# Mario Niepel

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7858547/publications.pdf

Version: 2024-02-01

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|---|---|---|---|
| 45<br>papers | 5,054<br>citations | 147566<br>31<br>h-index | 253896<br>43<br>g-index |
| 54<br>all docs | 54<br>docs citations | 54<br>times ranked | 8919<br>citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Growth rate inhibition metrics correct for confounders in measuring sensitivity to cancer drugs. Nature Methods, 2016, 13, 521-527. | 9.0 | 489 |
| 2 | The nuclear pore complex: bridging nuclear transport and gene regulation. Nature Reviews Molecular Cell Biology, 2010, 11, 490-501. | 16.1 | 473 |
| 3 | Inputâ€“output behavior of ErbB signaling pathways as revealed by a mass action model trained against dynamic data. Molecular Systems Biology, 2009, 5, 239. | 3.2 | 332 |
| 4 | 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. | 2.9 | 327 |
| 5 | Discovery of Potent and Selective Covalent Inhibitors of JNK. Chemistry and Biology, 2012, 19, 140-154. | 6.2 | 286 |
| 6 | LINCS Canvas Browser: interactive web app to query, browse and interrogate LINCS L1000 gene expression signatures. Nucleic Acids Research, 2014, 42, W449-W460. | 6.5 | 280 |
| 7 | Classic and contemporary approaches to modeling biochemical reactions. Genes and Development, 2010, 24, 1861-1875. | 2.7 | 255 |
| 8 | L1000CDS2: LINCS L1000 characteristic direction signatures search engine. Npj Systems Biology and Applications, 2016, 2, . | 1.4 | 250 |
| 9 | Non-genetic cell-to-cell variability and the consequences for pharmacology. Current Opinion in Chemical Biology, 2009, 13, 556-561. | 2.8 | 200 |
| 10 | Discovering causal pathways linking genomic events to transcriptional states using Tied Diffusion Through Interacting Events (TieDIE). Bioinformatics, 2013, 29, 2757-2764. | 1.8 | 189 |
| 11 | Characterization of Torin2, an ATP-Competitive Inhibitor of mTOR, ATM, and ATR. Cancer Research, 2013, 73, 2574-2586. | 0.4 | 170 |
| 12 | ADPâ€ribosyltransferases, an update on function and nomenclature. FEBS Journal, 2022, 289, 7399-7410. | 2.2 | 150 |
| 13 | Conservation of protein abundance patterns reveals the regulatory architecture of the EGFR-MAPK pathway. Science Signaling, 2016, 9, rs6. | 1.6 | 119 |
| 14 | 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. | 0.9 | 100 |
| 15 | A Multi-center Study on the Reproducibility of Drug-Response Assays in Mammalian Cell Lines. Cell Systems, 2019, 9, 35-48.e5. | 2.9 | 95 |
| 16 | Profiles of Basal and Stimulated Receptor Signaling Networks Predict Drug Response in Breast Cancer Lines. Science Signaling, 2013, 6, ra84. | 1.6 | 90 |
| 17 | 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. | 1.6 | 89 |
| 18 | A Cell Cycle Phosphoproteome of the Yeast Centrosome. Science, 2011, 332, 1557-1561. | 6.0 | 88 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Systematic analysis of <scp>BRAF<sup>V</sup></scp><sup>600E</sup> melanomas reveals a role for <scp>JNK</scp>/câ€Jun pathway in adaptive resistance to drugâ€induced apoptosis. Molecular Systems Biology, 2015, 11, 797. | 3.2 | 84 |
| 20 | 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. | 2.3 | 81 |
| 21 | Common and cell-type specific responses to anti-cancer drugs revealed by high throughput transcript profiling. Nature Communications, 2017, 8, 1186. | 5.8 | 78 |
| 22 | PARP7 negatively regulates the type I interferon response in cancer cells and its inhibition triggers antitumor immunity. Cancer Cell, 2021, 39, 1214-1226.e10. | 7.7 | 72 |
| 23 | 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. | 1.5 | 71 |
| 24 | Alternative drug sensitivity metrics improve preclinical cancer pharmacogenomics. Nature Biotechnology, 2017, 35, 500-502. | 9.4 | 68 |
| 25 | Adaptive informatics for multifactorial and high-content biological data. Nature Methods, 2011, 8, 487-492. | 9.0 | 65 |
| 26 | GRcalculator: an online tool for calculating and mining doseâ€“response data. BMC Cancer, 2017, 17, 698. | 1.1 | 64 |
| 27 | Dissecting Variability in Responses to Cancer Chemotherapy Through Systems Pharmacology. Clinical Pharmacology and Therapeutics, 2010, 88, 34-38. | 2.3 | 59 |
| 28 | Enabling drug discovery for the PARP protein family through the detection of mono-ADP-ribosylation. Biochemical Pharmacology, 2019, 167, 97-106. | 2.0 | 38 |
| 29 | 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. | 2.5 | 37 |
| 30 | 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. | 6.5 | 36 |
| 31 | 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. | 1.3 | 34 |
| 32 | Analysis of growth factor signaling in genetically diverse breast cancer lines. BMC Biology, 2014, 12, 20. | 1.7 | 34 |
| 33 | Quantification of sensitivity and resistance of breast cancer cell lines to anti-cancer drugs using GR metrics. Scientific Data, 2017, 4, 170166. | 2.4 | 34 |
| 34 | Measuring Cancer Drug Sensitivity and Resistance in Cultured Cells. Current Protocols in Chemical Biology, 2017, 9, 55-74. | 1.7 | 31 |
| 35 | Mass Spectrometry Based Method to Increase Throughput for Kinome Analyses Using ATP Probes. Analytical Chemistry, 2013, 85, 4666-4674. | 3.2 | 30 |
| 36 | Designing Drugâ€Response Experiments and Quantifying their Results. Current Protocols in Chemical Biology, 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. Cell Systems, 2020, 10, 204-212.e8. | 2.9 | 26 |
| 38 | Torin2 Exploits Replication and Checkpoint Vulnerabilities to Cause Death of PI3K-Activated Triple-Negative Breast Cancer Cells. Cell Systems, 2020, 10, 66-81.e11. | 2.9 | 26 |
| 39 | Receptor-based mechanism of relative sensing and cell memory in mammalian signaling networks. ELife, 2020, 9, . | 2.8 | 24 |
| 40 | InÂVitro and Cellular Probes to Study PARP Enzyme Target Engagement. Cell Chemical Biology, 2020, 27, 877-887.e14. | 2.5 | 18 |
| 41 | Targeted Degradation of PARP14 Using a Heterobifunctional Small Molecule. ChemBioChem, 2021, 22, 2107-2110. | 1.3 | 12 |
| 42 | 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. | 0.8 | 4 |
| 43 | Tensor clustering with algebraic constraints gives interpretable groups of crosstalk mechanisms in breast cancer. Journal of the Royal Society Interface, 2019, 16, 20180661. | 1.5 | 3 |
| 44 | IQGAP1 is a Novel HER2 Binding Partner and Regulates HER2â€Mediated Cell Proliferation. FASEB Journal, 2010, 24, 421.10. | 0.2 | 0 |
| 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 |