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	MSPypeline: a python package for streamlined data analysis of mass spectrometry-based proteomics. Bioinformatics Advances, 2022, 2, .	2.4	6
2	Deciphering signal transduction networks in the liver by mechanistic mathematical modelling. Biochemical Journal, 2022, 479, 1361-1374.	3.7	4
3	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
4	Identification of Interleukin1Î² as an Amplifier of Interferon alpha-induced Antiviral Responses. PLoS Pathogens, 2020, 16, e1008461.	4.7	5
5	Disentangling molecular mechanisms regulating sensitization of interferon alpha signal transduction. Molecular Systems Biology, 2020, 16, e8955.	7.2	41
6	Prediction of Pathway Desensitization by Mathematical Modeling of IFNÎ± Signal Transduction. Zeitschrift Fur Gastroenterologie, 2019, 57, .	0.5	0
7	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
8	Expression ratio of the TGFÎ²-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
9	Model-based identification of TNFÎ±-induced IKKÎ²-mediated and IÎºBÎ±-mediated regulation of NFÎºB 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
10	Protein abundance of AKT and ERK pathway components governs cell type–specific regulation ofÂproliferation. Molecular Systems Biology, 2017, 13, 904.	7.2	72
11	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
12	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
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 the Complexity of HGF Signaling by Combining Qualitative and Quantitative Modeling. PLoS Computational Biology, 2015, 11, e1004192.	3.2	15
15	Data2Dynamics: a modeling environment tailored to parameter estimation in dynamical systems. Bioinformatics, 2015, 31, 3558-3560.	4.1	206
16	T160â€phosphorylated <scp>CDK</scp>2 defines threshold for <scp>HGF</scp>â€dependent proliferation in primary hepatocytes. Molecular Systems Biology, 2015, 11, 795.	7.2	19
17	Biological Foundations of Signal Transduction, Systems Biology and Aberrations in Disease. , 2014, , 45-64.		1
18	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

#	ARTICLE	IF	CITATIONS
19	Cellular ERK Phospho-Form Profiles with Conserved Preference for a Switch-Like Pattern. Journal of Proteome Research, 2013, 12, 637-646.	3.7	18
20	Lessons Learned from Quantitative Dynamical Modeling in Systems Biology. PLoS ONE, 2013, 8, e74335.	2.5	275
21	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
22	Mathematical modeling of hematological malignancies. Frontiers in Bioscience - Elite, 2012, E4, 1648.	1.8	0
23	Short-term information processing, long-term responses: Insights by mathematical modeling of signal transduction. BioEssays, 2012, 34, 542-550.	2.5	16
24	Predictive mathematical models of cancer signalling pathways. Journal of Internal Medicine, 2012, 271, 155-165.	6.0	56
25	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
26	Division of labor by dual feedback regulators controls JAK2/STAT5 signaling over broad ligand range. Molecular Systems Biology, 2011, 7, 516.	7.2	110
27	Covering a Broad Dynamic Range: Information Processing at the Erythropoietin Receptor. Science, 2010, 328, 1404-1408.	12.6	152
28	Theoretical and experimental analysis links isoform-specific ERK signalling to cell fate decisions. Molecular Systems Biology, 2009, 5, 334.	7.2	72
29	Structural and practical identifiability analysis of partially observed dynamical models by exploiting the profile likelihood. Bioinformatics, 2009, 25, 1923-1929.	4.1	1,061
30	Standardizing experimental protocols. Current Opinion in Biotechnology, 2008, 19, 354-359.	6.6	20
31	Computational processing and error reduction strategies for standardized quantitative data in biological networks. FEBS Journal, 2005, 272, 6400-6411.	4.7	66
32	Quantitative data generation for systems biology: the impact of randomisation, calibrators and normalisers. IET Systems Biology, 2005, 152, 193.	2.0	33
33	Facilitation of mRNA Deadenylation and Decay by the Exosome-Bound, DExH Protein RHAU. Molecular Cell, 2004, 13, 101-111.	9.7	170