5	111
15	Role of Hexose Transport in Control of Glycolytic Flux in <i>Saccharomyces cerevisiae</i>. Applied and Environmental Microbiology, 2004, 70, 5323-5330.	3.1	107
16	Towards building the silicon cell: A modular approach. BioSystems, 2006, 83, 207-216.	2.0	107
17	Construction and Characterization of an Effector Strain of Streptococcus mutans for Replacement Therapy of Dental Caries. Infection and Immunity, 2000, 68, 543-549.	2.2	104
18	FAIRDOMHub: a repository and collaboration environment for sharing systems biology research. Nucleic Acids Research, 2017, 45, D404-D407.	14.5	98

#	Article	IF	Citations
19	Identifiers for the 21st century: How to design, provision, and reuse persistent identifiers to maximize utility and impact of life science data. PLoS Biology, 2017, 15, e2001414.	5.6	97
20	DNA supercoiling inEscherichia coliis under tight and subtle homeostatic control, involving gene-expression and metabolic regulation of both topoisomeraseâ€ƒI and DNA gyrase. FEBS Journal, 2002, 269, 1662-1669.	0.2	96
21	Characterization of the Zymomonas mobilis glucose facilitator gene product (glf) in recombinant Escherichia coli: examination of transport mechanism, kinetics and the role of glucokinase in glucose transport. Molecular Microbiology, 1995, 15, 795-802.	2.5	93
22	Involvement of pyruvate dehydrogenase in product formation in pyruvate-limited anaerobic chemostat cultures of Enterococcus faecalis NCTC 775. Archives of Microbiology, 1990, 154, 50-5.	2.2	84
23	Systems biology towards life in silico: mathematics of the control of living cells. Journal of Mathematical Biology, 2009, 58, 7-34.	1.9	77
24	Control of Glycolytic Dynamics by Hexose Transport in Saccharomyces cerevisiae. Biophysical Journal, 2001, 80, 626-634.	0.5	75
25	SEEK: a systems biology data and model management platform. BMC Systems Biology, 2015, 9, 33.	3.0	75
26	Differences in sensitivity to NADH of purified pyruvate dehydrogenase complexes ofEnterococcus faecalis,Lactococcus lactis,Azotobacter vinelandiiandEscherichia coli: Implications for their activity in vivo. FEMS Microbiology Letters, 1993, 114, 279-283.	1.8	73
27	Control Analysis for Autonomously Oscillating Biochemical Networks. Biophysical Journal, 2002, 82, 99-108.	0.5	69
28	RightField: embedding ontology annotation in spreadsheets. Bioinformatics, 2011, 27, 2021-2022.	4.1	69
29	Sustained glycolytic oscillations in individual isolated yeast cells. FEBS Journal, 2012, 279, 2837-2847.	4.7	64
30	The Silicon Cell initiative: working towards a detailed kinetic description at the cellular level. Current Opinion in Biotechnology, 2005, 16, 336-343.	6.6	60
31	Harmonizing semantic annotations for computational models in biology. Briefings in Bioinformatics, 2019, 20, 540-550.	6.5	52
32	11-Oxygenated androgen precursors are the preferred substrates for aldo-keto reductase 1C3 (AKR1C3): Implications for castration resistant prostate cancer. Journal of Steroid Biochemistry and Molecular Biology, 2018, 183, 192-201.	2.5	51
33	Reconstruction of glucose uptake and phosphorylation in a glucose-negative mutant of Escherichia coli by using Zymomonas mobilis genes encoding the glucose facilitator protein and glucokinase. Journal of Bacteriology, 1994, 176, 2133-2135.	2.2	50
34	Catabolism of Branched-Chain Î±-Keto Acids in <i>Enterococcus faecalis</i> : the <i>bkd</i> Gene Cluster, Enzymes, and Metabolic Route. Journal of Bacteriology, 1999, 181, 5433-5442.	2.2	47
35	DNA supercoiling by gyrase is linked to nucleoid compaction. Molecular Biology Reports, 2002, 29, 79-82.	2.3	45
36	Restriction point control of the mammalian cell cycle via the cyclin E/Cdk2:p27 complex. FEBS Journal, 2010, 277, 357-367.	4.7	44

#	Article	IF	Citations
37	The SEEK. Methods in Enzymology, 2011, 500, 629-655.	1.0	44
38	Branched-Chain Î±-Keto Acid Catabolism via the Gene Products of the <i>bkd</i> Operon in <i>Enterococcus faecalis</i> : a New, Secreted Metabolite Serving as a Temporary Redox Sink. Journal of Bacteriology, 2000, 182, 3239-3246.	2.2	42
39	Targeting pathogen metabolism without collateral damage to the host. Scientific Reports, 2017, 7, 40406.	3.3	42
40	Effect of the energy source on the NADH/NAD ratio and on pyruvate catabolism in anaerobic chemostat cultures ofEnterococcus faecalisNCTC 775. FEMS Microbiology Letters, 1991, 81, 63-66.	1.8	41
41	Systems biology tools for toxicology. Archives of Toxicology, 2012, 86, 1251-1271.	4.2	41
42	A combined experimental and modelling approach for the Weimberg pathway optimisation. Nature Communications, 2020, 11, 1098.	12.8	41
43	Competition for phosphorus between the nitrogen-fixing cyanobacteria Anabaena and Aphanizomenon. FEMS Microbiology Ecology, 1997, 24, 259-267.	2.7	40
44	The extent to which ATP demand controls the glycolytic flux depends strongly on the organism and conditions for growth. Molecular Biology Reports, 2002, 29, 41-45.	2.3	40
45	Glucose and the ATP paradox in yeast. Biochemical Journal, 2000, 352, 593-599.	3.7	39
46	Time dependent responses of glycolytic intermediates in a detailed glycolytic model of Lactococcus lactis during glucose run-out experiments. Molecular Biology Reports, 2002, 29, 157-161.	2.3	37
47	Putting Intentions into Cell Biochemistry: An Artificial Intelligence Perspective. Journal of Theoretical Biology, 2002, 214, 105-134.	1.7	36
48	Physiological implications of class IIa bacteriocin resistance in Listeria monocytogenes strains. Microbiology (United Kingdom), 2004, 150, 335-340.	1.8	36
49	The evolution of standards and data management practices in systems biology. Molecular Systems Biology, 2015, 11, 851.	7.2	35
50	Targeting glycolysis in the malaria parasite <i>Plasmodium falciparum</i>. FEBS Journal, 2016, 283, 634-646.	4.7	35
51	Isolation and characterisation of the pyruvate dehydrogenase complex of anaerobically grown Enterococcus faecalis NCTC 775. FEBS Journal, 1992, 203, 245-250.	0.2	33
52	Allosteric regulation of phosphofructokinase controls the emergence of glycolytic oscillations in isolated yeast cells. FEBS Journal, 2014, 281, 2784-2793.	4.7	33
53	Construction and validation of a detailed kinetic model of glycolysis in <i>PlasmodiumÂfalciparum</i>. FEBS Journal, 2015, 282, 1481-1511.	4.7	33
54	Design principles of nuclear receptor signaling: how complex networking improves signal transduction. Molecular Systems Biology, 2010, 6, 446.	7.2	32

#	Article	IF	Citations
55	Emergence of the silicon human and network targeting drugs. European Journal of Pharmaceutical Sciences, 2012, 46, 190-197.	4.0	32
56	Genetic and physiological analysis of the lethal effect of L-(+)-lactate dehydrogenase deficiency in Streptococcus mutans: complementation by alcohol dehydrogenase from Zymomonas mobilis. Infection and Immunity, 1996, 64, 4319-4323.	2.2	32
57	Extensive regulation compromises the extent to which DNA gyrase controls DNA supercoiling and growth rate ofEscherichia coli. FEBS Journal, 1999, 266, 865-877.	0.2	31
58	Yeast glycolytic oscillations that are not controlled by a single oscillophore: a new definition of oscillophore strength. Journal of Theoretical Biology, 2005, 232, 385-398.	1.7	31
59	From isolation to integration, a systems biology approach for building the Silicon Cell. , 0, , 13-30.		31
60	From steadyâ€state to synchronized yeast glycolytic oscillations I: model construction. FEBS Journal, 2012, 279, 2810-2822.	4.7	30
61	Effect of culture conditions on the NADH/NAD ratio and total amounts of NAD(H) in chemostat cultures ofEnterococcus faecalisNCTC 775. FEMS Microbiology Letters, 1994, 116, 263-267.	1.8	29
62	Regulation of energy source metabolism in streptococci. Journal of Applied Microbiology, 1997, 83, 12S-19S.	3.1	29
63	Glutathione metabolism modeling: A mechanism for liver drug-robustness and a new biomarker strategy. Biochimica Et Biophysica Acta - General Subjects, 2013, 1830, 4943-4959.	2.4	28
64	Variation in pantothenate kinase type determines the pantothenamide mode of action and impacts on coenzymeÂA salvage biosynthesis. FEBS Journal, 2014, 281, 4731-4753.	4.7	28
65	The JWS online simulation database. Bioinformatics, 2017, 33, 1589-1590.	4.1	28
66	Control, responses and modularity of cellular regulatory networks: a control analysis perspective. IET Systems Biology, 2008, 2, 397-410.	1.5	27
67	Control of glycolytic flux inZymomonas mobilis by glucose 6-phosphate dehydrogenase activity. , 1996, 51, 190-197.		26
68	JWS Online Cellular Systems Modelling and Microbiology. Microbiology (United Kingdom), 2003, 149, 3045-3047.	1.8	26
69	Enzymes or redox couples? The kinetics of thioredoxin and glutaredoxin reactions in a systems biology context. Biochemical Journal, 2009, 417, 269-277.	3.7	25
70	BDI-modelling of complex intracellular dynamics. Journal of Theoretical Biology, 2008, 251, 1-23.	1.7	24
71	Evaluation of a simplified generic bi-substrate rate equation for computational systems biology. IET Systems Biology, 2006, 153, 338.	2.0	23
72	Pyruvate relieves the necessity of high induction levels of catalase and enables Campylobacter jejuni to grow under fully aerobic conditions. Letters in Applied Microbiology, 2008, 46, 377-382.	2.2	23

#	Article	IF	Citations
73	A mathematical modelling approach to assessing the reliability of biomarkers of glutathione metabolism. European Journal of Pharmaceutical Sciences, 2012, 46, 233-243.	4.0	23
74	An ffh mutant of Streptococcus mutans is viable and able to physiologically adapt to low pH in continuous culture. FEMS Microbiology Letters, 2004, 234, 315-324.	1.8	23
75	Java Web Simulation (JWS); a web based database of kinetic models. Molecular Biology Reports, 2002, 29, 259-263.	2.3	22
76	Intermediate instability at high temperature leads to low pathway efficiency for an <i>in vitro</i> reconstituted system of gluconeogenesis in <i>Sulfolobus solfataricus</i>. FEBS Journal, 2013, 280, 4666-4680.	4.7	22
77	Selectivity in Overlapping MAP Kinase Cascades. Journal of Theoretical Biology, 2002, 218, 343-354.	1.7	21
78	From steadyâ€state to synchronized yeast glycolytic oscillations II: model validation. FEBS Journal, 2012, 279, 2823-2836.	4.7	21
79	Determining Enzyme Kinetics for Systems Biology with Nuclear Magnetic Resonance Spectroscopy. Metabolites, 2012, 2, 818-843.	2.9	20
80	Metabolic control in integrated biochemical systems. FEBS Journal, 2002, 269, 4399-4408.	0.2	19
81	A comparative analysis of kinetic models of erythrocyte glycolysis. Journal of Theoretical Biology, 2008, 252, 488-496.	1.7	18
82	Tradeâ€off of dynamic fragility but not of robustness in metabolic pathways <i>inÂsilico</i>. FEBS Journal, 2013, 280, 160-173.	4.7	18
83	Quantitative aspects of glucose metabolism by Escherichia coli B/r, grown in the presence of pyrroloquinoline quinone. Antonie Van Leeuwenhoek, 1991, 60, 373-382.	1.7	16
84	Thermodynamics of complexity. The live cell. Thermochimica Acta, 1998, 309, 111-120.	2.7	15
85	Flux balance analysis for ethylene formation in genetically engineered Saccharomyces cerevisiae. IET Systems Biology, 2011, 5, 245-251.	1.5	13
86	The A-ring reduction of 11-ketotestosterone is efficiently catalysed by AKR1D1 and SRD5A2 but not SRD5A1. Journal of Steroid Biochemistry and Molecular Biology, 2020, 202, 105724.	2.5	13
87	The Silicon Cell Initiative. Current Genomics, 2004, 5, 687-697.	1.6	13
88	Energy, control and DNA structure in the living cell. Biophysical Chemistry, 1995, 55, 153-165.	2.8	12
89	The Development of Computational Biology in South Africa: Successes Achieved and Lessons Learnt. PLoS Computational Biology, 2016, 12, e1004395.	3.2	12
90	Intercellular communication induces glycolytic synchronization waves between individually oscillating cells. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2010075118.	7.1	12

#	Article	IF	Citations
91	Control analysis of trophic chains. Ecological Modelling, 2003, 168, 153-171.	2.5	11
92	Glycolysis and Flux Control. EcoSal Plus, 2005, 1, .	5.4	11
93	Heterogeneity of glycolytic oscillatory behaviour in individual yeast cells. FEBS Letters, 2014, 588, 3-7.	2.8	11
94	BioSimulators: a central registry of simulation engines and services for recommending specific tools. Nucleic Acids Research, 2022, 50, W108-W114.	14.5	11
95	Summation theorems for flux and concentration control coefficients of dynamic systems. IET Systems Biology, 2006, 153, 314.	2.0	10
96	Systems biology model databases and resources. Essays in Biochemistry, 2008, 45, 223-236.	4.7	10
97	A turbo engine with automatic transmission? How to marry chemicomotion to the subtleties and robustness of life. Biochimica Et Biophysica Acta - Bioenergetics, 2002, 1555, 75-82.	1.0	8
98	Experimental supply-demand analysis of anaerobic yeast energy metabolism. Molecular Biology Reports, 2002, 29, 203-209.	2.3	8
99	What it takes to understand and cure a living system: computational systems biology and a systems biology-driven pharmacokineticsâ€"pharmacodynamics platform. Interface Focus, 2011, 1, 16-23.	3.0	8
100	Fourth-Generation Progestins Inhibit 3Î²-Hydroxysteroid Dehydrogenase Type 2 and Modulate the Biosynthesis of Endogenous Steroids. PLoS ONE, 2016, 11, e0164170.	2.5	8
101	Workflows for optimization of enzyme cascades and whole cell catalysis based on enzyme kinetic characterization and pathway modelling. Current Opinion in Biotechnology, 2022, 74, 55-60.	6.6	8
102	Molecular biology for flux control. Biochemical Society Transactions, 1995, 23, 367-370.	3.4	7
103	Glucose and the ATP paradox in yeast. Biochemical Journal, 2000, 352, 593.	3.7	7
104	The Peculiar Glycolytic Pathway in Hyperthermophylic Archaea: Understanding Its Whims by Experimentation In Silico. International Journal of Molecular Sciences, 2017, 18, 876.	4.1	7
105	Live control of the living cell. Biochemical Society Transactions, 1999, 27, 261-264.	3.4	6
106	Semantic Data and Models Sharing in Systems Biology: The Just Enough Results Model and the SEEK Platform. Lecture Notes in Computer Science, 2013, , 212-227.	1.3	6
107	Data and model integration using JWS Online. In Silico Biology, 2007, 7, S27-35.	0.9	6
108	Experimental evidence for allosteric modifier saturation as predicted by the bi-substrate Hill equation. IET Systems Biology, 2006, 153, 342.	2.0	5

#	Article	IF	Citations
109	Phosphofructokinase controls the acetaldehyde-induced phase shift in isolated yeast glycolytic oscillators. Biochemical Journal, 2019, 476, 353-363.	3.7	5
110	How to distinguish between the vacuum cleaner and flippase mechanisms of the lmrA multi-drug transporter in Lactococcus lactis. Molecular Biology Reports, 2002, 29, 107-112.	2.3	4
111	Conditions for effective allosteric feedforward and feedback in metabolic pathways. IET Systems Biology, 2006, 153, 327.	2.0	4
112	From Silicon Cell to Silicon Human. , 2011, , 437-458.		4
113	Differences in sensitivity to NADH of purified pyruvate dehydrogenase complexes of Enterococcus faecalis, Lactococcus lactis, Azotobacter vinelandii and Escherichia coli: Implications for their activity in vivo. FEMS Microbiology Letters, 1993, 114, 279-283.	1.8	4
114	Phosphoglycerate kinase acts as a futile cycle at high temperature. Microbiology (United Kingdom), 2017, 163, 1604-1612.	1.8	4
115	ECA: control in ecosystems. Molecular Biology Reports, 2002, 29, 113-117.	2.3	3
116	Attractive Models: How to Make the Silicon Cell Relevant and Dynamic. Comparative and Functional Genomics, 2003, 4, 155-158.	2.0	3
117	Comparing the regulatory behaviour of two cooperative, reversible enzyme mechanisms. IET Systems Biology, 2006, 153, 335.	2.0	3
118	Stealthy annotation of experimental biology by spreadsheets. Concurrency Computation Practice and Experience, 2013, 25, 467-480.	2.2	3
119	Transcriptional and Metabolic Response of Wine-Related Lactiplantibacillus plantarum to Different Conditions of Aeration and Nitrogen Availability. Fermentation, 2021, 7, 68.	3.0	3
120	Effect of the energy source on the NADH/NAD ratio and on pyruvate catabolism in anaerobic chemostat cultures of Enterococcus faecalis NCTC 775. FEMS Microbiology Letters, 1991, 81, 63-66.	1.8	3
121	Data Management in Computational Systems Biology: Exploring Standards, Tools, Databases, and Packaging Best Practices. Methods in Molecular Biology, 2019, 2049, 285-314.	0.9	3
122	Is there an optimal ribosome concentration for maximal protein production?. IET Systems Biology, 2006, 153, 398.	2.0	2
123	Quantitative analysis of drug effects at the whole-body level: a case study for glucose metabolism in malaria patients. Biochemical Society Transactions, 2015, 43, 1157-1163.	3.4	2
124	Modelling the variable incorporation of aromatic amino acids in the tyrocidines and analogous cyclodecapeptides. Journal of Applied Microbiology, 2019, 127, 1665-1676.	3.1	2
125	Studying Glycolytic Oscillations in Individual Yeast Cells by Combining Fluorescence Microscopy with Microfluidics and Optical Tweezers. Current Protocols in Cell Biology, 2019, 82, e70.	2.3	2
126	Uncovering the effects of heterogeneity and parameter sensitivity on within-host dynamics of disease: malaria as a case study. BMC Bioinformatics, 2021, 22, 384.	2.6	2

#	Article	IF	Citations
127	Enhanced underground metabolism challenges life at high temperatureâ€“metabolic thermoadaptation in hyperthermophilic Archaea. Current Opinion in Systems Biology, 2022, 30, 100423.	2.6	2
128	Editorial: 12th BTK Meeting: â€˜Systems Biology: redefining BioThermoKineticsâ€™. IET Systems Biology, 2006, 153, 312.	2.0	1
129	Software tools that facilitate kinetic modelling with large data sets: an example using growth modelling in sugarcane. IET Systems Biology, 2006, 153, 385.	2.0	1
130	Computational modelling of the Î”4 and Î”5 adrenal steroidogenic pathways provides insight into hypocortisolism. Molecular and Cellular Endocrinology, 2021, 526, 111194.	3.2	1
131	Metabolic Control From The Back Benches: Biochemistry Towards Biocomplexity. , 2000, , 235-242.		1
132	Detailed Kinetic Models Using Metabolomics Data Sets. , 2005, , 215-242.		0
133	OneStop:JWS Online's access point to SBML,SBGN and MIRIAM compliant annotation. Nature Precedings, 2011, , .	0.1	0
134	SupraBiology 2014: Promoting UKâ€China collaboration on Systems Biology and High Performance Computing. Quantitative Biology, 2015, 3, 46-53.	0.5	0
135	Estimating merozoite release number and reinvasion efficiency in <i>Plasmodium falciparum</i> cell culture. Transactions of the Royal Society of South Africa, 2021, 76, 147-155.	1.1	0
136	Quantifying the Importance of Regulatory Loops in homeostatic Control Mechanisms: Hierarchical Control of DNA Supercoiling. , 2000, , 67-72.		0
137	Databases for Kinetic Models. , 2013, , 537-544.		0