

Mario Niepel

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

5,054
citations

147801

31
h-index

254184

43
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54
all docs

54
docs citations

54
times ranked

8919
citing authors

#	ARTICLE	IF	CITATIONS
1	Growth rate inhibition metrics correct for confounders in measuring sensitivity to cancer drugs. <i>Nature Methods</i> , 2016, 13, 521-527.	19.0	489
2	The nuclear pore complex: bridging nuclear transport and gene regulation. <i>Nature Reviews Molecular Cell Biology</i> , 2010, 11, 490-501.	37.0	473
3	Input-output behavior of ErbB signaling pathways as revealed by a mass action model trained against dynamic data. <i>Molecular Systems Biology</i> , 2009, 5, 239.	7.2	332
4	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. <i>Cell Systems</i> , 2018, 6, 13-24.	6.2	327
5	Discovery of Potent and Selective Covalent Inhibitors of JNK. <i>Chemistry and Biology</i> , 2012, 19, 140-154.	6.0	286
6	LINCS Canvas Browser: interactive web app to query, browse and interrogate LINCS L1000 gene expression signatures. <i>Nucleic Acids Research</i> , 2014, 42, W449-W460.	14.5	280
7	Classic and contemporary approaches to modeling biochemical reactions. <i>Genes and Development</i> , 2010, 24, 1861-1875.	5.9	255
8	L1000CDS2: LINCS L1000 characteristic direction signatures search engine. <i>Npj Systems Biology and Applications</i> , 2016, 2, .	3.0	250
9	Non-genetic cell-to-cell variability and the consequences for pharmacology. <i>Current Opinion in Chemical Biology</i> , 2009, 13, 556-561.	6.1	200
10	Discovering causal pathways linking genomic events to transcriptional states using Tied Diffusion Through Interacting Events (TieDIE). <i>Bioinformatics</i> , 2013, 29, 2757-2764.	4.1	189
11	Characterization of Torin2, an ATP-Competitive Inhibitor of mTOR, ATM, and ATR. <i>Cancer Research</i> , 2013, 73, 2574-2586.	0.9	170
12	ADP-ribosyltransferases, an update on function and nomenclature. <i>FEBS Journal</i> , 2022, 289, 7399-7410.	4.7	150
13	Conservation of protein abundance patterns reveals the regulatory architecture of the EGFR-MAPK pathway. <i>Science Signaling</i> , 2016, 9, rs6.	3.6	119
14	The nuclear basket proteins Mlp1p and Mlp2p are part of a dynamic interactome including Esc1p and the proteasome. <i>Molecular Biology of the Cell</i> , 2013, 24, 3920-3938.	2.1	100
15	A Multi-center Study on the Reproducibility of Drug-Response Assays in Mammalian Cell Lines. <i>Cell Systems</i> , 2019, 9, 35-48.e5.	6.2	95
16	Profiles of Basal and Stimulated Receptor Signaling Networks Predict Drug Response in Breast Cancer Lines. <i>Science Signaling</i> , 2013, 6, ra84.	3.6	90
17	Kinome-wide Selectivity Profiling of ATP-competitive Mammalian Target of Rapamycin (mTOR) Inhibitors and Characterization of Their Binding Kinetics. <i>Journal of Biological Chemistry</i> , 2012, 287, 9742-9752.	3.4	89
18	A Cell Cycle Phosphoproteome of the Yeast Centrosome. <i>Science</i> , 2011, 332, 1557-1561.	12.6	88

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19	Systematic analysis of $\langle \text{scp} \rangle \text{BRAF}^V \langle / \text{scp} \rangle \langle \text{sup} \rangle 600E \langle / \text{sup} \rangle$ melanomas reveals a role for $\langle \text{scp} \rangle \text{JNK} \langle / \text{scp} \rangle$ pathway in adaptive resistance to drug-induced apoptosis. <i>Molecular Systems Biology</i> , 2015, 11, 797.	7.2	84
20	The nuclear pore complex-associated protein, Mlp2p, binds to the yeast spindle pole body and promotes its efficient assembly. <i>Journal of Cell Biology</i> , 2005, 170, 225-235.	5.2	81
21	Common and cell-type specific responses to anti-cancer drugs revealed by high throughput transcript profiling. <i>Nature Communications</i> , 2017, 8, 1186.	12.8	78
22	PARP7 negatively regulates the type I interferon response in cancer cells and its inhibition triggers antitumor immunity. <i>Cancer Cell</i> , 2021, 39, 1214-1226.e10.	16.8	72
23	Identification and Characterization of the Functional Elements within the Tobacco Etch Virus 5' Leader Required for Cap-Independent Translation. <i>Journal of Virology</i> , 1999, 73, 9080-9088.	3.4	71
24	Alternative drug sensitivity metrics improve preclinical cancer pharmacogenomics. <i>Nature Biotechnology</i> , 2017, 35, 500-502.	17.5	68
25	Adaptive informatics for multifactorial and high-content biological data. <i>Nature Methods</i> , 2011, 8, 487-492.	19.0	65
26	GRcalculator: an online tool for calculating and mining dose-response data. <i>BMC Cancer</i> , 2017, 17, 698.	2.6	64
27	Dissecting Variability in Responses to Cancer Chemotherapy Through Systems Pharmacology. <i>Clinical Pharmacology and Therapeutics</i> , 2010, 88, 34-38.	4.7	59
28	Enabling drug discovery for the PARP protein family through the detection of mono-ADP-ribosylation. <i>Biochemical Pharmacology</i> , 2019, 167, 97-106.	4.4	38
29	A potent and selective PARP14 inhibitor decreases protumor macrophage gene expression and elicits inflammatory responses in tumor explants. <i>Cell Chemical Biology</i> , 2021, 28, 1158-1168.e13.	5.2	37
30	The role of 5'-leader length, secondary structure and PABP concentration on cap and poly(A) tail function during translation in <i>Xenopus</i> oocytes. <i>Nucleic Acids Research</i> , 2000, 28, 2943-2953.	14.5	36
31	Secondary structure in the 5'-leader or 3'-untranslated region reduces protein yield but does not affect the functional interaction between the 5'-cap and the poly(A) tail. <i>FEBS Letters</i> , 1999, 462, 79-84.	2.8	34
32	Analysis of growth factor signaling in genetically diverse breast cancer lines. <i>BMC Biology</i> , 2014, 12, 20.	3.8	34
33	Quantification of sensitivity and resistance of breast cancer cell lines to anti-cancer drugs using GR metrics. <i>Scientific Data</i> , 2017, 4, 170166.	5.3	34
34	Measuring Cancer Drug Sensitivity and Resistance in Cultured Cells. <i>Current Protocols in Chemical Biology</i> , 2017, 9, 55-74.	1.7	31
35	Mass Spectrometry Based Method to Increase Throughput for Kinome Analyses Using ATP Probes. <i>Analytical Chemistry</i> , 2013, 85, 4666-4674.	6.5	30
36	Designing Drug-Response Experiments and Quantifying their Results. <i>Current Protocols in Chemical Biology</i> , 2017, 9, 96-116.	1.7	30

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37	Maximum Entropy Framework for Predictive Inference of Cell Population Heterogeneity and Responses in Signaling Networks. <i>Cell Systems</i> , 2020, 10, 204-212.e8.	6.2	26
38	Torin2 Exploits Replication and Checkpoint Vulnerabilities to Cause Death of PI3K-Activated Triple-Negative Breast Cancer Cells. <i>Cell Systems</i> , 2020, 10, 66-81.e11.	6.2	26
39	Receptor-based mechanism of relative sensing and cell memory in mammalian signaling networks. <i>ELife</i> , 2020, 9, .	6.0	24
40	InÂVitro and Cellular Probes to Study PARP Enzyme Target Engagement. <i>Cell Chemical Biology</i> , 2020, 27, 877-887.e14.	5.2	18
41	Targeted Degradation of PARP14 Using a Heterobifunctional Small Molecule. <i>ChemBioChem</i> , 2021, 22, 2107-2110.	2.6	12
42	Selective Pharmaceutical Inhibition of PARP14 Mitigates Allergen-Induced IgE and Mucus Overproduction in a Mouse Model of Pulmonary Allergic Response. <i>ImmunoHorizons</i> , 2022, 6, 432-446.	1.8	4
43	Tensor clustering with algebraic constraints gives interpretable groups of crosstalk mechanisms in breast cancer. <i>Journal of the Royal Society Interface</i> , 2019, 16, 20180661.	3.4	3
44	IQGAP1 is a Novel HER2 Binding Partner and Regulates HER2â€Mediated Cell Proliferation. <i>FASEB Journal</i> , 2010, 24, 421.10.	0.5	0
45	Targeting Vulnerabilities in Successive Cell Cycle Stages to Induce Death of PI3K-Activated Basal-Like Breast Cancer Cells. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0