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	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
2	BioSimulators: a central registry of simulation engines and services for recommending specific tools. Nucleic Acids Research, 2022, 50, W108-W114.	14.5	11
3	Enhanced underground metabolism challenges life at high temperatureâ€“metabolic thermoadaptation in hyperthermophilic Archaea. Current Opinion in Systems Biology, 2022, 30, 100423.	2.6	2
4	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
5	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
6	Transcriptional and Metabolic Response of Wine-Related Lactiplantibacillus plantarum to Different Conditions of Aeration and Nitrogen Availability. Fermentation, 2021, 7, 68.	3.0	3
7	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
8	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
9	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
10	A combined experimental and modelling approach for the Weimberg pathway optimisation. Nature Communications, 2020, 11, 1098.	12.8	41
11	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
12	Harmonizing semantic annotations for computational models in biology. Briefings in Bioinformatics, 2019, 20, 540-550.	6.5	52
13	Phosphofructokinase controls the acetaldehyde-induced phase shift in isolated yeast glycolytic oscillators. Biochemical Journal, 2019, 476, 353-363.	3.7	5
14	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
15	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
16	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
17	Targeting pathogen metabolism without collateral damage to the host. Scientific Reports, 2017, 7, 40406.	3.3	42
18	The JWS online simulation database. Bioinformatics, 2017, 33, 1589-1590.	4.1	28

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19	FAIRDOMHub: a repository and collaboration environment for sharing systems biology research. Nucleic Acids Research, 2017, 45, D404-D407.	14.5	98
20	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
21	Phosphoglycerate kinase acts as a futile cycle at high temperature. Microbiology (United Kingdom), 2017, 163, 1604-1612.	1.8	4
22	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
23	The Development of Computational Biology in South Africa: Successes Achieved and Lessons Learnt. PLoS Computational Biology, 2016, 12, e1004395.	3.2	12
24	Fourth-Generation Progestins Inhibit 3Î²-Hydroxysteroid Dehydrogenase Type 2 and Modulate the Biosynthesis of Endogenous Steroids. PLoS ONE, 2016, 11, e0164170.	2.5	8
25	Targeting glycolysis in the malaria parasite <i>Plasmodium falciparum</i>. FEBS Journal, 2016, 283, 634-646.	4.7	35
26	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
27	The evolution of standards and data management practices in systems biology. Molecular Systems Biology, 2015, 11, 851.	7.2	35
28	Construction and validation of a detailed kinetic model of glycolysis in <i>PlasmodiumÂfalciparum</i>. FEBS Journal, 2015, 282, 1481-1511.	4.7	33
29	SupraBiology 2014: Promoting UKâ€China collaboration on Systems Biology and High Performance Computing. Quantitative Biology, 2015, 3, 46-53.	0.5	0
30	SEEK: a systems biology data and model management platform. BMC Systems Biology, 2015, 9, 33.	3.0	75
31	Allosteric regulation of phosphofructokinase controls the emergence of glycolytic oscillations in isolated yeast cells. FEBS Journal, 2014, 281, 2784-2793.	4.7	33
32	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
33	Heterogeneity of glycolytic oscillatory behaviour in individual yeast cells. FEBS Letters, 2014, 588, 3-7.	2.8	11
34	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
35	Tradeâ€off of dynamic fragility but not of robustness in metabolic pathways <i>inÂsilico</i>. FEBS Journal, 2013, 280, 160-173.	4.7	18
36	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

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37	Stealthy annotation of experimental biology by spreadsheets. Concurrency Computation Practice and Experience, 2013, 25, 467-480.	2.2	3
38	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
39	Databases for Kinetic Models. , 2013, , 537-544.		0
40	Systems biology tools for toxicology. Archives of Toxicology, 2012, 86, 1251-1271.	4.2	41
41	Determining Enzyme Kinetics for Systems Biology with Nuclear Magnetic Resonance Spectroscopy. Metabolites, 2012, 2, 818-843.	2.9	20
42	Emergence of the silicon human and network targeting drugs. European Journal of Pharmaceutical Sciences, 2012, 46, 190-197.	4.0	32
43	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
44	Sustained glycolytic oscillations in individual isolated yeast cells. FEBS Journal, 2012, 279, 2837-2847.	4.7	64
45	From steadyâ€state to synchronized yeast glycolytic oscillations II: model validation. FEBS Journal, 2012, 279, 2823-2836.	4.7	21
46	From steadyâ€state to synchronized yeast glycolytic oscillations I: model construction. FEBS Journal, 2012, 279, 2810-2822.	4.7	30
47	The SEEK. Methods in Enzymology, 2011, 500, 629-655.	1.0	44
48	From Silicon Cell to Silicon Human. , 2011, , 437-458.		4
49	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
50	OneStop:JWS Online's access point to SBML,SBGN and MIRIAM compliant annotation. Nature Precedings, 2011, , .	0.1	0
51	Flux balance analysis for ethylene formation in genetically engineered Saccharomyces cerevisiae. IET Systems Biology, 2011, 5, 245-251.	1.5	13
52	Reproducible computational biology experiments with SED-ML - The Simulation Experiment Description Markup Language. BMC Systems Biology, 2011, 5, 198.	3.0	211
53	Minimum Information About a Simulation Experiment (MIASE). PLoS Computational Biology, 2011, 7, e1001122.	3.2	133
54	RightField: embedding ontology annotation in spreadsheets. Bioinformatics, 2011, 27, 2021-2022.	4.1	69

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55	BioModels Database: An enhanced, curated and annotated resource for published quantitative kinetic models. BMC Systems Biology, 2010, 4, 92.	3.0	467
56	Restriction point control of the mammalian cell cycle via the cyclin E/Cdk2:p27 complex. FEBS Journal, 2010, 277, 357-367.	4.7	44
57	Design principles of nuclear receptor signaling: how complex networking improves signal transduction. Molecular Systems Biology, 2010, 6, 446.	7.2	32
58	Systems biology towards life in silico: mathematics of the control of living cells. Journal of Mathematical Biology, 2009, 58, 7-34.	1.9	77
59	The Systems Biology Graphical Notation. Nature Biotechnology, 2009, 27, 735-741.	17.5	828
60	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
61	A comparative analysis of kinetic models of erythrocyte glycolysis. Journal of Theoretical Biology, 2008, 252, 488-496.	1.7	18
62	BDI-modelling of complex intracellular dynamics. Journal of Theoretical Biology, 2008, 251, 1-23.	1.7	24
63	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
64	Control, responses and modularity of cellular regulatory networks: a control analysis perspective. IET Systems Biology, 2008, 2, 397-410.	1.5	27
65	Systems biology model databases and resources. Essays in Biochemistry, 2008, 45, 223-236.	4.7	10
66	Data and model integration using JWS Online. In Silico Biology, 2007, 7, S27-35.	0.9	6
67	Towards building the silicon cell: A modular approach. BioSystems, 2006, 83, 207-216.	2.0	107
68	Is there an optimal ribosome concentration for maximal protein production?. IET Systems Biology, 2006, 153, 398.	2.0	2
69	Editorial: 12th BTK Meeting: â€˜Systems Biology: redefining BioThermoKineticsâ€™. IET Systems Biology, 2006, 153, 312.	2.0	1
70	Conditions for effective allosteric feedforward and feedback in metabolic pathways. IET Systems Biology, 2006, 153, 327.	2.0	4
71	Comparing the regulatory behaviour of two cooperative, reversible enzyme mechanisms. IET Systems Biology, 2006, 153, 335.	2.0	3
72	Summation theorems for flux and concentration control coefficients of dynamic systems. IET Systems Biology, 2006, 153, 314.	2.0	10

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73	Evaluation of a simplified generic bi-substrate rate equation for computational systems biology. IET Systems Biology, 2006, 153, 338.	2.0	23
74	Experimental evidence for allosteric modifier saturation as predicted by the bi-substrate Hill equation. IET Systems Biology, 2006, 153, 342.	2.0	5
75	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
76	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
77	Glycolysis and Flux Control. EcoSal Plus, 2005, 1, .	5.4	11
78	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
79	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
80	Minimum information requested in the annotation of biochemical models (MIRIAM). Nature Biotechnology, 2005, 23, 1509-1515.	17.5	553
81	Detailed Kinetic Models Using Metabolomics Data Sets. , 2005, , 215-242.		0
82	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
83	Physiological implications of class IIa bacteriocin resistance in Listeria monocytogenes strains. Microbiology (United Kingdom), 2004, 150, 335-340.	1.8	36
84	Web-based kinetic modelling using JWS Online. Bioinformatics, 2004, 20, 2143-2144.	4.1	295
85	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
86	The Silicon Cell Initiative. Current Genomics, 2004, 5, 687-697.	1.6	13
87	Control analysis of trophic chains. Ecological Modelling, 2003, 168, 153-171.	2.5	11
88	Attractive Models: How to Make the Silicon Cell Relevant and Dynamic. Comparative and Functional Genomics, 2003, 4, 155-158.	2.0	3
89	JWS Online Cellular Systems Modelling and Microbiology. Microbiology (United Kingdom), 2003, 149, 3045-3047.	1.8	26
90	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

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91	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
92	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
93	Control Analysis for Autonomously Oscillating Biochemical Networks. Biophysical Journal, 2002, 82, 99-108.	0.5	69
94	Putting Intentions into Cell Biochemistry: An Artificial Intelligence Perspective. Journal of Theoretical Biology, 2002, 214, 105-134.	1.7	36
95	Selectivity in Overlapping MAP Kinase Cascades. Journal of Theoretical Biology, 2002, 218, 343-354.	1.7	21
96	Metabolic control in integrated biochemical systems. FEBS Journal, 2002, 269, 4399-4408.	0.2	19
97	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
98	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
99	DNA supercoiling by gyrase is linked to nucleoid compaction. Molecular Biology Reports, 2002, 29, 79-82.	2.3	45
100	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
101	Java Web Simulation (JWS); a web based database of kinetic models. Molecular Biology Reports, 2002, 29, 259-263.	2.3	22
102	Experimental supply-demand analysis of anaerobic yeast energy metabolism. Molecular Biology Reports, 2002, 29, 203-209.	2.3	8
103	ECA: control in ecosystems. Molecular Biology Reports, 2002, 29, 113-117.	2.3	3
104	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
105	Control of Glycolytic Dynamics by Hexose Transport in Saccharomyces cerevisiae. Biophysical Journal, 2001, 80, 626-634.	0.5	75
106	Glucose and the ATP paradox in yeast. Biochemical Journal, 2000, 352, 593.	3.7	7
107	Glucose and the ATP paradox in yeast. Biochemical Journal, 2000, 352, 593-599.	3.7	39
108	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

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109	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
110	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
111	Transduction of Intracellular and Intercellular Dynamics in Yeast Glycolytic Oscillations. Biophysical Journal, 2000, 78, 1145-1153.	0.5	116
112	Metabolic Control From The Back Benches: Biochemistry Towards Biocomplexity. , 2000, , 235-242.		1
113	Quantifying the Importance of Regulatory Loops in homeostatic Control Mechanisms: Hierarchical Control of DNA Supercoiling. , 2000, , 67-72.		0
114	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
115	Live control of the living cell. Biochemical Society Transactions, 1999, 27, 261-264.	3.4	6
116	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
117	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
118	Thermodynamics of complexity. The live cell. Thermochimica Acta, 1998, 309, 111-120.	2.7	15
119	Competition for phosphorus between the nitrogen-fixing cyanobacteria Anabaena and Aphanizomenon. FEMS Microbiology Ecology, 1997, 24, 259-267.	2.7	40
120	Regulation of energy source metabolism in streptococci. Journal of Applied Microbiology, 1997, 83, 12S-19S.	3.1	29
121	Control of glycolytic flux inZymomonas mobilis by glucose 6-phosphate dehydrogenase activity. , 1996, 51, 190-197.		26
122	DNA supercoiling depends on the phosphorylation potential in Escherichia coli. Molecular Microbiology, 1996, 20, 351-360.	2.5	111
123	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
124	Molecular biology for flux control. Biochemical Society Transactions, 1995, 23, 367-370.	3.4	7
125	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
126	Energy, control and DNA structure in the living cell. Biophysical Chemistry, 1995, 55, 153-165.	2.8	12

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127	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
128	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
129	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
130	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
131	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
132	Isolation and characterisation of the pyruvate dehydrogenase complex of anaerobically grown Enterococcus faecalis NCTC 775. FEBS Journal, 1992, 203, 245-250.	0.2	33
133	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
134	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
135	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
136	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
137	From isolation to integration, a systems biology approach for building the Silicon Cell. , 0, , 13-30.		31