

Bernd Bodenmiller

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

11,111
citations

101543

36
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114465

63
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87
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87
docs citations

87
times ranked

16724
citing authors

#	ARTICLE	IF	CITATIONS
1	Cutaneous and systemic hyperinflammation drives maculopapular drug exanthema in severely ill COVID-19 patients. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2022, 77, 595-608.	5.7	21
2	Mass cytometric and transcriptomic profiling of epithelial-mesenchymal transitions in human mammary cell lines. <i>Scientific Data</i> , 2022, 9, 44.	5.3	5
3	Three-dimensional imaging mass cytometry for highly multiplexed molecular and cellular mapping of tissues and the tumor microenvironment. <i>Nature Cancer</i> , 2022, 3, 122-133.	13.2	92
4	Multiplexed imaging mass cytometry of the chemokine milieu in melanoma characterizes features of the response to immunotherapy. <i>Science Immunology</i> , 2022, 7, eabk1692.	11.9	100
5	Single-cell proteomics defines the cellular heterogeneity of localized prostate cancer. <i>Cell Reports Medicine</i> , 2022, 3, 100604.	6.5	7
6	Breast tumor microenvironment structures are associated with genomic features and clinical outcome. <i>Nature Genetics</i> , 2022, 54, 660-669.	21.4	88
7	T-cell recovery and evidence of persistent immune activation 12 months after severe COVID-19. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2022, 77, 2468-2481.	5.7	20
8	A distinct innate immune signature marks progression from mild to severe COVID-19. <i>Cell Reports Medicine</i> , 2021, 2, 100166.	6.5	102
9	The Tumor Profiler Study: integrated, multi-omic, functional tumor profiling for clinical decision support. <i>Cancer Cell</i> , 2021, 39, 288-293.	16.8	71
10	Deciphering the signaling network of breast cancer improves drug sensitivity prediction. <i>Cell Systems</i> , 2021, 12, 401-418.e12.	6.2	22
11	Profound dysregulation of T cell homeostasis and function in patients with severe COVID-19. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021, 76, 2866-2881.	5.7	59
12	Multi-omics reveals clinically relevant proliferative drive associated with mTOR-MYC-OXPHOS activity in chronic lymphocytic leukemia. <i>Nature Cancer</i> , 2021, 2, 853-864.	13.2	32
13	<i>cytomapper</i> : an R/Bioconductor package for visualization of highly multiplexed imaging data. <i>Bioinformatics</i> , 2021, 36, 5706-5708.	4.1	33
14	Cell-to-cell and type-to-type heterogeneity of signaling networks: insights from the crowd. <i>Molecular Systems Biology</i> , 2021, 17, e10402.	7.2	9
15	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , 2020, 587, 377-386.	27.8	108
16	Imaging mass cytometry and multiplatform genomics define the phenogenomic landscape of breast cancer. <i>Nature Cancer</i> , 2020, 1, 163-175.	13.2	209
17	Uncovering axes of variation among single-cell cancer specimens. <i>Nature Methods</i> , 2020, 17, 302-310.	19.0	39
18	Stabilized Reconstruction of Signaling Networks from Single-Cell Cue-Response Data. <i>Scientific Reports</i> , 2020, 10, 1233.	3.3	1

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19	The single-cell pathology landscape of breast cancer. <i>Nature</i> , 2020, 578, 615-620.	27.8	582
20	Profiling Cell Signaling Networks at Single-cell Resolution. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 744-756.	3.8	39
21	A quantitative analysis of the interplay of environment, neighborhood, and cell state in 3D spheroids. <i>Molecular Systems Biology</i> , 2020, 16, e9798.	7.2	17
22	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. <i>Cell</i> , 2019, 179, 1207-1221.e22.	28.9	162
23	Modeling Cell-Cell Interactions from Spatial Molecular Data with Spatial Variance Component Analysis. <i>Cell Reports</i> , 2019, 29, 202-211.e6.	6.4	133
24	A Map of Human Type 1 Diabetes Progression by Imaging Mass Cytometry. <i>Cell Metabolism</i> , 2019, 29, 755-768.e5.	16.2	217
25	Analysis of the Human Kinome and Phosphatome by Mass Cytometry Reveals Overexpression-Induced Effects on Cancer-Related Signaling. <i>Molecular Cell</i> , 2019, 74, 1086-1102.e5.	9.7	32
26	IL6 and CXCR1 expression is associated with cancer stem cell-like properties of clear cell renal cancer. <i>Journal of Pathology</i> , 2019, 248, 377-389.	4.5	32
27	A Single-Cell Atlas of the Tumor and Immune Ecosystem of Human Breast Cancer. <i>Cell</i> , 2019, 177, 1330-1345.e18.	28.9	547
28	In-Depth Characterization of Monocyte-Derived Macrophages using a Mass Cytometry-Based Phagocytosis Assay. <i>Scientific Reports</i> , 2019, 9, 1925.	3.3	114
29	Hair eruption initiates and commensal skin microbiota aggravate adverse events of anti-EGFR therapy. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	23
30	CellCycleTRACER accounts for cell cycle and volume in mass cytometry data. <i>Nature Communications</i> , 2018, 9, 632.	12.8	36
31	Ruthenium counterstaining for imaging mass cytometry. <i>Journal of Pathology</i> , 2018, 244, 479-484.	4.5	33
32	Simultaneous Multiplexed Imaging of mRNA and Proteins with Subcellular Resolution in Breast Cancer Tissue Samples by Mass Cytometry. <i>Cell Systems</i> , 2018, 6, 25-36.e5.	6.2	214
33	High-Dimensional Phenotyping Identifies Age-Emergent Cells in Human Mammary Epithelia. <i>Cell Reports</i> , 2018, 23, 1205-1219.	6.4	39
34	Compensation of Signal Spillover in Suspension and Imaging Mass Cytometry. <i>Cell Systems</i> , 2018, 6, 612-620.e5.	6.2	272
35	Learning time-varying information flow from single-cell epithelial to mesenchymal transition data. <i>PLoS ONE</i> , 2018, 13, e0203389.	2.5	18
36	Limited utility of tissue micro-arrays in detecting intra-tumoral heterogeneity in stem cell characteristics and tumor progression markers in breast cancer. <i>Journal of Translational Medicine</i> , 2018, 16, 118.	4.4	15

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37	Influence of node abundance on signaling network state and dynamics analyzed by mass cytometry. <i>Nature Biotechnology</i> , 2017, 35, 164-172.	17.5	39
38	An Immune Atlas of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2017, 169, 736-749.e18.	28.9	751
39	histoCAT: analysis of cell phenotypes and interactions in multiplex image cytometry data. <i>Nature Methods</i> , 2017, 14, 873-876.	19.0	470
40	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	6.0	1,547
41	Enhanced multiplexing in mass cytometry using osmium and ruthenium tetroxide species. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2016, 89, 491-497.	1.5	36
42	Phosphorylation of residues inside the <scp>SNARE</scp> complex suppresses secretory vesicle fusion. <i>EMBO Journal</i> , 2016, 35, 1810-1821.	7.8	40
43	AirLab: a cloud-based platform to manage and share antibody-based single-cell research. <i>Genome Biology</i> , 2016, 17, 142.	8.8	21
44	Multiplexed Epitope-Based Tissue Imaging for Discovery and Healthcare Applications. <i>Cell Systems</i> , 2016, 2, 225-238.	6.2	201
45	Automatic single cell segmentation on highly multiplexed tissue images. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2015, 87, 936-942.	1.5	53
46	Target of Rapamycin Complex 2 Regulates Actin Polarization and Endocytosis via Multiple Pathways. <i>Journal of Biological Chemistry</i> , 2015, 290, 14963-14978.	3.4	72
47	Palladium-based mass tag cell barcoding with a doublet-filtering scheme and single-cell deconvolution algorithm. <i>Nature Protocols</i> , 2015, 10, 316-333.	12.0	466
48	Unraveling cell populations in tumors by single-cell mass cytometry. <i>Current Opinion in Biotechnology</i> , 2015, 31, 122-129.	6.6	102
49	Kinome-wide Decoding of Network-Attacking Mutations Rewiring Cancer Signaling. <i>Cell</i> , 2015, 163, 202-217.	28.9	168
50	An internal standardisation strategy for quantitative immunoassay tissue imaging using laser ablation inductively coupled plasma mass spectrometry. <i>Journal of Analytical Atomic Spectrometry</i> , 2015, 30, 254-259.	3.0	39
51	Highly multiplexed imaging of tumor tissues with subcellular resolution by mass cytometry. <i>Nature Methods</i> , 2014, 11, 417-422.	19.0	1,430
52	Automated identification of stratifying signatures in cellular subpopulations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2770-7.	7.1	421
53	The Calcineurin Signaling Network Evolves via Conserved Kinase-Phosphatase Modules that Transcend Substrate Identity. <i>Molecular Cell</i> , 2014, 55, 422-435.	9.7	102
54	Fast Chemical Imaging at High Spatial Resolution by Laser Ablation Inductively Coupled Plasma Mass Spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 10107-10116.	6.5	174

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55	A Practical Guide to Multiplexed Mass Cytometry. Current Topics in Microbiology and Immunology, 2013, 377, 95-109.	1.1	30
56	Multiplexed mass cytometry profiling of cellular states perturbed by small-molecule regulators. Nature Biotechnology, 2012, 30, 858-867.	17.5	502
57	A platinum-based covalent viability reagent for single-cell mass cytometry. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2012, 81A, 467-475.	1.5	177
58	Phosphoproteome Resource for Systems Biology Research. Methods in Molecular Biology, 2011, 694, 307-322.	0.9	11
59	Orm family proteins mediate sphingolipid homeostasis.. FASEB Journal, 2011, 25, 197.2.	0.5	0
60	Phosphoproteomic Analysis Reveals Interconnected System-Wide Responses to Perturbations of Kinases and Phosphatases in Yeast. Science Signaling, 2010, 3, rs4.	3.6	277
61	Quantitative Analysis of Protein Phosphorylation on a System-Wide Scale by Mass Spectrometry-Based Proteomics. Methods in Enzymology, 2010, 470, 317-334.	1.0	44
62	An integrated chemical, mass spectrometric and computational strategy for (quantitative) phosphoproteomics: application to Drosophila melanogaster Kc167 cells. Molecular BioSystems, 2007, 3, 275.	2.9	76
63	PhosphoPep—a phosphoproteome resource for systems biology research in <i>Drosophila</i> Kc167 cells. Molecular Systems Biology, 2007, 3, 139.	7.2	168
64	An R-based reproducible and user-friendly preprocessing pipeline for CyTOF data. F1000Research, 0, 9, 1263.	1.6	25