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	Identification of periodic attractors in Boolean networks using a priori information. PLoS Computational Biology, 2022, 18, e1009702.	3.2	1
2	Control of COVIDâ€19 Outbreaks under Stochastic Community Dynamics, Bimodality, or Limited Vaccination. Advanced Science, 2022, 9, .	11.2	9
3	Loss of hepatic Mboat7 leads to liver fibrosis. Gut, 2021, 70, 940-950.	12.1	73
4	Nonalcoholic fatty liver disease stratification by liver lipidomics. Journal of Lipid Research, 2021, 62, 100104.	4.2	39
5	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
6	Deep Hidden Physics Modeling of Cell Signaling Networks. Current Genomics, 2021, 22, 239-243.	1.6	0
7	Sperm migration in the genital tractâ€"In silico experiments identify key factors for reproductive success. PLoS Computational Biology, 2021, 17, e1009109.	3.2	4
8	Shapes of cell signaling. Current Opinion in Systems Biology, 2021, 27, 100354.	2.6	3
9	Data Management and Modeling in Plant Biology. Frontiers in Plant Science, 2021, 12, 717958.	3.6	10
10	Acclimation in plants â€" the Green Hub consortium. Plant Journal, 2021, 106, 23-40.	5.7	44
11	Moonlighting proteins - an approach to systematize the concept. In Silico Biology, 2020, 13, 71-83.	0.9	4
12	Identification of small nonâ€coding RNAs responsive to *GUN1* and *GUN5* related retrograde signals in *Arabidopsis thaliana*. Plant Journal, 2020, 104, 138-155.	5.7	10
13	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	17.5	314
14	Chemical Reaction Networks Possess Intrinsic, Temperature-Dependent Functionality. Entropy, 2020, 22, 117.	2.2	5
15	SBML Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
16	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
17	A comprehensive, mechanistically detailed, and executable model of the cell division cycle in Saccharomyces cerevisiae. Nature Communications, 2019, 10, 1308.	12.8	41
18	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

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19	Information Thermodynamics for Time Series of Signal-Response Models. Entropy, 2019, 21, 177.	2.2	7
20	Signaling pathways in context. Current Opinion in Biotechnology, 2019, 58, 155-160.	6.6	2
21	Cybrides virtuels : simuler l'influence du fond génétique mitochondrial sur le métabolisme. Les Cahiers De Myologie, 2019, , 44-46.	0.0	0
22	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
23	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
24	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
25	Modelling the Central Carbon Metabolism of three Cancer Cells using 13C Data. IFAC-PapersOnLine, 2018, 51, 80-81.	0.9	0
26	Dynamic Modelling of Mitochondrial Metabolism. IFAC-PapersOnLine, 2018, 51, 126-127.	0.9	5
27	Spatial modeling of the membrane-cytosolic interface in protein kinase signal transduction. PLoS Computational Biology, 2018, 14, e1006075.	3.2	16
28	Alterations of mTOR signaling impact metabolic stress resistance in colorectal carcinomas with BRAF and KRAS mutations. Scientific Reports, 2018, 8, 9204.	3.3	22
29	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
30	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
31	Interaction Dynamics Determine Signaling and Output Pathway Responses. Cell Reports, 2017, 19, 136-149.	6.4	15
32	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
33	Causal influence in linear Langevin networks without feedback. Physical Review E, 2017, 95, 042315.	2.1	2
34	Estimation of immune cell content in tumour tissue using single-cell RNA-seq data. Nature Communications, 2017, 8, 2032.	12.8	225
35	Comprehensive mathematical model of oxidative phosphorylation valid for physiological and pathological conditions. FEBS Journal, 2017, 284, 2802-2828.	4.7	22
36	Computational Modeling of Lipid Metabolism in Yeast. Frontiers in Molecular Biosciences, 2016, 3, 57.	3.5	11

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37	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
38	The game theory of Candida albicans colonization dynamics reveals host status-responsive gene expression. BMC Systems Biology, 2016, 10, 20.	3.0	14
39	Dynamics of cell wall elasticity pattern shapes the cell during yeast mating morphogenesis. Open Biology, 2016, 6, 160136.	3.6	36
40	Systems Level Analysis of the Yeast Osmo-Stat. Scientific Reports, 2016, 6, 30950.	3.3	26
41	Computational Lipidomics and Lipid Bioinformatics: Filling In the Blanks. Journal of Integrative Bioinformatics, 2016, 13, 34-51.	1.5	3
42	SBtab: a flexible table format for data exchange in systems biology. Bioinformatics, 2016, 32, 2559-2561.	4.1	31
43	Micro- and nano-tubules built from loosely and tightly rolled up thin sheets. Physical Chemistry Chemical Physics, 2016, 18, 1292-1301.	2.8	1
44	A Thermodynamic Model of Monovalent Cation Homeostasis in the Yeast Saccharomyces cerevisiae. PLoS Computational Biology, 2016, 12, e1004703.	3.2	10
45	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
46	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
47	Influence of cell shape, inhomogeneities and diffusion barriers in cell polarization models. Physical Biology, 2015, 12, 066014.	1.8	42
48	Stochastic simulation of Boolean rxncon models: towards quantitative analysis of large signaling networks. BMC Systems Biology, 2015, 9, 45.	3.0	18
49	Dynamic metabolic models in context: biomass backtracking. Integrative Biology (United Kingdom), 2015, 7, 940-951.	1.3	4
50	Bud-Localization of CLB2 mRNA Can Constitute a Growth Rate Dependent Daughter Sizer. PLoS Computational Biology, 2015, 11, e1004223.	3.2	24
51	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
52	Role of gB and pUS3 in Equine Herpesvirus 1 Transfer between Peripheral Blood Mononuclear Cells and Endothelial Cells: a Dynamic *In Vitro* Model. Journal of Virology, 2015, 89, 11899-11908.	3.4	18
53	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
54	Assessing the advantage of morphological changes in Candida albicans: a game theoretical study. Frontiers in Microbiology, 2014, 5, 41.	3.5	17

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55	Phosphoproteomic analyses reveal novel cross‐modulation mechanisms between two signaling pathways in yeast. Molecular Systems Biology, 2014, 10, 767.	7.2	58
56	Yeast Mating and Image-Based Quantification of Spatial Pattern Formation. PLoS Computational Biology, 2014, 10, e1003690.	3.2	25
57	SensA: web-based sensitivity analysis of SBML models. Bioinformatics, 2014, 30, 2830-2831.	4.1	3
58	Global dynamic optimization approach to predict activation in metabolic pathways. BMC Systems Biology, 2014, 8, 1.	3.0	211
59	Bridging the gaps in systems biology. Molecular Genetics and Genomics, 2014, 289, 727-734.	2.1	38
60	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
61	New types of experimental data shape the use of enzyme kinetics for dynamic network modeling. FEBS Journal, 2014, 281, 549-571.	4.7	51
62	Mathematical Models of Mitochondrial Aging and Dynamics. Progress in Molecular Biology and Translational Science, 2014, 127, 63-92.	1.7	15
63	Impact of Acute Metal Stress in Saccharomyces cerevisiae. PLoS ONE, 2014, 9, e83330.	2.5	74
64	Reaction-contingency based bipartite Boolean modelling. BMC Systems Biology, 2013, 7, 58.	3.0	12
65	Quantitative Analysis of Glycerol Accumulation, Glycolysis and Growth under Hyper Osmotic Stress. PLoS Computational Biology, 2013, 9, e1003084.	3.2	95
66	Dissecting the energy metabolism in <i>Mycoplasma pneumoniae</i> through genome‐scale metabolic modeling. Molecular Systems Biology, 2013, 9, 653.	7.2	69
67	Systematic Construction of Kinetic Models from Genome-Scale Metabolic Networks. PLoS ONE, 2013, 8, e79195.	2.5	102
68	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
69	A framework for mapping, visualisation and automatic model creation of signal‐transduction networks. Molecular Systems Biology, 2012, 8, 578.	7.2	54
70	Global Network Reorganization During Dynamic Adaptations of <i>Bacillus subtilis</i> Metabolism. Science, 2012, 335, 1099-1103.	12.6	255
71	Sic1 plays a role in timing and oscillatory behaviour of B-type cyclins. Biotechnology Advances, 2012, 30, 108-130.	11.7	29
72	Modelling reveals novel roles of two parallel signalling pathways and homeostatic feedbacks in yeast. Molecular Systems Biology, 2012, 8, 622.	7.2	56

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73	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
74	A systems biological analysis links ROS metabolism to mitochondrial protein quality control. Mechanisms of Ageing and Development, 2012, 133, 331-337.	4.6	43
75	Zooming in on Yeast Osmoadaptation. Advances in Experimental Medicine and Biology, 2012, 736, 293-310.	1.6	10
76	Modelling the Regulation of Thermal Adaptation in Candida albicans, a Major Fungal Pathogen of Humans. PLoS ONE, 2012, 7, e32467.	2.5	52
77	Information theory based approaches to cellular signaling. Biochimica Et Biophysica Acta - General Subjects, 2011, 1810, 924-932.	2.4	84
78	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
79	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
80	Computational Yeast Systems Biology: A Case Study for the MAP Kinase Cascade. Methods in Molecular Biology, 2011, 759, 323-343.	0.9	2
81	Automated Ensemble Modeling with modelMaGe: Analyzing Feedback Mechanisms in the Sho1 Branch of the HOG Pathway. PLoS ONE, 2011, 6, e14791.	2.5	20
82	Biophysical properties of Saccharomyces cerevisiae and their relationship with HOG pathway activation. European Biophysics Journal, 2010, 39, 1547-1556.	2.2	90
83	Biochemical network-based drug-target prediction. Current Opinion in Biotechnology, 2010, 21, 511-516.	6.6	68
84	What Influences DNA Replication Rate in Budding Yeast?. PLoS ONE, 2010, 5, e10203.	2.5	5
85	Modular rate laws for enzymatic reactions: thermodynamics, elasticities and implementation. Bioinformatics, 2010, 26, 1528-1534.	4.1	110
86	Annotation and merging of SBML models with semanticSBML. Bioinformatics, 2010, 26, 421-422.	4.1	88
87	Parameter Balancing in Kinetic Models of Cell Metabolism. Journal of Physical Chemistry B, 2010, 114, 16298-16303.	2.6	43
88	DIFFERENT GROUPS OF METABOLIC GENES CLUSTER AROUND EARLY AND LATE FIRING ORIGINS OF REPLICATION IN BUDDING YEAST. , 2010, , .		1
89	G1 AND G2 ARRESTS IN RESPONSE TO OSMOTIC SHOCK ARE ROBUST PROPERTIES OF THE BUDDING YEAST CELL CYCLE. , 2010, , .		2
90	A Quantitative Study of the Hog1 MAPK Response to Fluctuating Osmotic Stress in Saccharomyces cerevisiae. PLoS ONE, 2010, 5, e9522.	2.5	64

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91	GRAPHICAL ANALYSIS AND EXPERIMENTAL EVALUATION OF SACCHAROMYCES CEREVISIAE PTRK1|2 AND PBMH1|2 PROMOTER REGION. , 2010, , .		0
92	Robustness and fragility in the yeast high osmolarity glycerol (HOG) signal‑transduction pathway. Molecular Systems Biology, 2009, 5, 281.	7.2	56
93	TIde: a software for the systematic scanning of drug targets in kinetic network models. BMC Bioinformatics, 2009, 10, 344.	2.6	15
94	Timing matters. FEBS Letters, 2009, 583, 4013-4018.	2.8	10
95	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. Nature Biotechnology, 2008, 26, 1155-1160.	17.5	530
96	EXPLORING THE IMPACT OF OSMOADAPTATION ON GLYCOLYSIS USING TIME-VARYING RESPONSE-COEFFICIENTS. , 2008, , .		3
97	EXPLORING THE EFFECT OF VARIABLE ENZYME CONCENTRATIONS IN A KINETIC MODEL OF YEAST GLYCOLYSIS. , 2008, , .		7
98	ModelMage: A TOOL FOR AUTOMATIC MODEL GENERATION, SELECTION AND MANAGEMENT. , 2008, , .		6
99	Short-term volume and turgor regulation in yeast. Essays in Biochemistry, 2008, 45, 147-160.	4.7	18
100	ModelMage: a tool for automatic model generation, selection and management. Genome Informatics, 2008, 20, 52-63.	0.4	11
101	Exploring the impact of osmoadaptation on glycolysis using time-varying response-coefficients. Genome Informatics, 2008, 20, 77-90.	0.4	4
102	Cell Size at S Phase Initiation: An Emergent Property of the G1/S Network. PLoS Computational Biology, 2007, 3, e64.	3.2	96
103	STEADY STATE ANALYSIS OF SIGNAL RESPONSE IN RECEPTOR TRAFFICKING NETWORKS. , 2007, , .		0
104	Modelling dynamic processes in yeast. Yeast, 2007, 24, 943-959.	1.7	26
105	Systems biology standards—the community speaks. Nature Biotechnology, 2007, 25, 390-391.	17.5	87
106	Modeling the Dynamics of Stress Activated Protein Kinases (SAPK) in Cellular Stress Response. , 2007, , 205-224.		3
107	INSIGHTS INTO THE NETWORK CONTROLLING THE G_1/S TRANSITION IN BUDDING YEAST. , 2007, , .		7
108	AUTOMATICALLY GENERATED MODEL OF A METABOLIC NETWORK. , 2007, , .		5

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109	Constraint-Based Modeling and Kinetic Analysis of the Smad Dependent TGF-Î² Signaling Pathway. PLoS ONE, 2007, 2, e936.	2.5	75
110	SBML-PET: a Systems Biology Markup Language-based parameter estimation tool. Bioinformatics, 2006, 22, 2704-2705.	4.1	74
111	Bringing metabolic networks to life: convenience rate law and thermodynamic constraints. Theoretical Biology and Medical Modelling, 2006, 3, 41.	2.1	191
112	Bringing metabolic networks to life: integration of kinetic, metabolic, and proteomic data. Theoretical Biology and Medical Modelling, 2006, 3, 42.	2.1	61
113	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
114	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
115	Mathematical modeling of intracellular signaling pathways. BMC Neuroscience, 2006, 7, S10.	1.9	119
116	SBMLmerge, a system for combining biochemical network models. Genome Informatics, 2006, 17, 62-71.	0.4	21
117	Integrative model of the response of yeast to osmotic shock. Nature Biotechnology, 2005, 23, 975-982.	17.5	408
118	Minimum information requested in the annotation of biochemical models (MIRIAM). Nature Biotechnology, 2005, 23, 1509-1515.	17.5	553
119	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
120	Modelling the dynamics of the yeast pheromone pathway. Yeast, 2004, 21, 831-850.	1.7	107
121	Prediction of temporal gene expression. FEBS Journal, 2002, 269, 5406-5413.	0.2	98
122	Theoretical Approaches to the Evolutionary Optimization of Glycolysis. Thermodynamic and Kinetic Constraints. FEBS Journal, 1997, 243, 191-201.	0.2	70
123	A yeast cell cycle model integrating stress, signaling, and physiology. FEMS Yeast Research, 0, , .	2.3	0