Clemens Kreutz

List of Publications by Year
in descending order

78 papers	4,848 citations	136950 32 h-index	106344 65 g-index
91 all docs	91 docs citations	91 times ranked	6388 citing authors

#	ARTICLE	IF	CITATIONS
1	Using Differentiable Programming for Flexible Statistical Modeling. American Statistician, 2022, 76, 270-279.	1.6	2
2	Preventing COVID-19 outbreaks through surveillance testing in healthcare facilities: a modelling study. BMC Infectious Diseases, 2022, 22, 105.	2.9	13
3	Optimal Experimental Design Based on Two-Dimensional Likelihood Profiles. Frontiers in Molecular Biosciences, 2022, 9, 800856.	3.5	1
4	Data-driven prediction of COVID-19 cases in Germany for decision making. BMC Medical Research Methodology, 2022, 22, 116.	3.1	7
5	Benchmarking of analysis strategies for data-independent acquisition proteomics using a large-scale dataset comprising inter-patient heterogeneity. Nature Communications, 2022, 13, 2622.	12.8	34
6	PEtab—Interoperable specification of parameter estimation problems in systems biology. PLoS Computational Biology, 2021, 17, e1008646.	3.2	55
7	Changes in Gut Microbiota after a Four-Week Intervention with Vegan vs. Meat-Rich Diets in Healthy Participants: A Randomized Controlled Trial. Microorganisms, 2021, 9, 727.	3.6	16
8	DIMA: Data-Driven Selection of an Imputation Algorithm. Journal of Proteome Research, 2021, 20, 3489-3496.	3.7	13
9	Non-pharmacological measures implemented in the setting of long-term care facilities to prevent SARS-CoV-2 infections and their consequences: a rapid review. The Cochrane Library, 2021, 2021, CD015085.	2.8	26
10	Identification of Interleukin1β as an Amplifier of Interferon alpha-induced Antiviral Responses. PLoS Pathogens, 2020, 16, e1008461.	4.7	5
11	Tail–Robust Quantile Normalization. Proteomics, 2020, 20, e2000068.	2.2	4
12	Phosphoproteomics identifies dual-site phosphorylation in an extended basophilic motif regulating FILIP1-mediated degradation of filamin-C. Communications Biology, 2020, 3, 253.	4.4	25
13	A blind and independent benchmark study for detecting differentially methylated regions in plants. Bioinformatics, 2020, 36, 3314-3321.	4.1	7
14	A New Approximation Approach for Transient Differential Equation Models. Frontiers in Physics, 2020, 8, .	2.1	9
15	Conditional deletion of Nedd4-2 in lung epithelial cells causes progressive pulmonary fibrosis in adult mice. Nature Communications, 2020, 11, 2012.	12.8	52
16	Recipes for Analysis of Molecular Networks Using the Data2Dynamics Modeling Environment. Methods in Molecular Biology, 2019, 1945, 341-362.	0.9	4
17	Optimal Paths Between Parameter Estimates in Non-linear ODE Systems Using the Nudged Elastic Band Method. Frontiers in Physics, 2019, 7, .	2.1	5
18	Guidelines for benchmarking of optimization-based approaches for fitting mathematical models. Genome Biology, 2019, 20, 281.	8.8	11

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19	Functional Proteomics of Breast Cancer Metabolism Identifies GLUL as Responder during Hypoxic Adaptation. Journal of Proteome Research, 2019, 18, 1352-1362.	3.7	9
20	Benchmark problems for dynamic modeling of intracellular processes. Bioinformatics, 2019, 35, 3073-3082.	4.1	61
21	Profile likelihood-based analyses of infectious disease models. Statistical Methods in Medical Research, 2018, 27, 1979-1998.	1.5	22
22	An easy and efficient approach for testing identifiability. Bioinformatics, 2018, 34, 1913-1921.	4.1	22
23	Resolving the Combinatorial Complexity of Smad Protein Complex Formation and Its Link to Gene Expression. Cell Systems, 2018, 6, 75-89.e11.	6.2	55
24	Quantifying post-transcriptional regulation in the development of Drosophila melanogaster. Nature Communications, 2018, 9, 4970.	12.8	63
25	BRAF V600E Mutations in Nevi and Melanocytic Tumors of Uncertain Malignant Potential. Journal of Investigative Dermatology, 2018, 138, 2489-2491.	0.7	5
26	Partial break in tolerance of NKG2Aâˆ'/LIR-1âˆ' single KIR+ NK cells early in the course of HLA-matched, KIR-mismatched hematopoietic cell transplantation. Bone Marrow Transplantation, 2017, 52, 1144-1155.	2.4	3
27	Hepatocyte Ploidy Is a Diversity Factor for Liver Homeostasis. Frontiers in Physiology, 2017, 8, 862.	2.8	35
28	L 1 regularization facilitates detection of cell type-specific parameters in dynamical systems. Bioinformatics, 2016, 32, i718-i726.	4.1	26
29	New Concepts for Evaluating the Performance of Computational Methods * *The author acknowledge financial support by the by the German Ministry of Education and Research (BMBF) via e:Bio Grant No. 031L0080.. IFAC-PapersOnLine, 2016, 49, 63-70.	0.9	19
30	Fast integration-based prediction bands for ordinary differential equation models. Bioinformatics, 2016, 32, 1204-1210.	4.1	21
31	A Thymic Epithelial Stem Cell Pool Persists throughout Ontogeny and Is Modulated by TGF-Î². Cell Reports, 2016, 17, 448-457.	6.4	12
32	Dealing with prognostic signature instability: a strategy illustrated for cardiovascular events in patients with end-stage renal disease. BMC Medical Genomics, 2016, 9, 43.	1.5	0
33	Identification of Cell Type-Specific Differences in Erythropoietin Receptor Signaling in Primary Erythroid and Lung Cancer Cells. PLoS Computational Biology, 2016, 12, e1005049.	3.2	41
34	Driving the Model to Its Limit: Profile Likelihood Based Model Reduction. PLoS ONE, 2016, 11, e0162366.	2.5	79
35	Representative Sinusoids for Hepatic Four-Scale Pharmacokinetics Simulations. PLoS ONE, 2015, 10, e0133653.	2.5	47
36	Data2Dynamics: a modeling environment tailored to parameter estimation in dynamical systems. Bioinformatics, 2015, 31, 3558-3560.	4.1	206

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37	Summary of the DREAM8 Parameter Estimation Challenge: Toward Parameter Identification for Whole-Cell Models. PLoS Computational Biology, 2015, 11, e1004096.	3.2	35
38	<scp>USP</scp> 18 lack in microglia causes destructive interferonopathy of the mouse brain. EMBO Journal, 2015, 34, 1612-1629.	7.8	178
39	Statistics for Model Calibration. Contributions in Mathematical and Computational Sciences, 2015, , 355-375.	0.3	0
40	Cause and cure of sloppiness in ordinary differential equation models. Physical Review E, 2014, 90, 023303.	2.1	27
41	PI3Kâ€‘p110â€‘alphaâ€‘subtype signalling mediates survival, proliferation and neurogenesis of cortical progenitor cells via activation of <scp>mTORC</scp>2. Journal of Neurochemistry, 2014, 130, 255-267.	3.9	55
42	Network topology and parameter estimation: from experimental design methods to gene regulatory network kinetics using a community based approach. BMC Systems Biology, 2014, 8, 13.	3.0	62
43	Profile likelihood in systems biology. FEBS Journal, 2013, 280, 2564-2571.	4.7	124
44	MeDIP coupled with a promoter tiling array as a platform to investigate global DNA methylation patterns in AML cells. Leukemia Research, 2013, 37, 102-111.	0.8	14
45	Subcellular mislocalization of the transcription factor NF-E2 in erythroid cells discriminates prefibrotic primary myelofibrosis from essential thrombocythemia. Blood, 2013, 122, 93-99.	1.4	21
46	Joining forces of Bayesian and frequentist methodology: a study for inference in the presence of non-identifiability. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2013, 371, 20110544.	3.4	94
47	Lessons Learned from Quantitative Dynamical Modeling in Systems Biology. PLoS ONE, 2013, 8, e74335.	2.5	275
48	Optimal Experiment Design, Fisher Information. , 2013, , 1576-1579.		4
49	Input. , 2013, , 1035-1036.		0
50	Observable. , 2013, , 1557-1558.		0
51	TSSiâ€"an R package for transcription start site identification from 5â€² mRNA tag data. Bioinformatics, 2012, 28, 1641-1642.	4.1	2
52	Comprehensive estimation of input signals and dynamics in biochemical reaction networks. Bioinformatics, 2012, 28, i529-i534.	4.1	33
53	Likelihood based observability analysis and confidence intervals for predictions of dynamic models. BMC Systems Biology, 2012, 6, 120.	3.0	104
54	Caspase-3 feeds back on caspase-8, Bid and XIAP in type I Fas signaling in primary mouse hepatocytes. Apoptosis: an International Journal on Programmed Cell Death, 2012, 17, 503-515.	4.9	72

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55	Experimental Design for Parameter Estimation of Gene Regulatory Networks. PLoS ONE, 2012, 7, e40052.	2.5	62
56	Division of labor by dual feedback regulators controls JAK2/STAT5 signaling over broad ligand range. Molecular Systems Biology, 2011, 7, 516.	7.2	110
57	Addressing parameter identifiability by model-based experimentation. IET Systems Biology, 2011, 5, 120-130.	1.5	126
58	Transcription factors ETF, E2F, and SP-1 are involved in cytokine-independent proliferation of murine hepatocytes. Hepatology, 2010, 52, 2127-2136.	7.3	95
59	Estimation of Gene Induction Enables a Relevance-Based Ranking of Gene Sets. Journal of Computational Biology, 2009, 16, 959-967.	1.6	4
60	Theoretical and experimental analysis links isoformâ€•specific ERK signalling to cell fate decisions. Molecular Systems Biology, 2009, 5, 334.	7.2	72
61	A novel approach for reliable microarray analysis of microdissected tumor cells from formalin-fixed and paraffin-embedded colorectal cancer resection specimens. Journal of Molecular Medicine, 2009, 87, 211-224.	3.9	38
62	Systems biology: experimental design. FEBS Journal, 2009, 276, 923-942.	4.7	220
63	Combination of immunosuppressive drugs leaves specific â€œfingerprintâ€•on gene expressionin vitro. Immunopharmacology and Immunotoxicology, 2009, 31, 283-292.	2.4	3
64	Structural and practical identifiability analysis of partially observed dynamical models by exploiting the profile likelihood. Bioinformatics, 2009, 25, 1923-1929.	4.1	1,061
65	Using Optimal Transformations and Multi-Experiment Fitting to Detect and Reduce Effects of Non-Identifiable Parameters in Non-Linear Dynamical Models. Biophysical Journal, 2009, 96, 307a.	0.5	0
66	An error model for protein quantification. Bioinformatics, 2007, 23, 2747-2753.	4.1	101
67	cDNA Microarray Analysis of Adaptive Changes after Renal Ablation in a Sclerosis-Resistant Mouse Strain. Kidney and Blood Pressure Research, 2007, 30, 377-387.	2.0	8
68	Microarray analysis reveals influence of the sesquiterpene lactone parthenolide on gene transcription profiles in human epithelial cells. Life Sciences, 2007, 80, 1608-1618.	4.3	7
69	Data-based identifiability analysis of non-linear dynamical models. Bioinformatics, 2007, 23, 2612-2618.	4.1	143
70	Genome-wide analysis of DNA copy number changes and LOH in CLL using high-density SNP arrays. Blood, 2007, 109, 1202-1210.	1.4	219
71	Dynamic Pathway Modeling: Feasibility Analysis and Optimal Experimental Design. Annals of the New York Academy of Sciences, 2007, 1115, 212-220.	3.8	13
72	Primary mouse hepatocytes for systems biology approaches: a standardized in vitro system for modelling of signal transduction pathways. IET Systems Biology, 2006, 153, 433.	2.0	122

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73	Host cell responses induced by hepatitis C virus binding. Hepatology, 2006, 43, 1326-1336.	7.3	20
74	Gene profiling of polycystic kidneys. Nephrology Dialysis Transplantation, 2006, 21, 1816-1824.	0.7	61
75	Controlling the Continuos Positive Airway Pressure-Device Using Partial Observable Markov Decision Processes. , 2005, , 273-286.		1
76	Gene expression profiling in polycythaemia vera: overexpression of transcription factor NF-E2. British Journal of Haematology, 2005, 129, 138-150.	2.5	101
77	Computational processing and error reduction strategies for standardized quantitative data in biological networks. FEBS Journal, 2005, 272, 6400-6411.	4.7	66
78	Quantitative data generation for systems biology: the impact of randomisation, calibrators and normalisers. IET Systems Biology, 2005, 152, 193.	2.0	33