

Sean C Bendall

List of Publications by Year in descending order

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117
papers

18,714
citations

46918

47
h-index

33814

99
g-index

140
all docs

140
docs citations

140
times ranked

24475
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-Cell Mass Cytometry of Differential Immune and Drug Responses Across a Human Hematopoietic Continuum. <i>Science</i> , 2011, 332, 687-696.	6.0	2,097
2	Data-Driven Phenotypic Dissection of AML Reveals Progenitor-like Cells that Correlate with Prognosis. <i>Cell</i> , 2015, 162, 184-197.	13.5	1,791
3	viSNE enables visualization of high dimensional single-cell data and reveals phenotypic heterogeneity of leukemia. <i>Nature Biotechnology</i> , 2013, 31, 545-552.	9.4	1,481
4	Extracting a cellular hierarchy from high-dimensional cytometry data with SPADE. <i>Nature Biotechnology</i> , 2011, 29, 886-891.	9.4	905
5	Multiplexed ion beam imaging of human breast tumors. <i>Nature Medicine</i> , 2014, 20, 436-442.	15.2	881
6	Single-Cell Trajectory Detection Uncovers Progression and Regulatory Coordination in Human B Cell Development. <i>Cell</i> , 2014, 157, 714-725.	13.5	838
7	A Structured Tumor-Immune Microenvironment in Triple Negative Breast Cancer Revealed by Multiplexed Ion Beam Imaging. <i>Cell</i> , 2018, 174, 1373-1387.e19.	13.5	729
8	Systemic Immunity Is Required for Effective Cancer Immunotherapy. <i>Cell</i> , 2017, 168, 487-502.e15.	13.5	708
9	Normalization of mass cytometry data with bead standards. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2013, 83A, 483-494.	1.1	655
10	A deep profiler's guide to cytometry. <i>Trends in Immunology</i> , 2012, 33, 323-332.	2.9	596
11	IGF and FGF cooperatively establish the regulatory stem cell niche of pluripotent human cells in vitro. <i>Nature</i> , 2007, 448, 1015-1021.	13.7	552
12	Cytometry by Time-of-Flight Shows Combinatorial Cytokine Expression and Virus-Specific Cell Niches within a Continuum of CD8+ T Cell Phenotypes. <i>Immunity</i> , 2012, 36, 142-152.	6.6	534
13	Wishbone identifies bifurcating developmental trajectories from single-cell data. <i>Nature Biotechnology</i> , 2016, 34, 637-645.	9.4	523
14	Multiplexed mass cytometry profiling of cellular states perturbed by small-molecule regulators. <i>Nature Biotechnology</i> , 2012, 30, 858-867.	9.4	502
15	A HUPO test sample study reveals common problems in mass spectrometry-based proteomics. <i>Nature Methods</i> , 2009, 6, 423-430.	9.0	316
16	Whole-cell segmentation of tissue images with human-level performance using large-scale data annotation and deep learning. <i>Nature Biotechnology</i> , 2022, 40, 555-565.	9.4	297
17	Clinical recovery from surgery correlates with single-cell immune signatures. <i>Science Translational Medicine</i> , 2014, 6, 255ra131.	5.8	285
18	The transcriptional landscape of $\hat{1}\pm\hat{1}^2$ T cell differentiation. <i>Nature Immunology</i> , 2013, 14, 619-632.	7.0	256

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19	MIBI-TOF: A multiplexed imaging platform relates cellular phenotypes and tissue structure. <i>Science Advances</i> , 2019, 5, eaax5851.	4.7	252
20	An interactive reference framework for modeling a dynamic immune system. <i>Science</i> , 2015, 349, 1259425.	6.0	214
21	From single cells to deep phenotypes in cancer. <i>Nature Biotechnology</i> , 2012, 30, 639-647.	9.4	197
22	Single-cell mass cytometry adapted to measurements of the cell cycle. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2012, 81A, 552-566.	1.1	196
23	Conditional density-based analysis of T cell signaling in single-cell data. <i>Science</i> , 2014, 346, 1250689.	6.0	188
24	Single-cell metabolic profiling of human cytotoxic T cells. <i>Nature Biotechnology</i> , 2021, 39, 186-197.	9.4	187
25	Prevention of Amino Acid Conversion in SILAC Experiments with Embryonic Stem Cells. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1587-1597.	2.5	172
26	Metal-isotope-tagged monoclonal antibodies for high-dimensional mass cytometry. <i>Nature Protocols</i> , 2018, 13, 2121-2148.	5.5	171
27	Mutant IDH1 Downregulates ATM and Alters DNA Repair and Sensitivity to DNA Damage Independent of TET2. <i>Cancer Cell</i> , 2016, 30, 337-348.	7.7	166
28	Mapping lung cancer epithelial-mesenchymal transition states and trajectories with single-cell resolution. <i>Nature Communications</i> , 2019, 10, 5587.	5.8	162
29	An Integrated Multi-omic Single-Cell Atlas of Human B Cell Identity. <i>Immunity</i> , 2020, 53, 217-232.e5.	6.6	161
30	Transition to invasive breast cancer is associated with progressive changes in the structure and composition of tumor stroma. <i>Cell</i> , 2022, 185, 299-310.e18.	13.5	161
31	Clonal isolation of hESCs reveals heterogeneity within the pluripotent stem cell compartment. <i>Nature Methods</i> , 2006, 3, 807-815.	9.0	155
32	Immune monitoring using mass cytometry and related high-dimensional imaging approaches. <i>Nature Reviews Rheumatology</i> , 2020, 16, 87-99.	3.5	131
33	Single-cell developmental classification of B cell precursor acute lymphoblastic leukemia at diagnosis reveals predictors of relapse. <i>Nature Medicine</i> , 2018, 24, 474-483.	15.2	112
34	The immunoregulatory landscape of human tuberculosis granulomas. <i>Nature Immunology</i> , 2022, 23, 318-329.	7.0	110
35	High-resolution myogenic lineage mapping by single-cell mass cytometry. <i>Nature Cell Biology</i> , 2017, 19, 558-567.	4.6	108
36	Visualization and cellular hierarchy inference of single-cell data using SPADE. <i>Nature Protocols</i> , 2016, 11, 1264-1279.	5.5	99

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37	Glucose Metabolism Drives Histone Acetylation Landscape Transitions that Dictate Muscle Stem Cell Function. <i>Cell Reports</i> , 2019, 27, 3939-3955.e6.	2.9	94
38	Comprehensive Immune Monitoring of Clinical Trials to Advance Human Immunotherapy. <i>Cell Reports</i> , 2019, 28, 819-831.e4.	2.9	91
39	Single-Cell Mass Cytometry Analysis of Human Tonsil T Cell Remodeling by Varicella Zoster Virus. <i>Cell Reports</i> , 2014, 8, 633-645.	2.9	82
40	An Enhanced Mass Spectrometry Approach Reveals Human Embryonic Stem Cell Growth Factors in Culture. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 421-432.	2.5	80
41	A Universal Live Cell Barcoding-Platform for Multiplexed Human Single Cell Analysis. <i>Scientific Reports</i> , 2018, 8, 10770.	1.6	75
42	Immune-stimulating antibody conjugates elicit robust myeloid activation and durable antitumor immunity. <i>Nature Cancer</i> , 2021, 2, 18-33.	5.7	74
43	The basis of cellular and regional vulnerability in Alzheimer's disease. <i>Acta Neuropathologica</i> , 2019, 138, 729-749.	3.9	73
44	Assessing basophil activation by using flow cytometry and mass cytometry in blood stored 24 hours before analysis. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 889-899.e11.	1.5	71
45	Macrophages are metabolically heterogeneous within the tumor microenvironment. <i>Cell Reports</i> , 2021, 37, 110171.	2.9	69
46	Single-cell systems-level analysis of human Toll-like receptor activation defines a chemokine signature in patients with systemic lupus erythematosus. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 136, 1326-1336.	1.5	66
47	Deconstructing human embryonic stem cell cultures: niche regulation of self-renewal and pluripotency. <i>Journal of Molecular Medicine</i> , 2008, 86, 875-886.	1.7	58
48	Integration of mechanistic immunological knowledge into a machine learning pipeline improves predictions. <i>Nature Machine Intelligence</i> , 2020, 2, 619-628.	8.3	52
49	Single-cell mass cytometry reveals cross-talk between inflammation-dampening and inflammation-amplifying cells in osteoarthritic cartilage. <i>Science Advances</i> , 2020, 6, eaay5352.	4.7	52
50	Single-cell mass cytometry of TCR signaling: Amplification of small initial differences results in low ERK activation in NOD mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 16466-16471.	3.3	50
51	Proliferation tracing with single-cell mass cytometry optimizes generation of stem cell memory-like T cells. <i>Nature Biotechnology</i> , 2019, 37, 259-266.	9.4	49
52	DRUG-NEM: Optimizing drug combinations using single-cell perturbation response to account for intratumoral heterogeneity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4294-E4303.	3.3	42
53	Synthetically Modified Viral Capsids as Versatile Carriers for Use in Antibody-Based Cell Targeting. <i>Bioconjugate Chemistry</i> , 2015, 26, 1590-1596.	1.8	36
54	Distinct signaling programs control human hematopoietic stem cell survival and proliferation. <i>Blood</i> , 2017, 129, 307-318.	0.6	35

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55	The Split Virus Influenza Vaccine rapidly activates immune cells through Fc γ 3 receptors. <i>Vaccine</i> , 2014, 32, 5989-5997.	1.7	34
56	Scalable Conjugation and Characterization of Immunoglobulins with Stable Mass Isotope Reporters for Single-Cell Mass Cytometry Analysis. <i>Methods in Molecular Biology</i> , 2019, 1989, 55-81.	0.4	32
57	Multiplexed single-cell morphometry for hematopathology diagnostics. <i>Nature Medicine</i> , 2020, 26, 408-417.	15.2	32
58	Parallel analysis of tri-molecular biosynthesis with cell identity and function in single cells. <i>Nature Communications</i> , 2019, 10, 1185.	5.8	29
59	Antigen-Dependent Integration of Opposing Proximal TCR-Signaling Cascades Determines the Functional Fate of T Lymphocytes. <i>Journal of Immunology</i> , 2014, 192, 2109-2119.	0.4	27
60	Human IL-10-producing B cells have diverse states that are induced from multiple B cell subsets. <i>Cell Reports</i> , 2022, 39, 110728.	2.9	27
61	Human embryonic stem cells: lessons from stem cell niches <i>in vivo</i> . <i>Regenerative Medicine</i> , 2008, 3, 365-376.	0.8	26
62	Mass synaptometry: High-dimensional multi parametric assay for single synapses. <i>Journal of Neuroscience Methods</i> , 2019, 312, 73-83.	1.3	26
63	Clonal tracking of hESCs reveals differential contribution to functional assays. <i>Nature Methods</i> , 2010, 7, 917-922.	9.0	24
64	NRAS G12V oncogene facilitates self-renewal in a murine model of acute myelogenous leukemia. <i>Blood</i> , 2014, 124, 3274-3283.	0.6	24
65	High-Parameter Immune Profiling with CyTOF. <i>Methods in Molecular Biology</i> , 2020, 2055, 351-368.	0.4	23
66	Complement targeting of nonhuman sialic acid does not mediate cell death of human embryonic stem cells. <i>Nature Medicine</i> , 2006, 12, 1113-1114.	15.2	20
67	GateFinder: projection-based gating strategy optimization for flow and mass cytometry. <i>Bioinformatics</i> , 2018, 34, 4131-4133.	1.8	20
68	Mass Cytometry Phenotyping of Human Granulocytes Reveals Novel Basophil Functional Heterogeneity. <i>iScience</i> , 2020, 23, 101724.	1.9	19
69	A topological view of human CD34+ cell state trajectories from integrated single-cell output and proteomic data. <i>Blood</i> , 2019, 133, 927-939.	0.6	17
70	Multiplexed Ion Beam Imaging: Insights into Pathobiology. <i>Annual Review of Pathology: Mechanisms of Disease</i> , 2022, 17, 403-423.	9.6	16
71	Reproducible, high-dimensional imaging in archival human tissue by multiplexed ion beam imaging by time-of-flight (MIBI-TOF). <i>Laboratory Investigation</i> , 2022, 102, 762-770.	1.7	16
72	Serial transplantation reveals a critical role for endoglin in hematopoietic stem cell quiescence. <i>Blood</i> , 2019, 133, 688-696.	0.6	15

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73	Single-synapse analyses of Alzheimer's disease implicate pathologic tau, DJ1, CD47, and ApoE. <i>Science Advances</i> , 2021, 7, eabk0473.	4.7	14
74	Network for Biomarker Immunoprofiling for Cancer Immunotherapy: Cancer Immune Monitoring and Analysis Centers and Cancer Immunologic Data Commons (CIMAC-CIDC). <i>Clinical Cancer Research</i> , 2021, 27, 5038-5048.	3.2	13
75	TRAIL-induced variation of cell signaling states provides nonheritable resistance to apoptosis. <i>Life Science Alliance</i> , 2019, 2, e201900554.	1.3	11
76	Multiplexed Ion Beam Imaging Readout of Single-Cell Immunoblotting. <i>Analytical Chemistry</i> , 2021, 93, 8517-8525.	3.2	9
77	Multiplexed imaging reveals an IFN- γ -driven inflammatory state in nivolumab-associated gastritis. <i>Cell Reports Medicine</i> , 2021, 2, 100419.	3.3	9
78	Mass Cytometry Analysis Of Myelofibrosis and Secondary Acute Myeloid Leukemia Reveals Constitutive and Cytokine Induced Signaling Abnormalities With Differential Sensitivities To Ruxolitinib. <i>Blood</i> , 2013, 122, 1610-1610.	0.6	9
79	Integrating transcription-factor abundance with chromatin accessibility in human erythroid lineage commitment. <i>Cell Reports Methods</i> , 2022, 2, 100188.	1.4	9
80	Immune Profiling Mass Cytometry Assay Harmonization: Multicenter Experience from CIMAC-CIDC. <i>Clinical Cancer Research</i> , 2021, 27, 5062-5071.	3.2	8
81	CytofIn enables integrated analysis of public mass cytometry datasets using generalized anchors. <i>Nature Communications</i> , 2022, 13, 934.	5.8	8
82	Supervised dimensionality reduction for exploration of single-cell data by HSS-LDA. <i>Patterns</i> , 2022, 3, 100536.	3.1	8
83	Diamonds in the doublets. <i>Nature Biotechnology</i> , 2020, 38, 559-561.	9.4	7
84	Mass ϵ tag barcoding for multiplexed analysis of human synaptosomes and other anuclear events. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2021, 99, 939-945.	1.1	7
85	Identification of Two CAR T-Cell Populations Associated with Complete Response or Progressive Disease in Adult Lymphoma Patients Treated with Axi-Cel. <i>Blood</i> , 2019, 134, 779-779.	0.6	6
86	Natural Killer Cell Receptors and Ligands Are Associated With Markers of HIV-1 Persistence in Chronically Infected ART Suppressed Patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 757846.	1.8	5
87	Ikaros Mediates Antigen Escape Following CD19 CAR T Cell Therapy in r/r B-ALL. <i>Blood</i> , 2021, 138, 613-613.	0.6	4
88	Mass Synaptometry: Applying Mass Cytometry to Single Synapse Analysis. <i>Methods in Molecular Biology</i> , 2022, 2417, 69-88.	0.4	4
89	Variation of Immune Cell Responses in Humans Reveals Sex-Specific Coordinated Signaling Across Cell Types. <i>Frontiers in Immunology</i> , 2022, 13, 867016.	2.2	4
90	OR40 Applying single-cell mass cytometry to investigate the immune system of highly sensitized patients who undergo intravenous immunoglobulin desensitization treatment. <i>Human Immunology</i> , 2017, 78, 37-38.	1.2	3

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91	Single Cell Trajectory Detection Orders Hallmarks of Early Human B Cell Development. <i>Blood</i> , 2012, 120, 1044-1044.	0.6	3
92	Proteomic Analysis of Pluripotent Stem Cells. , 2007, Chapter 1, Unit 1B.1.		2
93	An optimized protocol for phenotyping human granulocytes by mass cytometry. <i>STAR Protocols</i> , 2022, 3, 101280.	0.5	2
94	Revealing new biology from multiplexed, metal-isotope-tagged, single-cell readouts. <i>Trends in Cell Biology</i> , 2022, 32, 501-512.	3.6	2
95	The Interaction of SWI/SNF with the Ribosome Regulates Translation and Confers Sensitivity to Translation Pathway Inhibitors in Cancers with Complex Perturbations. <i>Cancer Research</i> , 2022, 82, 2829-2837.	0.4	2
96	Single-Cell Developmental Classification of B-Cell Precursor Acute Lymphoblastic Leukemia at Diagnosis Reveals Predictors of Relapse. <i>Experimental Hematology</i> , 2018, 64, S33-S34.	0.2	1
97	Single Cell Mass Cytometry of Dysregulated Signaling Networks in Myeloproliferative Neoplasms and Secondary Acute Myeloid Leukemia. <i>Blood</i> , 2012, 120, 703-703.	0.6	1
98	Comprehensive Immune Monitoring of Clinical Trials to Advance Human Immunotherapy. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
99	CIMAC-CIDC CyTOF harmonization.. <i>Journal of Clinical Oncology</i> , 2020, 38, e15242-e15242.	0.8	1
100	Abstract CT142: GD2.Ox40.CD28.z CAR T cell trial in neuroblastoma and osteosarcoma. <i>Cancer Research</i> , 2022, 82, CT142-CT142.	0.4	1
101	SESSION INTRODUCTION. , 2017, 22, 557-563.		0
102	Assessing basophil activation by flow cytometry and mass cytometry in blood stored 24 hours before analysis. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, AB124.	1.5	0
103	High-Dimensional Analysis of Intracellular Signaling and Dasatinib Inhibition In High-Risk Pediatric Leukemia by 31-Parameter Mass Cytometry. <i>Blood</i> , 2010, 116, 2761-2761.	0.6	0
104	Oncogene Withdrawal Selectively Alters Phosphoprotein States and Shifts Differentiation Status In Myeloid Leukemia Subpopulations. <i>Blood</i> , 2010, 116, 3160-3160.	0.6	0
105	Application of Mass Cytometry to Measure Proliferation During Normal and Malignant Hematopoietic Differentiation. <i>Blood</i> , 2011, 118, 4782-4782.	0.6	0
106	Mass Cytometry Organizes the Heterogeneity of Pediatric B Cell Acute Lymphoblastic Leukemia. <i>Blood</i> , 2011, 118, 753-753.	0.6	0
107	Signaling and Immunophenotypic Diversity in Pediatric Acute Myeloid Leukemia As Defined by 31-Parameter Single-Cell Mass Cytometry. <i>Blood</i> , 2011, 118, 2565-2565.	0.6	0
108	Activated NRAS Mediates Self-Renewal Capacity in AML by Facilitating the Mll/AF9-Specified Gene Expression Signature. <i>Blood</i> , 2012, 120, 5116-5116.	0.6	0

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109	Dimensionality Reduction Reveals Distinct Shapes of Normal and Malignant Hematopoietic Cell Populations. <i>Blood</i> , 2012, 120, 1451-1451.	0.6	0
110	Short Term Signalling Responses of the Most Primitive Subsets of Human Hematopoietic Cells Stimulated in Vitro Correlate with Their Subsequent Self-Renewal Behaviour.. <i>Blood</i> , 2012, 120, 2341-2341.	0.6	0
111	Network-Based Discovery of Prognostic Markers in Pediatric AML by Multi-Dimensional Single Cell Mass Cytometry. <i>Blood</i> , 2012, 120, 1411-1411.	0.6	0
112	Ras-Pathway Inhibition With Targeted Therapies Abrogates Self-Renewal In Acute Myelogenous Leukemia. <i>Blood</i> , 2013, 122, 819-819.	0.6	0
113	Abstract B15: NRASG12V oncogene mediates self-renewal in a murine model of acute myelogenous leukemia. , 2014, , .		0
114	Single Cell Developmental Classification of B Cell Precursor Acute Lymphoblastic Leukemia (BCP ALL) Reveals Link Between Phenotype, Signaling, and Drug Response. <i>Blood</i> , 2014, 124, 488-488.	0.6	0
115	Inhibition of Pre-BCR Signaling Mediates a Metabolic Switch in B-Cell Progenitor Acute Lymphoblastic Leukemia. <i>Blood</i> , 2021, 138, 615-615.	0.6	0
116	Chromatin Content Capture Reveals Acute Leukaemia Oncogenic Vulnerability Point in Human B Cell Development. <i>Blood</i> , 2021, 138, 673-673.	0.6	0
117	3011 “ SINGLE CELL PROTEOMIC MAP OF PHENOTYPIC IDENTITY AND MOLECULAR REGULATORS TO REDEFINE HUMAN HEMATOPOIETIC PROGENITORS. <i>Experimental Hematology</i> , 2021, 100, S48.	0.2	0