Edda Klipp

List of Publications by Year
in descending order

123 papers	6,309 citations	87888 38 h-index	79698 73 g-index
138 all docs	138 docs citations	138 times ranked	7627 citing authors

#	Article	IF	Citations
1	Minimum information requested in the annotation of biochemical models (MIRIAM). Nature Biotechnology, 2005, 23, 1509-1515.	17.5	553
2	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. Nature Biotechnology, 2008, 26, 1155-1160.	17.5	530
3	Integrative model of the response of yeast to osmotic shock. Nature Biotechnology, 2005, 23, 975-982.	17.5	408
4	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	17.5	314
5	Global Network Reorganization During Dynamic Adaptations of <i>Bacillus subtilis</i> Metabolism. Science, 2012, 335, 1099-1103.	12.6	255
6	Estimation of immune cell content in tumour tissue using single-cell RNA-seq data. Nature Communications, 2017, 8, 2032.	12.8	225
7	Global dynamic optimization approach to predict activation in metabolic pathways. BMC Systems Biology, 2014, 8, 1.	3.0	211
8	Bringing metabolic networks to life: convenience rate law and thermodynamic constraints. Theoretical Biology and Medical Modelling, 2006, 3, 41.	2.1	191
9	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
10	Mathematical modeling of intracellular signaling pathways. BMC Neuroscience, 2006, 7, S10.	1.9	119
11	Modular rate laws for enzymatic reactions: thermodynamics, elasticities and implementation. Bioinformatics, 2010, 26, 1528-1534.	4.1	110
12	Modelling the dynamics of the yeast pheromone pathway. Yeast, 2004, 21, 831-850.	1.7	107
13	Systematic Construction of Kinetic Models from Genome-Scale Metabolic Networks. PLoS ONE, 2013, 8, e79195.	2.5	102
14	Prediction of temporal gene expression. FEBS Journal, 2002, 269, 5406-5413.	0.2	98
15	Cell Size at S Phase Initiation: An Emergent Property of the G1/S Network. PLoS Computational Biology, 2007, 3, e64.	3.2	96
16	Quantitative Analysis of Glycerol Accumulation, Glycolysis and Growth under Hyper Osmotic Stress. PLoS Computational Biology, 2013, 9, e1003084.	3.2	95
17	Biophysical properties of Saccharomyces cerevisiae and their relationship with HOG pathway activation. European Biophysics Journal, 2010, 39, 1547-1556.	2.2	90
18	Annotation and merging of SBML models with semanticSBML. Bioinformatics, 2010, 26, 421-422.	4.1	88

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19	Systems biology standards—the community speaks. Nature Biotechnology, 2007, 25, 390-391.	17.5	87
20	Information theory based approaches to cellular signaling. Biochimica Et Biophysica Acta - General Subjects, 2011, 1810, 924-932.	2.4	84
21	Constraint-Based Modeling and Kinetic Analysis of the Smad Dependent TGF-β Signaling Pathway. PLoS ONE, 2007, 2, e936.	2.5	75
22	SBML-PET: a Systems Biology Markup Language-based parameter estimation tool. Bioinformatics, 2006, 22, 2704-2705.	4.1	74
23	Impact of Acute Metal Stress in Saccharomyces cerevisiae. PLoS ONE, 2014, 9, e83330.	2.5	74
24	Loss of hepatic Mboat7 leads to liver fibrosis. Gut, 2021, 70, 940-950.	12.1	73
25	Theoretical Approaches to the Evolutionary Optimization of Glycolysis. Thermodynamic and Kinetic Constraints. FEBS Journal, 1997, 243, 191-201.	0.2	70
26	Dissecting the energy metabolism in *Mycoplasma pneumoniae* through genome–scale metabolic modeling. Molecular Systems Biology, 2013, 9, 653.	7.2	69
27	Biochemical network-based drug-target prediction. Current Opinion in Biotechnology, 2010, 21, 511-516.	6.6	68
28	A Quantitative Study of the Hog1 MAPK Response to Fluctuating Osmotic Stress in Saccharomyces cerevisiae. PLoS ONE, 2010, 5, e9522.	2.5	64
29	Bringing metabolic networks to life: integration of kinetic, metabolic, and proteomic data. Theoretical Biology and Medical Modelling, 2006, 3, 42.	2.1	61
30	Phosphoproteomic analyses reveal novel cross–modulation mechanisms between two signaling pathways in yeast. Molecular Systems Biology, 2014, 10, 767.	7.2	58
31	Robustness and fragility in the yeast high osmolarity glycerol (HOG) signal–transduction pathway. Molecular Systems Biology, 2009, 5, 281.	7.2	56
32	Modelling reveals novel roles of two parallel signalling pathways and homeostatic feedbacks in yeast. Molecular Systems Biology, 2012, 8, 622.	7.2	56
33	A framework for mapping, visualisation and automatic model creation of signal–transduction networks. Molecular Systems Biology, 2012, 8, 578.	7.2	54
34	Modelling the Regulation of Thermal Adaptation in Candida albicans, a Major Fungal Pathogen of Humans. PLoS ONE, 2012, 7, e32467.	2.5	52
35	New types of experimental data shape the use of enzyme kinetics for dynamic network modeling. FEBS Journal, 2014, 281, 549-571.	4.7	51
36	Time-Dependent Quantitative Multicomponent Control of the G_1-S Network by the Stress-Activated Protein Kinase Hog1 upon Osmostress. Science Signaling, 2011, 4, ra63.	3.6	48

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37	Acclimation in plants – the Green Hub consortium. Plant Journal, 2021, 106, 23-40.	5.7	44
38	Parameter Balancing in Kinetic Models of Cell Metabolism. Journal of Physical Chemistry B, 2010, 114, 16298-16303.	2.6	43
39	A systems biological analysis links ROS metabolism to mitochondrial protein quality control. Mechanisms of Ageing and Development, 2012, 133, 331-337.	4.6	43
40	Alternative pathways as mechanism for the negative effects associated with overexpression of superoxide dismutase. Journal of Theoretical Biology, 2006, 238, 828-840.	1.7	42
41	Influence of cell shape, inhomogeneities and diffusion barriers in cell polarization models. Physical Biology, 2015, 12, 066014.	1.8	42
42	A comprehensive, mechanistically detailed, and executable model of the cell division cycle in Saccharomyces cerevisiae. Nature Communications, 2019, 10, 1308.	12.8	41
43	Nonalcoholic fatty liver disease stratification by liver lipidomics. Journal of Lipid Research, 2021, 62, 100104.	4.2	39
44	Alteration of Protein Levels during Influenza Virus H1N1 Infection in Host Cells: A Proteomic Survey of Host and Virus Reveals Differential Dynamics. PLoS ONE, 2014, 9, e94257.	2.5	38
45	Bridging the gaps in systems biology. Molecular Genetics and Genomics, 2014, 289, 727-734.	2.1	38
46	Dynamics of cell wall elasticity pattern shapes the cell during yeast mating morphogenesis. Open Biology, 2016, 6, 160136.	3.6	36
47	A Clb/Cdk1-mediated regulation of Fkh2 synchronizes CLB expression in the budding yeast cell cycle. Npj Systems Biology and Applications, 2017, 3, 7.	3.0	32
48	A modelling approach to quantify dynamic crosstalk between the pheromone and the starvation pathway in baker's yeast. FEBS Journal, 2006, 273, 3520-3533.	4.7	31
49	SBtab: a flexible table format for data exchange in systems biology. Bioinformatics, 2016, 32, 2559-2561.	4.1	31
50	Model-based inference of biochemical parameters and dynamic properties of microbial signal transduction networks. Current Opinion in Biotechnology, 2011, 22, 109-116.	6.6	30
51	Sic1 plays a role in timing and oscillatory behaviour of B-type cyclins. Biotechnology Advances, 2012, 30, 108-130.	11.7	29
52	Alternative Pathways Might Mediate Toxicity of High Concentrations of Superoxide Dismutase. Annals of the New York Academy of Sciences, 2004, 1019, 370-374.	3.8	28
53	Viral RNA Degradation and Diffusion Act as a Bottleneck for the Influenza A Virus Infection Efficiency. PLoS Computational Biology, 2016, 12, e1005075.	3.2	27
54	Modelling dynamic processes in yeast. Yeast, 2007, 24, 943-959.	1.7	26

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55	Systems Level Analysis of the Yeast Osmo-Stat. Scientific Reports, 2016, 6, 30950.	3.3	26
56	Yeast Mating and Image-Based Quantification of Spatial Pattern Formation. PLoS Computational Biology, 2014, 10, e1003690.	3.2	25
57	Bud-Localization of CLB2 mRNA Can Constitute a Growth Rate Dependent Daughter Sizer. PLoS Computational Biology, 2015, 11, e1004223.	3.2	24
58	Comprehensive mathematical model of oxidative phosphorylation valid for physiological and pathological conditions. FEBS Journal, 2017, 284, 2802-2828.	4.7	22
59	Alterations ofÂmTOR signaling impact metabolic stress resistance in colorectal carcinomas with BRAF and KRAS mutations. Scientific Reports, 2018, 8, 9204.	3.3	22
60	SBMLmerge, a system for combining biochemical network models. Genome Informatics, 2006, 17, 62-71.	0.4	21
61	Network reconstruction and validation of the Snf1/AMPK pathway in baker's yeast based on a comprehensive literature review. Npj Systems Biology and Applications, 2015, 1, 15007.	3.0	20
62	The discrepancy between data for and expectations on metabolic models: How to match experiments and computational efforts to arrive at quantitative predictions?. Current Opinion in Systems Biology, 2018, 8, 1-6.	2.6	20
63	Automated Ensemble Modeling with modelMaGe: Analyzing Feedback Mechanisms in the Sho1 Branch of the HOG Pathway. PLoS ONE, 2011, 6, e14791.	2.5	20
64	Stochastic simulation of Boolean rxncon models: towards quantitative analysis of large signaling networks. BMC Systems Biology, 2015, 9, 45.	3.0	18
65	Role of gB and pUS3 in Equine Herpesvirus 1 Transfer between Peripheral Blood Mononuclear Cells and Endothelial Cells: a Dynamic <i>In Vitro</i> Model. Journal of Virology, 2015, 89, 11899-11908.	3.4	18
66	Short-term volume and turgor regulation in yeast. Essays in Biochemistry, 2008, 45, 147-160.	4.7	18
67	Assessing the advantage of morphological changes in Candida albicans: a game theoretical study. Frontiers in Microbiology, 2014, 5, 41.	3.5	17
68	Osmolyte homeostasis controls single-cell growth rate and maximum cell size of Saccharomyces cerevisiae. Npj Systems Biology and Applications, 2019, 5, 34.	3.0	17
69	Spatial modeling of the membrane-cytosolic interface in protein kinase signal transduction. PLoS Computational Biology, 2018, 14, e1006075.	3.2	16
70	TIde: a software for the systematic scanning of drug targets in kinetic network models. BMC Bioinformatics, 2009, 10, 344.	2.6	15
71	Size homeostasis can be intrinsic to growing cell populations and explained without size sensing or signalling. FEBS Journal, 2012, 279, 4213-4230.	4.7	15
72	Mathematical Models of Mitochondrial Aging and Dynamics. Progress in Molecular Biology and Translational Science, 2014, 127, 63-92.	1.7	15

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73	Identification of 2-[4-[(4-Methoxyphenyl)methoxy]-phenyl]acetonitrile and Derivatives as Potent Oct3/4 Inducers. Journal of Medicinal Chemistry, 2015, 58, 4976-4983.	6.4	15
74	Interaction Dynamics Determine Signaling and Output Pathway Responses. Cell Reports, 2017, 19, 136-149.	6.4	15
75	Unraveling interactions of cell cycle–regulating proteins Sic1 and B–type cyclins in living yeast cells: a FLIM–FRET approach. FASEB Journal, 2012, 26, 546-554.	0.5	14
76	The game theory of Candida albicans colonization dynamics reveals host status-responsive gene expression. BMC Systems Biology, 2016, 10, 20.	3.0	14
77	Differential T cell response against BK virus regulatory and structural antigens: A viral dynamics modelling approach. PLoS Computational Biology, 2018, 14, e1005998.	3.2	13
78	Reaction-contingency based bipartite Boolean modelling. BMC Systems Biology, 2013, 7, 58.	3.0	12
79	Computational Modeling of Lipid Metabolism in Yeast. Frontiers in Molecular Biosciences, 2016, 3, 57.	3.5	11
80	General solution of the chemical master equation and modality of marginal distributions for hierarchic first-order reaction networks. Journal of Mathematical Biology, 2018, 77, 377-419.	1.9	11
81	ModelMage: a tool for automatic model generation, selection and management. Genome Informatics, 2008, 20, 52-63.	0.4	11
82	Timing matters. FEBS Letters, 2009, 583, 4013-4018.	2.8	10
83	Identification of small non–coding RNAs responsive to *GUN1* and *GUN5* related retrograde signals in *Arabidopsis thaliana*. Plant Journal, 2020, 104, 138-155.	5.7	10
84	Data Management and Modeling in Plant Biology. Frontiers in Plant Science, 2021, 12, 717958.	3.6	10
85	Zooming in on Yeast Osmoadaptation. Advances in Experimental Medicine and Biology, 2012, 736, 293-310.	1.6	10
86	A Thermodynamic Model of Monovalent Cation Homeostasis in the Yeast Saccharomyces cerevisiae. PLoS Computational Biology, 2016, 12, e1004703.	3.2	10
87	A transcriptome-wide analysis deciphers distinct roles of G1 cyclins in temporal organization of the yeast cell cycle. Scientific Reports, 2019, 9, 3343.	3.3	9
88	Control of COVID–19 Outbreaks under Stochastic Community Dynamics, Bimodality, or Limited Vaccination. Advanced Science, 2022, 9, .	11.2	9
89	Information processing in the adaptation of Saccharomyces cerevisiae to osmotic stress: an analysis of the phosphorelay system. Systems and Synthetic Biology, 2014, 8, 297-306.	1.0	8
90	EXPLORING THE EFFECT OF VARIABLE ENZYME CONCENTRATIONS IN A KINETIC MODEL OF YEAST GLYCOLYSIS. , 2008, , .		7

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91	Transcriptional timing and noise of yeast cell cycle regulators—a single cell and single molecule approach. Npj Systems Biology and Applications, 2018, 4, 17.	3.0	7
92	Information Thermodynamics for Time Series of Signal-Response Models. Entropy, 2019, 21, 177.	2.2	7
93	INSIGHTS INTO THE NETWORK CONTROLLING THE G_1/S TRANSITION IN BUDDING YEAST. , 2007, , .		7
94	ModelMage: A TOOL FOR AUTOMATIC MODEL GENERATION, SELECTION AND MANAGEMENT. , 2008, , .		6
95	The MYpop toolbox: Putting yeast stress responses in cellular context on single cell and population scales. Biotechnology Journal, 2016, 11, 1158-1168.	3.5	6
96	Monitoring cytochrome P450 activity in living hepatocytes by chromogenic substrates in response to drug treatment or during cell maturation. Archives of Toxicology, 2018, 92, 1133-1149.	4.2	6
97	What Influences DNA Replication Rate in Budding Yeast?. PLoS ONE, 2010, 5, e10203.	2.5	5
98	Dynamic Modelling of Mitochondrial Metabolism. IFAC-PapersOnLine, 2018, 51, 126-127.	0.9	5
99	Chemical Reaction Networks Possess Intrinsic, Temperature-Dependent Functionality. Entropy, 2020, 22, 117.	2.2	5
100	AUTOMATICALLY GENERATED MODEL OF A METABOLIC NETWORK. , 2007, , .		5
101	Dynamic metabolic models in context: biomass backtracking. Integrative Biology (United Kingdom), 2015, 7, 940-951.	1.3	4
102	Moonlighting proteins - an approach to systematize the concept. In Silico Biology, 2020, 13, 71-83.	0.9	4
103	Modeling indicates degradation of mRNA and protein as a potential regulation mechanisms during cold acclimation. Journal of Plant Research, 2021, 134, 873-883.	2.4	4
104	Sperm migration in the genital tract—In silico experiments identify key factors for reproductive success. PLoS Computational Biology, 2021, 17, e1009109.	3.2	4
105	Exploring the impact of osmoadaptation on glycolysis using time-varying response-coefficients. Genome Informatics, 2008, 20, 77-90.	0.4	4
106	EXPLORING THE IMPACT OF OSMOADAPTATION ON GLYCOLYSIS USING TIME-VARYING RESPONSE-COEFFICIENTS. , 2008, , .		3
107	Modeling the Dynamics of Stress Activated Protein Kinases (SAPK) in Cellular Stress Response. , 2007, , 205-224.		3
108	SensA: web-based sensitivity analysis of SBML models. Bioinformatics, 2014, 30, 2830-2831.	4.1	3

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109	Computational Lipidomics and Lipid Bioinformatics: Filling In the Blanks. Journal of Integrative Bioinformatics, 2016, 13, 34-51.	1.5	3
110	Shapes of cell signaling. Current Opinion in Systems Biology, 2021, 27, 100354.	2.6	3
111	Causal influence in linear Langevin networks without feedback. Physical Review E, 2017, 95, 042315.	2.1	2
112	Signaling pathways in context. Current Opinion in Biotechnology, 2019, 58, 155-160.	6.6	2
113	Computational Yeast Systems Biology: A Case Study for the MAP Kinase Cascade. Methods in Molecular Biology, 2011, 759, 323-343.	0.9	2
114	G1 AND G2 ARRESTS IN RESPONSE TO OSMOTIC SHOCK ARE ROBUST PROPERTIES OF THE BUDDING YEAST CELL CYCLE. , 2010, , .		2
115	Micro- and nano-tubules built from loosely and tightly rolled up thin sheets. Physical Chemistry Chemical Physics, 2016, 18, 1292-1301.	2.8	1
116	DIFFERENT GROUPS OF METABOLIC GENES CLUSTER AROUND EARLY AND LATE FIRING ORIGINS OF REPLICATION IN BUDDING YEAST. , 2010, , .		1
117	Identification of periodic attractors in Boolean networks using a priori information. PLoS Computational Biology, 2022, 18, e1009702.	3.2	1
118	STEADY STATE ANALYSIS OF SIGNAL RESPONSE IN RECEPTOR TRAFFICKING NETWORKS. , 2007, , .		0
119	Modelling the Central Carbon Metabolism of three Cancer Cells using 13C Data. IFAC-PapersOnLine, 2018, 51, 80-81.	0.9	0
120	Deep Hidden Physics Modeling of Cell Signaling Networks. Current Genomics, 2021, 22, 239-243.	1.6	0
121	GRAPHICAL ANALYSIS AND EXPERIMENTAL EVALUATION OF SACCHAROMYCES CEREVISIAE PTRK1|2 AND PBMH1|2 PROMOTER REGION. , 2010, , .		0
122	Cybrides virtuels : simuler l'influence du fond génétique mitochondrial sur le métabolisme. Les Cahiers De Myologie, 2019, , 44-46.	0.0	0
123	A yeast cell cycle model integrating stress, signaling, and physiology. FEMS Yeast Research, 0, , .	2.3	0