Andreas Raue

List of Publications by Year
in descending order

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	Antibody-mediated targeting of TNFR2 activates CD8 [+] T cells in mice and promotes antitumor immunity. Science Translational Medicine, 2019, 11, .	12.4	39
2	MM-131, a bispecific anti-Met/EpCAM mAb, inhibits HGF-dependent and HGF-independent Met signaling through concurrent binding to EpCAM. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7533-7542.	7.1	26
3	Recipes for Analysis of Molecular Networks Using the Data2Dynamics Modeling Environment. Methods in Molecular Biology, 2019, 1945, 341-362.	0.9	4
4	Analysis of Single-Cell RNA-Seq Identifies Cell-Cell Communication Associated with Tumor Characteristics. Cell Reports, 2018, 25, 1458-1468.e4.	6.4	315
5	Predicting Tumor Growth and Ligand Dependence from mRNA by Combining Machine Learning with Mechanistic Modeling. Methods in Pharmacology and Toxicology, 2018, , 1.	0.2	0
6	Modeling chemotherapy-induced stress to identify rational combination therapies in the DNA damage response pathway. Science Signaling, 2018, 11, .	3.6	46
7	IL-1β-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. Journal of Biological Chemistry, 2017, 292, 6291-6302.	3.4	14
8	Predicting ligand-dependent tumors from multi-dimensional signaling features. Npj Systems Biology and Applications, 2017, 3, 27.	3.0	39
9	Estimation of immune cell content in tumour tissue using single-cell RNA-seq data. Nature Communications, 2017, 8, 2032.	12.8	225
10	Model calibration and uncertainty analysis in signaling networks. Current Opinion in Biotechnology, 2016, 39, 143-149.	6.6	13
11	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
12	Driving the Model to Its Limit: Profile Likelihood Based Model Reduction. PLoS ONE, 2016, 11, e0162366.	2.5	79
13	Disentangling the Complexity of HGF Signaling by Combining Qualitative and Quantitative Modeling. PLoS Computational Biology, 2015, 11, e1004192.	3.2	15
14	Summary of the DREAM8 Parameter Estimation Challenge: Toward Parameter Identification for Whole-Cell Models. PLoS Computational Biology, 2015, 11, e1004096.	3.2	35
15	Comparison of approaches for parameter identifiability analysis of biological systems. Bioinformatics, 2014, 30, 1440-1448.	4.1	149
16	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
17	Lessons Learned from Quantitative Dynamical Modeling in Systems Biology. PLoS ONE, 2013, 8, e74335.	2.5	275
18	Likelihood based observability analysis and confidence intervals for predictions of dynamic models. BMC Systems Biology, 2012, 6, 120.	3.0	104

#	Article	IF	Citations
19	Experimental Design for Parameter Estimation of Gene Regulatory Networks. PLoS ONE, 2012, 7, e40052.	2.5	62
20	Dynamic Mathematical Modeling of IL13-Induced Signaling in Hodgkin and Primary Mediastinal B-Cell Lymphoma Allows Prediction of Therapeutic Targets. Cancer Research, 2011, 71, 693-704.	0.9	82
21	Division of labor by dual feedback regulators controls JAK2/STAT5 signaling over broad ligand range. Molecular Systems Biology, 2011, 7, 516.	7.2	110
22	Covering a Broad Dynamic Range: Information Processing at the Erythropoietin Receptor. Science, 2010, 328, 1404-1408.	12.6	152