Marcel Schilling

List of Publications by Year
in descending order

33 papers	2,718 citations	471509 17 h-index	454955 30 g-index
36 all docs	36 docs citations	36 times ranked	3245 citing authors

#	Article	IF	Citations
1	Structural and practical identifiability analysis of partially observed dynamical models by exploiting the profile likelihood. Bioinformatics, 2009, 25, 1923-1929.	4.1	1,061
2	Lessons Learned from Quantitative Dynamical Modeling in Systems Biology. PLoS ONE, 2013, 8, e74335.	2.5	275
3	Data2Dynamics: a modeling environment tailored to parameter estimation in dynamical systems. Bioinformatics, 2015, 31, 3558-3560.	4.1	206
4	Facilitation of mRNA Deadenylation and Decay by the Exosome-Bound, DExH Protein RHAU. Molecular Cell, 2004, 13, 101-111.	9.7	170
5	Covering a Broad Dynamic Range: Information Processing at the Erythropoietin Receptor. Science, 2010, 328, 1404-1408.	12.6	152
6	Division of labor by dual feedback regulators controls JAK2/STAT5 signaling over broad ligand range. Molecular Systems Biology, 2011, 7, 516.	7.2	110
7	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
8	Theoretical and experimental analysis links isoform-specific ERK signalling to cell fate decisions. Molecular Systems Biology, 2009, 5, 334.	7.2	72
9	Protein abundance of AKT and ERK pathway components governs cell type-specific regulation of proliferation. Molecular Systems Biology, 2017, 13, 904.	7.2	72
10	Computational processing and error reduction strategies for standardized quantitative data in biological networks. FEBS Journal, 2005, 272, 6400-6411.	4.7	66
11	Predictive mathematical models of cancer signalling pathways. Journal of Internal Medicine, 2012, 271, 155-165.	6.0	56
12	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
13	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
14	Disentangling molecular mechanisms regulating sensitization of interferon alpha signal transduction. Molecular Systems Biology, 2020, 16, e8955.	7.2	41
15	Identification of Isoform-Specific Dynamics in Phosphorylation-Dependent STAT5 Dimerization by Quantitative Mass Spectrometry and Mathematical Modeling. Journal of Proteome Research, 2014, 13, 5685-5694.	3.7	38
16	Quantitative data generation for systems biology: the impact of randomisation, calibrators and normalisers. IET Systems Biology, 2005, 152, 193.	2.0	33
17	Standardizing experimental protocols. Current Opinion in Biotechnology, 2008, 19, 354-359.	6.6	20
18	T160-phosphorylated CDK2 defines threshold for HGF-dependent proliferation in primary hepatocytes. Molecular Systems Biology, 2015, 11, 795.	7.2	19

#	Article	IF	Citations
19	Model Based Targeting of IL-6-Induced Inflammatory Responses in Cultured Primary Hepatocytes to Improve Application of the JAK Inhibitor Ruxolitinib. Frontiers in Physiology, 2017, 8, 775.	2.8	19
20	Model-based identification of TNFα-induced IKKβ-mediated and IκBα-mediated regulation of NFκB signal transduction as a tool to quantify the impact of drug-induced liver injury compounds. Npj Systems Biology and Applications, 2018, 4, 23.	3.0	19
21	Cellular ERK Phospho-Form Profiles with Conserved Preference for a Switch-Like Pattern. Journal of Proteome Research, 2013, 12, 637-646.	3.7	18
22	Context-specific flow through the MEK/ERK module produces cell- and ligand-specific patterns of ERK single and double phosphorylation. Science Signaling, 2016, 9, ra13.	3.6	18
23	Short‐term information processing, long‐term responses: Insights by mathematical modeling of signal transduction. BioEssays, 2012, 34, 542-550.	2.5	16
24	Disentangling the Complexity of HGF Signaling by Combining Qualitative and Quantitative Modeling. PLoS Computational Biology, 2015, 11, e1004192.	3.2	15
25	Expression ratio of the TGFβ-inducible gene MYO10 is prognostic for overall survival of squamous cell lung cancer patients and predicts chemotherapy response. Scientific Reports, 2018, 8, 9517.	3.3	11
26	Cell-to-cell variability in JAK2/STAT5 pathway components and cytoplasmic volumes defines survival threshold in erythroid progenitor cells. Cell Reports, 2021, 36, 109507.	6.4	10
27	In silico labeling reveals the time-dependent label half-life and transit-time in dynamical systems. BMC Systems Biology, 2012, 6, 13.	3.0	6
28	MSPypeline: a python package for streamlined data analysis of mass spectrometry-based proteomics. Bioinformatics Advances, 2022, 2, .	2.4	6
29	Identification of Interleukin1β as an Amplifier of Interferon alpha-induced Antiviral Responses. PLoS Pathogens, 2020, 16, e1008461.	4.7	5
30	Deciphering signal transduction networks in the liver by mechanistic mathematical modelling. Biochemical Journal, 2022, 479, 1361-1374.	3.7	4
31	Biological Foundations of Signal Transduction, Systems Biology and Aberrations in Disease. , 2014, , 45-64.		1
32	Mathematical modeling of hematological malignancies. Frontiers in Bioscience - Elite, 2012, E4, 1648.	1.8	0
33	Prediction of Pathway Desensitization by Mathematical Modeling of IFNα Signal Transduction. Zeitschrift Fur Gastroenterologie, 2019, 57, .	0.5	0