

Edda Klipp

List of Publications by Year in descending order

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Version: 2024-02-01

123
papers

6,309
citations

87843

38
h-index

79644

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). <i>Nature Biotechnology</i> , 2005, 23, 1509-1515.	9.4	553
2	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. <i>Nature Biotechnology</i> , 2008, 26, 1155-1160.	9.4	530
3	Integrative model of the response of yeast to osmotic shock. <i>Nature Biotechnology</i> , 2005, 23, 975-982.	9.4	408
4	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	9.4	314
5	Global Network Reorganization During Dynamic Adaptations of <i>Bacillus subtilis</i> Metabolism. <i>Science</i> , 2012, 335, 1099-1103.	6.0	255
6	Estimation of immune cell content in tumour tissue using single-cell RNA-seq data. <i>Nature Communications</i> , 2017, 8, 2032.	5.8	225
7	Global dynamic optimization approach to predict activation in metabolic pathways. <i>BMC Systems Biology</i> , 2014, 8, 1.	3.0	211
8	Bringing metabolic networks to life: convenience rate law and thermodynamic constraints. <i>Theoretical Biology and Medical Modelling</i> , 2006, 3, 41.	2.1	191
9	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	3.2	178
10	Mathematical modeling of intracellular signaling pathways. <i>BMC Neuroscience</i> , 2006, 7, S10.	0.8	119
11	Modular rate laws for enzymatic reactions: thermodynamics, elasticities and implementation. <i>Bioinformatics</i> , 2010, 26, 1528-1534.	1.8	110
12	Modelling the dynamics of the yeast pheromone pathway. <i>Yeast</i> , 2004, 21, 831-850.	0.8	107
13	Systematic Construction of Kinetic Models from Genome-Scale Metabolic Networks. <i>PLoS ONE</i> , 2013, 8, e79195.	1.1	102
14	Prediction of temporal gene expression. <i>FEBS Journal</i> , 2002, 269, 5406-5413.	0.2	98
15	Cell Size at S Phase Initiation: An Emergent Property of the G1/S Network. <i>PLoS Computational Biology</i> , 2007, 3, e64.	1.5	96
16	Quantitative Analysis of Glycerol Accumulation, Glycolysis and Growth under Hyper Osmotic Stress. <i>PLoS Computational Biology</i> , 2013, 9, e1003084.	1.5	95
17	Biophysical properties of <i>Saccharomyces cerevisiae</i> and their relationship with HOG pathway activation. <i>European Biophysics Journal</i> , 2010, 39, 1547-1556.	1.2	90
18	Annotation and merging of SBML models with semanticSBML. <i>Bioinformatics</i> , 2010, 26, 421-422.	1.8	88

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19	Systems biology standardsâ€”the community speaks. <i>Nature Biotechnology</i> , 2007, 25, 390-391.	9.4	87
20	Information theory based approaches to cellular signaling. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2011, 1810, 924-932.	1.1	84
21	Constraint-Based Modeling and Kinetic Analysis of the Smad Dependent TGF-Î² Signaling Pathway. <i>PLoS ONE</i> , 2007, 2, e936.	1.1	75
22	SBML-PET: a Systems Biology Markup Language-based parameter estimation tool. <i>Bioinformatics</i> , 2006, 22, 2704-2705.	1.8	74
23	Impact of Acute Metal Stress in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2014, 9, e83330.	1.1	74
24	Loss of hepatic Mboat7 leads to liver fibrosis. <i>Gut</i> , 2021, 70, 940-950.	6.1	73
25	Theoretical Approaches to the Evolutionary Optimization of Glycolysis. Thermodynamic and Kinetic Constraints. <i>FEBS Journal</i> , 1997, 243, 191-201.	0.2	70
26	Dissecting the energy metabolism in <i>Mycoplasma pneumoniae</i> through genome-scale metabolic modeling. <i>Molecular Systems Biology</i> , 2013, 9, 653.	3.2	69
27	Biochemical network-based drug-target prediction. <i>Current Opinion in Biotechnology</i> , 2010, 21, 511-516.	3.3	68
28	A Quantitative Study of the Hog1 MAPK Response to Fluctuating Osmotic Stress in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2010, 5, e9522.	1.1	64
29	Bringing metabolic networks to life: integration of kinetic, metabolic, and proteomic data. <i>Theoretical Biology and Medical Modelling</i> , 2006, 3, 42.	2.1	61
30	Phosphoproteomic analyses reveal novel cross-modulation mechanisms between two signaling pathways in yeast. <i>Molecular Systems Biology</i> , 2014, 10, 767.	3.2	58
31	Robustness and fragility in the yeast high osmolarity glycerol (HOG) signal transduction pathway. <i>Molecular Systems Biology</i> , 2009, 5, 281.	3.2	56
32	Modelling reveals novel roles of two parallel signalling pathways and homeostatic feedbacks in yeast. <i>Molecular Systems Biology</i> , 2012, 8, 622.	3.2	56
33	A framework for mapping, visualisation and automatic model creation of signal transduction networks. <i>Molecular Systems Biology</i> , 2012, 8, 578.	3.2	54
34	Modelling the Regulation of Thermal Adaptation in <i>Candida albicans</i> , a Major Fungal Pathogen of Humans. <i>PLoS ONE</i> , 2012, 7, e32467.	1.1	52
35	New types of experimental data shape the use of enzyme kinetics for dynamic network modeling. <i>FEBS Journal</i> , 2014, 281, 549-571.	2.2	51
36	Time-Dependent Quantitative Multicomponent Control of the G ₁ -S Network by the Stress-Activated Protein Kinase Hog1 upon Osmostress. <i>Science Signaling</i> , 2011, 4, ra63.	1.6	48

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37	Acclimation in plants – the Green Hub consortium. <i>Plant Journal</i> , 2021, 106, 23-40.	2.8	44
38	Parameter Balancing in Kinetic Models of Cell Metabolism. <i>Journal of Physical Chemistry B</i> , 2010, 114, 16298-16303.	1.2	43
39	A systems biological analysis links ROS metabolism to mitochondrial protein quality control. <i>Mechanisms of Ageing and Development</i> , 2012, 133, 331-337.	2.2	43
40	Alternative pathways as mechanism for the negative effects associated with overexpression of superoxide dismutase. <i>Journal of Theoretical Biology</i> , 2006, 238, 828-840.	0.8	42
41	Influence of cell shape, inhomogeneities and diffusion barriers in cell polarization models. <i>Physical Biology</i> , 2015, 12, 066014.	0.8	42
42	A comprehensive, mechanistically detailed, and executable model of the cell division cycle in <i>Saccharomyces cerevisiae</i> . <i>Nature Communications</i> , 2019, 10, 1308.	5.8	41
43	Nonalcoholic fatty liver disease stratification by liver lipidomics. <i>Journal of Lipid Research</i> , 2021, 62, 100104.	2.0	39
44	Alteration of Protein Levels during Influenza Virus H1N1 Infection in Host Cells: A Proteomic Survey of Host and Virus Reveals Differential Dynamics. <i>PLoS ONE</i> , 2014, 9, e94257.	1.1	38
45	Bridging the gaps in systems biology. <i>Molecular Genetics and Genomics</i> , 2014, 289, 727-734.	1.0	38
46	Dynamics of cell wall elasticity pattern shapes the cell during yeast mating morphogenesis. <i>Open Biology</i> , 2016, 6, 160136.	1.5	36
47	A Clb/Cdk1-mediated regulation of Fkh2 synchronizes CLB expression in the budding yeast cell cycle. <i>Npj Systems Biology and Applications</i> , 2017, 3, 7.	1.4	32
48	A modelling approach to quantify dynamic crosstalk between the pheromone and the starvation pathway in baker's yeast. <i>FEBS Journal</i> , 2006, 273, 3520-3533.	2.2	31
49	SBtab: a flexible table format for data exchange in systems biology. <i>Bioinformatics</i> , 2016, 32, 2559-2561.	1.8	31
50	Model-based inference of biochemical parameters and dynamic properties of microbial signal transduction networks. <i>Current Opinion in Biotechnology</i> , 2011, 22, 109-116.	3.3	30
51	Sic1 plays a role in timing and oscillatory behaviour of B-type cyclins. <i>Biotechnology Advances</i> , 2012, 30, 108-130.	6.0	29
52	Alternative Pathways Might Mediate Toxicity of High Concentrations of Superoxide Dismutase. <i>Annals of the New York Academy of Sciences</i> , 2004, 1019, 370-374.	1.8	28
53	Viral RNA Degradation and Diffusion Act as a Bottleneck for the Influenza A Virus Infection Efficiency. <i>PLoS Computational Biology</i> , 2016, 12, e1005075.	1.5	27
54	Modelling dynamic processes in yeast. <i>Yeast</i> , 2007, 24, 943-959.	0.8	26

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55	Systems Level Analysis of the Yeast Osmo-Stat. <i>Scientific Reports</i> , 2016, 6, 30950.	1.6	26
56	Yeast Mating and Image-Based Quantification of Spatial Pattern Formation. <i>PLoS Computational Biology</i> , 2014, 10, e1003690.	1.5	25
57	Bud-Localization of CLB2 mRNA Can Constitute a Growth Rate Dependent Daughter Sizer. <i>PLoS Computational Biology</i> , 2015, 11, e1004223.	1.5	24
58	Comprehensive mathematical model of oxidative phosphorylation valid for physiological and pathological conditions. <i>FEBS Journal</i> , 2017, 284, 2802-2828.	2.2	22
59	Alterations of mTOR signaling impact metabolic stress resistance in colorectal carcinomas with BRAF and KRAS mutations. <i>Scientific Reports</i> , 2018, 8, 9204.	1.6	22
60	SBMLmerge, a system for combining biochemical network models. <i>Genome Informatics</i> , 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. <i>Npj Systems Biology and Applications</i> , 2015, 1, 15007.	1.4	20
62	The discrepancy between data for and expectations on metabolic models: How to match experiments and computational efforts to arrive at quantitative predictions?. <i>Current Opinion in Systems Biology</i> , 2018, 8, 1-6.	1.3	20
63	Automated Ensemble Modeling with modelMaGe: Analyzing Feedback Mechanisms in the Sho1 Branch of the HOG Pathway. <i>PLoS ONE</i> , 2011, 6, e14791.	1.1	20
64	Stochastic simulation of Boolean rxncon models: towards quantitative analysis of large signaling networks. <i>BMC Systems Biology</i> , 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. <i>Journal of Virology</i> , 2015, 89, 11899-11908.	1.5	18
66	Short-term volume and turgor regulation in yeast. <i>Essays in Biochemistry</i> , 2008, 45, 147-160.	2.1	18
67	Assessing the advantage of morphological changes in <i>Candida albicans</i> : a game theoretical study. <i>Frontiers in Microbiology</i> , 2014, 5, 41.	1.5	17
68	Osmolyte homeostasis controls single-cell growth rate and maximum cell size of <i>Saccharomyces cerevisiae</i> . <i>Npj Systems Biology and Applications</i> , 2019, 5, 34.	1.4	17
69	Spatial modeling of the membrane-cytosolic interface in protein kinase signal transduction. <i>PLoS Computational Biology</i> , 2018, 14, e1006075.	1.5	16
70	Tlde: a software for the systematic scanning of drug targets in kinetic network models. <i>BMC Bioinformatics</i> , 2009, 10, 344.	1.2	15
71	Size homeostasis can be intrinsic to growing cell populations and explained without size sensing or signalling. <i>FEBS Journal</i> , 2012, 279, 4213-4230.	2.2	15
72	Mathematical Models of Mitochondrial Aging and Dynamics. <i>Progress in Molecular Biology and Translational Science</i> , 2014, 127, 63-92.	0.9	15

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73	Identification of 2-[4-[(4-Methoxyphenyl)methoxy]-phenyl]acetonitrile and Derivatives as Potent Oct3/4 Inducers. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 4976-4983.	2.9	15
74	Interaction Dynamics Determine Signaling and Output Pathway Responses. <i>Cell Reports</i> , 2017, 19, 136-149.	2.9	15
75	Unraveling interactions of cell cycle-regulating proteins Sic1 and B-type cyclins in living yeast cells: a FLIM-FRET approach. <i>FASEB Journal</i> , 2012, 26, 546-554.	0.2	14
76	The game theory of <i>Candida albicans</i> colonization dynamics reveals host status-responsive gene expression. <i>BMC Systems Biology</i> , 2016, 10, 20.	3.0	14
77	Differential T cell response against BK virus regulatory and structural antigens: A viral dynamics modelling approach. <i>PLoS Computational Biology</i> , 2018, 14, e1005998.	1.5	13
78	Reaction-contingency based bipartite Boolean modelling. <i>BMC Systems Biology</i> , 2013, 7, 58.	3.0	12
79	Computational Modeling of Lipid Metabolism in Yeast. <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 57.	1.6	11
80	General solution of the chemical master equation and modality of marginal distributions for hierarchic first-order reaction networks. <i>Journal of Mathematical Biology</i> , 2018, 77, 377-419.	0.8	11
81	ModelMage: a tool for automatic model generation, selection and management. <i>Genome Informatics</i> , 2008, 20, 52-63.	0.4	11
82	Timing matters. <i>FEBS Letters</i> , 2009, 583, 4013-4018.	1.3	10
83	Identification of small non-coding RNAs responsive to <i>GUN1</i> and <i>GUN5</i> related retrograde signals in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2020, 104, 138-155.	2.8	10
84	Data Management and Modeling in Plant Biology. <i>Frontiers in Plant Science</i> , 2021, 12, 717958.	1.7	10
85	Zooming in on Yeast Osmoadaptation. <i>Advances in Experimental Medicine and Biology</i> , 2012, 736, 293-310.	0.8	10
86	A Thermodynamic Model of Monovalent Cation Homeostasis in the Yeast <i>Saccharomyces cerevisiae</i> . <i>PLoS Computational Biology</i> , 2016, 12, e1004703.	1.5	10
87	A transcriptome-wide analysis deciphers distinct roles of G1 cyclins in temporal organization of the yeast cell cycle. <i>Scientific Reports</i> , 2019, 9, 3343.	1.6	9
88	Control of COVID-19 Outbreaks under Stochastic Community Dynamics, Bimodality, or Limited Vaccination. <i>Advanced Science</i> , 2022, 9, .	5.6	9
89	Information processing in the adaptation of <i>Saccharomyces cerevisiae</i> to osmotic stress: an analysis of the phosphorelay system. <i>Systems and Synthetic Biology</i> , 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. <i>Npj Systems Biology and Applications</i> , 2018, 4, 17.	1.4	7
92	Information Thermodynamics for Time Series of Signal-Response Models. <i>Entropy</i> , 2019, 21, 177.	1.1	7
93	INSIGHTS INTO THE NETWORK CONTROLLING THE G ₁ S ₁ 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. <i>Biotechnology Journal</i> , 2016, 11, 1158-1168.	1.8	6
96	Monitoring cytochrome P450 activity in living hepatocytes by chromogenic substrates in response to drug treatment or during cell maturation. <i>Archives of Toxicology</i> , 2018, 92, 1133-1149.	1.9	6
97	What Influences DNA Replication Rate in Budding Yeast?. <i>PLoS ONE</i> , 2010, 5, e10203.	1.1	5
98	Dynamic Modelling of Mitochondrial Metabolism. <i>IFAC-PapersOnLine</i> , 2018, 51, 126-127.	0.5	5
99	Chemical Reaction Networks Possess Intrinsic, Temperature-Dependent Functionality. <i>Entropy</i> , 2020, 22, 117.	1.1	5
100	AUTOMATICALLY GENERATED MODEL OF A METABOLIC NETWORK. , 2007, , .		5
101	Dynamic metabolic models in context: biomass backtracking. <i>Integrative Biology (United Kingdom)</i> , 2015, 7, 940-951.	0.6	4
102	Moonlighting proteins - an approach to systematize the concept. <i>In Silico Biology</i> , 2020, 13, 71-83.	0.4	4
103	Modeling indicates degradation of mRNA and protein as a potential regulation mechanisms during cold acclimation. <i>Journal of Plant Research</i> , 2021, 134, 873-883.	1.2	4
104	Sperm migration in the genital tract—In silico experiments identify key factors for reproductive success. <i>PLoS Computational Biology</i> , 2021, 17, e1009109.	1.5	4
105	Exploring the impact of osmoadaptation on glycolysis using time-varying response-coefficients. <i>Genome Informatics</i> , 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. <i>Bioinformatics</i> , 2014, 30, 2830-2831.	1.8	3

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109	Computational Lipidomics and Lipid Bioinformatics: Filling In the Blanks. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 34-51.	1.0	3
110	Shapes of cell signaling. <i>Current Opinion in Systems Biology</i> , 2021, 27, 100354.	1.3	3
111	Causal influence in linear Langevin networks without feedback. <i>Physical Review E</i> , 2017, 95, 042315.	0.8	2
112	Signaling pathways in context. <i>Current Opinion in Biotechnology</i> , 2019, 58, 155-160.	3.3	2
113	Computational Yeast Systems Biology: A Case Study for the MAP Kinase Cascade. <i>Methods in Molecular Biology</i> , 2011, 759, 323-343.	0.4	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. <i>Physical Chemistry Chemical Physics</i> , 2016, 18, 1292-1301.	1.3	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. <i>PLoS Computational Biology</i> , 2022, 18, e1009702.	1.5	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. <i>IFAC-PapersOnLine</i> , 2018, 51, 80-81.	0.5	0
120	Deep Hidden Physics Modeling of Cell Signaling Networks. <i>Current Genomics</i> , 2021, 22, 239-243.	0.7	0
121	GRAPHICAL ANALYSIS AND EXPERIMENTAL EVALUATION OF SACCHAROMYCES CEREVISIAE PTRK1 2 AND PBMH1 2 PROMOTER REGION. , 2010, , .		0
122	Cybrides virtuels : simuler lâ€™influence du fond gÃ©nÃ©tique mitochondrial sur le mÃ©tabolisme. <i>Les Cahiers De Myologie</i> , 2019, , 44-46.	0.0	0
123	A yeast cell cycle model integrating stress, signaling, and physiology. <i>FEMS Yeast Research</i> , 0, , .	1.1	0