Mario Niepel

List of Publications by Year
in descending order

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45	5,054	147801	254184
papers	citations	31 h-index	43 g-index

54	54	54	8919
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	ADPâ€ribosyltransferases, an update on function and nomenclature. FEBS Journal, 2022, 289, 7399-7410.	4.7	150
2	Selective Pharmaceutical Inhibition of PARP14 Mitigates Allergen-Induced IgE and Mucus Overproduction in a Mouse Model of Pulmonary Allergic Response. ImmunoHorizons, 2022, 6, 432-446.	1.8	4
3	Targeted Degradation of PARP14 Using a Heterobifunctional Small Molecule. ChemBioChem, 2021, 22, 2107-2110.	2.6	12
4	A potent and selective PARP14 inhibitor decreases protumor macrophage gene expression and elicits inflammatory responses in tumor explants. Cell Chemical Biology, 2021, 28, 1158-1168.e13.	5.2	37
5	PARP7 negatively regulates the type I interferon response in cancer cells and its inhibition triggers antitumor immunity. Cancer Cell, 2021, 39, 1214-1226.e10.	16.8	72
6	Maximum Entropy Framework for Predictive Inference of Cell Population Heterogeneity and Responses in Signaling Networks. Cell Systems, 2020, 10, 204-212.e8.	6.2	26
7	Torin2 Exploits Replication and Checkpoint Vulnerabilities to Cause Death of PI3K-Activated Triple-Negative Breast Cancer Cells. Cell Systems, 2020, 10, 66-81.e11.	6.2	26
8	InÂVitro and Cellular Probes to Study PARP Enzyme Target Engagement. Cell Chemical Biology, 2020, 27, 877-887.e14.	5.2	18
9	Receptor-based mechanism of relative sensing and cell memory in mammalian signaling networks. ELife, 2020, 9, .	6.0	24
10	A Multi-center Study on the Reproducibility of Drug-Response Assays in Mammalian Cell Lines. Cell Systems, 2019, 9, 35-48.e5.	6.2	95
11	Tensor clustering with algebraic constraints gives interpretable groups of crosstalk mechanisms in breast cancer. Journal of the Royal Society Interface, 2019, 16, 20180661.	3.4	3
12	Enabling drug discovery for the PARP protein family through the detection of mono-ADP-ribosylation. Biochemical Pharmacology, 2019, 167, 97-106.	4.4	38
13	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. Cell Systems, 2018, 6, 13-24.	6.2	327
14	Measuring Cancer Drug Sensitivity and Resistance in Cultured Cells. Current Protocols in Chemical Biology, 2017, 9, 55-74.	1.7	31
15	Alternative drug sensitivity metrics improve preclinical cancer pharmacogenomics. Nature Biotechnology, 2017, 35, 500-502.	17.5	68
16	Common and cell-type specific responses to anti-cancer drugs revealed by high throughput transcript profiling. Nature Communications, 2017, 8, 1186.	12.8	78
17	Quantification of sensitivity and resistance of breast cancer cell lines to anti-cancer drugs using GR metrics. Scientific Data, 2017, 4, 170166.	5.3	34
18	Designing Drugâ€Response Experiments and Quantifying their Results. Current Protocols in Chemical Biology, 2017, 9, 96-116.	1.7	30

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19	GRcalculator: an online tool for calculating and mining doseâ€“response data. BMC Cancer, 2017, 17, 698.	2.6	64
20	L1000CDS2: LINCS L1000 characteristic direction signatures search engine. Npj Systems Biology and Applications, 2016, 2, .	3.0	250
21	Growth rate inhibition metrics correct for confounders in measuring sensitivity to cancer drugs. Nature Methods, 2016, 13, 521-527.	19.0	489
22	Conservation of protein abundance patterns reveals the regulatory architecture of the EGFR-MAPK pathway. Science Signaling, 2016, 9, rs6.	3.6	119
23	Systematic analysis of <scp>BRAF^V</scp>^{600E} melanomas reveals a role for <scp>JNK</scp>/câ€Jun pathway in adaptive resistance to drugâ€induced apoptosis. Molecular Systems Biology, 2015, 11, 797.	7.2	84
24	LINCS Canvas Browser: interactive web app to query, browse and interrogate LINCS L1000 gene expression signatures. Nucleic Acids Research, 2014, 42, W449-W460.	14.5	280
25	Analysis of growth factor signaling in genetically diverse breast cancer lines. BMC Biology, 2014, 12, 20.	3.8	34
26	Profiles of Basal and Stimulated Receptor Signaling Networks Predict Drug Response in Breast Cancer Lines. Science Signaling, 2013, 6, ra84.	3.6	90
27	Characterization of Torin2, an ATP-Competitive Inhibitor of mTOR, ATM, and ATR. Cancer Research, 2013, 73, 2574-2586.	0.9	170
28	Discovering causal pathways linking genomic events to transcriptional states using Tied Diffusion Through Interacting Events (TieDIE). Bioinformatics, 2013, 29, 2757-2764.	4.1	189
29	Mass Spectrometry Based Method to Increase Throughput for Kinome Analyses Using ATP Probes. Analytical Chemistry, 2013, 85, 4666-4674.	6.5	30
30	The nuclear basket proteins Mlp1p and Mlp2p are part of a dynamic interactome including Esc1p and the proteasome. Molecular Biology of the Cell, 2013, 24, 3920-3938.	2.1	100
31	Kinome-wide Selectivity Profiling of ATP-competitive Mammalian Target of Rapamycin (mTOR) Inhibitors and Characterization of Their Binding Kinetics. Journal of Biological Chemistry, 2012, 287, 9742-9752.	3.4	89
32	Discovery of Potent and Selective Covalent Inhibitors of JNK. Chemistry and Biology, 2012, 19, 140-154.	6.0	286
33	Adaptive informatics for multifactorial and high-content biological data. Nature Methods, 2011, 8, 487-492.	19.0	65
34	A Cell Cycle Phosphoproteome of the Yeast Centrosome. Science, 2011, 332, 1557-1561.	12.6	88
35	Dissecting Variability in Responses to Cancer Chemotherapy Through Systems Pharmacology. Clinical Pharmacology and Therapeutics, 2010, 88, 34-38.	4.7	59
36	The nuclear pore complex: bridging nuclear transport and gene regulation. Nature Reviews Molecular Cell Biology, 2010, 11, 490-501.	37.0	473

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37	Classic and contemporary approaches to modeling biochemical reactions. Genes and Development, 2010, 24, 1861-1875.	5.9	255
38	IQGAP1 is a Novel HER2 Binding Partner and Regulates HER2â€Mediated Cell Proliferation. FASEB Journal, 2010, 24, 421.10.	0.5	0
39	Non-genetic cell-to-cell variability and the consequences for pharmacology. Current Opinion in Chemical Biology, 2009, 13, 556-561.	6.1	200
40	Inputâ€“output behavior of ErbB signaling pathways as revealed by a mass action model trained against dynamic data. Molecular Systems Biology, 2009, 5, 239.	7.2	332
41	The nuclear pore complexâ€“associated protein, Mlp2p, binds to the yeast spindle pole body and promotes its efficient assembly. Journal of Cell Biology, 2005, 170, 225-235.	5.2	81
42	The role of 5'-leader length, secondary structure and PABP concentration on cap and poly(A) tail function during translation in Xenopus oocytes. Nucleic Acids Research, 2000, 28, 2943-2953.	14.5	36
43	Secondary structure in the 5â€²-leader or 3â€²-untranslated region reduces protein yield but does not affect the functional interaction between the 5â€²-cap and the poly(A) tail. FEBS Letters, 1999, 462, 79-84.	2.8	34
44	Identification and Characterization of the Functional Elements within the Tobacco Etch Virus 5â€² Leader Required for Cap-Independent Translation. Journal of Virology, 1999, 73, 9080-9088.	3.4	71
45	Targeting Vulnerabilities in Successive Cell Cycle Stages to Induce Death of PI3K-Activated Basal-Like Breast Cancer Cells. SSRN Electronic Journal, 0, , .	0.4	0