

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
h-index

114465

63
g-index

87
all docs

87
docs citations

87
times ranked

16724
citing authors

#	ARTICLE	IF	CITATIONS
1	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	6.0	1,547
2	Highly multiplexed imaging of tumor tissues with subcellular resolution by mass cytometry. <i>Nature Methods</i> , 2014, 11, 417-422.	19.0	1,430
3	An Immune Atlas of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2017, 169, 736-749.e18.	28.9	751
4	The single-cell pathology landscape of breast cancer. <i>Nature</i> , 2020, 578, 615-620.	27.8	582
5	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
6	Multiplexed mass cytometry profiling of cellular states perturbed by small-molecule regulators. <i>Nature Biotechnology</i> , 2012, 30, 858-867.	17.5	502
7	histoCAT: analysis of cell phenotypes and interactions in multiplex image cytometry data. <i>Nature Methods</i> , 2017, 14, 873-876.	19.0	470
8	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
9	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
10	Phosphoproteomic Analysis Reveals Interconnected System-Wide Responses to Perturbations of Kinases and Phosphatases in Yeast. <i>Science Signaling</i> , 2010, 3, rs4.	3.6	277
11	Compensation of Signal Spillover in Suspension and Imaging Mass Cytometry. <i>Cell Systems</i> , 2018, 6, 612-620.e5.	6.2	272
12	A Map of Human Type 1 Diabetes Progression by Imaging Mass Cytometry. <i>Cell Metabolism</i> , 2019, 29, 755-768.e5.	16.2	217
13	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
14	Imaging mass cytometry and multiplatform genomics define the phenogenomic landscape of breast cancer. <i>Nature Cancer</i> , 2020, 1, 163-175.	13.2	209
15	Multiplexed Epitope-Based Tissue Imaging for Discovery and Healthcare Applications. <i>Cell Systems</i> , 2016, 2, 225-238.	6.2	201
16	A platinum-based covalent viability reagent for single-cell mass cytometry. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2012, 81A, 467-475.	1.5	177
17	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
18	PhosphoPepâ€”a phosphoproteome resource for systems biology research in <i>Drosophila</i> Kc167 cells. <i>Molecular Systems Biology</i> , 2007, 3, 139.	7.2	168

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19	Kinome-wide Decoding of Network-Attacking Mutations Rewiring Cancer Signaling. <i>Cell</i> , 2015, 163, 202-217.	28.9	168
20	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. <i>Cell</i> , 2019, 179, 1207-1221.e22.	28.9	162
21	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
22	In-Depth Characterization of Monocyte-Derived Macrophages using a Mass Cytometry-Based Phagocytosis Assay. <i>Scientific Reports</i> , 2019, 9, 1925.	3.3	114
23	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , 2020, 587, 377-386.	27.8	108
24	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
25	Unraveling cell populations in tumors by single-cell mass cytometry. <i>Current Opinion in Biotechnology</i> , 2015, 31, 122-129.	6.6	102
26	A distinct innate immune signature marks progression from mild to severe COVID-19. <i>Cell Reports Medicine</i> , 2021, 2, 100166.	6.5	102
27	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
28	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
29	Breast tumor microenvironment structures are associated with genomic features and clinical outcome. <i>Nature Genetics</i> , 2022, 54, 660-669.	21.4	88
30	An integrated chemical, mass spectrometric and computational strategy for (quantitative) phosphoproteomics: application to <i>Drosophila melanogaster</i> Kc167 cells. <i>Molecular BioSystems</i> , 2007, 3, 275.	2.9	76
31	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
32	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
33	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
34	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
35	Quantitative Analysis of Protein Phosphorylation on a System-Wide Scale by Mass Spectrometry-Based Proteomics. <i>Methods in Enzymology</i> , 2010, 470, 317-334.	1.0	44
36	Phosphorylation of residues inside the <sc>SNARE</sc> complex suppresses secretory vesicle fusion. <i>EMBO Journal</i> , 2016, 35, 1810-1821.	7.8	40

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37	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
38	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
39	High-Dimensional Phenotyping Identifies Age-Emergent Cells in Human Mammary Epithelia. <i>Cell Reports</i> , 2018, 23, 1205-1219.	6.4	39
40	Uncovering axes of variation among single-cell cancer specimens. <i>Nature Methods</i> , 2020, 17, 302-310.	19.0	39
41	Profiling Cell Signaling Networks at Single-cell Resolution. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 744-756.	3.8	39
42	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
43	CellCycleTRACER accounts for cell cycle and volume in mass cytometry data. <i>Nature Communications</i> , 2018, 9, 632.	12.8	36
44	Ruthenium counterstaining for imaging mass cytometry. <i>Journal of Pathology</i> , 2018, 244, 479-484.	4.5	33
45	<i>cytomapper</i> : an R/Bioconductor package for visualization of highly multiplexed imaging data. <i>Bioinformatics</i> , 2021, 36, 5706-5708.	4.1	33
46	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
47	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
48	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
49	A Practical Guide to Multiplexed Mass Cytometry. <i>Current Topics in Microbiology and Immunology</i> , 2013, 377, 95-109.	1.1	30
50	An R-based reproducible and user-friendly preprocessing pipeline for CyTOF data. <i>F1000Research</i> , 0, 9, 1263.	1.6	25
51	Hair eruption initiates and commensal skin microbiota aggravate adverse events of anti-EGFR therapy. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	23
52	Deciphering the signaling network of breast cancer improves drug sensitivity prediction. <i>Cell Systems</i> , 2021, 12, 401-418.e12.	6.2	22
53	AirLab: a cloud-based platform to manage and share antibody-based single-cell research. <i>Genome Biology</i> , 2016, 17, 142.	8.8	21
54	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

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55	Tâ€cell recovery and evidence of persistent immune activation 12â€months after severe COVID-19. Allergy: European Journal of Allergy and Clinical Immunology, 2022, 77, 2468-2481.	5.7	20
56	Learning time-varying information flow from single-cell epithelial to mesenchymal transition data. PLoS ONE, 2018, 13, e0203389.	2.5	18
57	A quantitative analysis of the interplay of environment, neighborhood, and cell state in 3D spheroids. Molecular Systems Biology, 2020, 16, e9798.	7.2	17
58	Limited utility of tissue micro-arrays in detecting intra-tumoral heterogeneity in stem cell characteristics and tumor progression markers in breast cancer. Journal of Translational Medicine, 2018, 16, 118.	4.4	15
59	Phosphoproteome Resource for Systems Biology Research. Methods in Molecular Biology, 2011, 694, 307-322.	0.9	11
60	Cellâ€cell and typeâ€type heterogeneity of signaling networks: insights from the crowd. Molecular Systems Biology, 2021, 17, e10402.	7.2	9
61	Single-cell proteomics defines the cellular heterogeneity of localized prostate cancer. Cell Reports Medicine, 2022, 3, 100604.	6.5	7
62	Mass cytometric and transcriptomic profiling of epithelial-mesenchymal transitions in human mammary cell lines. Scientific Data, 2022, 9, 44.	5.3	5
63	Stabilized Reconstruction of Signaling Networks from Single-Cell Cue-Response Data. Scientific Reports, 2020, 10, 1233.	3.3	1
64	Orm family proteins mediate sphingolipid homeostasis.. FASEB Journal, 2011, 25, 197.2.	0.5	0