

Andreas Raue

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6796954/publications.pdf>

Version: 2024-02-01

22
papers

1,919
citations

471509

17
h-index

713466

21
g-index

22
all docs

22
docs citations

22
times ranked

3003
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of Single-Cell RNA-Seq Identifies Cell-Cell Communication Associated with Tumor Characteristics. <i>Cell Reports</i> , 2018, 25, 1458-1468.e4.	6.4	315
2	Lessons Learned from Quantitative Dynamical Modeling in Systems Biology. <i>PLoS ONE</i> , 2013, 8, e74335.	2.5	275
3	Estimation of immune cell content in tumour tissue using single-cell RNA-seq data. <i>Nature Communications</i> , 2017, 8, 2032.	12.8	225
4	Covering a Broad Dynamic Range: Information Processing at the Erythropoietin Receptor. <i>Science</i> , 2010, 328, 1404-1408.	12.6	152
5	Comparison of approaches for parameter identifiability analysis of biological systems. <i>Bioinformatics</i> , 2014, 30, 1440-1448.	4.1	149
6	Division of labor by dual feedback regulators controls JAK2/STAT5 signaling over broad ligand range. <i>Molecular Systems Biology</i> , 2011, 7, 516.	7.2	110
7	Likelihood based observability analysis and confidence intervals for predictions of dynamic models. <i>BMC Systems Biology</i> , 2012, 6, 120.	3.0	104
8	Joining forces of Bayesian and frequentist methodology: a study for inference in the presence of non-identifiability. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2013, 371, 20110544.	3.4	94
9	Dynamic Mathematical Modeling of IL13-Induced Signaling in Hodgkin and Primary Mediastinal B-Cell Lymphoma Allows Prediction of Therapeutic Targets. <i>Cancer Research</i> , 2011, 71, 693-704.	0.9	82
10	Driving the Model to Its Limit: Profile Likelihood Based Model Reduction. <i>PLoS ONE</i> , 2016, 11, e0162366.	2.5	79
11	Experimental Design for Parameter Estimation of Gene Regulatory Networks. <i>PLoS ONE</i> , 2012, 7, e40052.	2.5	62
12	Modeling chemotherapy-induced stress to identify rational combination therapies in the DNA damage response pathway. <i>Science Signaling</i> , 2018, 11, .	3.6	46
13	Identification of Cell Type-Specific Differences in Erythropoietin Receptor Signaling in Primary Erythroid and Lung Cancer Cells. <i>PLoS Computational Biology</i> , 2016, 12, e1005049.	3.2	41
14	Predicting ligand-dependent tumors from multi-dimensional signaling features. <i>Npj Systems Biology and Applications</i> , 2017, 3, 27.	3.0	39
15	Antibody-mediated targeting of TNFR2 activates CD8 ⁺ T cells in mice and promotes antitumor immunity. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	39
16	Summary of the DREAM8 Parameter Estimation Challenge: Toward Parameter Identification for Whole-Cell Models. <i>PLoS Computational Biology</i> , 2015, 11, e1004096.	3.2	35
17	MM-131, a bispecific anti-Met/EpCAM mAb, inhibits HGF-dependent and HGF-independent Met signaling through concurrent binding to EpCAM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7533-7542.	7.1	26
18	Disentangling the Complexity of HGF Signaling by Combining Qualitative and Quantitative Modeling. <i>PLoS Computational Biology</i> , 2015, 11, e1004192.	3.2	15

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19	IL-1 β -induced and p38MAPK-dependent activation of the mitogen-activated protein kinase-activated protein kinase 2 (MK2) in hepatocytes: Signal transduction with robust and concentration-independent signal amplification. <i>Journal of Biological Chemistry</i> , 2017, 292, 6291-6302.	3.4	14
20	Model calibration and uncertainty analysis in signaling networks. <i>Current Opinion in Biotechnology</i> , 2016, 39, 143-149.	6.6	13
21	Recipes for Analysis of Molecular Networks Using the Data2Dynamics Modeling Environment. <i>Methods in Molecular Biology</i> , 2019, 1945, 341-362.	0.9	4
22	Predicting Tumor Growth and Ligand Dependence from mRNA by Combining Machine Learning with Mechanistic Modeling. <i>Methods in Pharmacology and Toxicology</i> , 2018, , 1.	0.2	0