Jonathan M. Irish

List of Publications by Year
in descending order

121 papers	6,407 citations	101496 36 h-index	71651 76 g-index
138 all docs	138 docs citations	138 times ranked	10985 citing authors

#	Article	IF	Citations
1	Single Cell Profiling of Potentiated Phospho-Protein Networks in Cancer Cells. Cell, 2004, 118, 217-228.	13.5	655
2	Web‐Based Analysis and Publication of Flow Cytometry Experiments. Current Protocols in Cytometry, 2010, 53, Unit10.17.	3.7	418
3	Melanoma-specific MHC-II expression represents a tumour-autonomous phenotype and predicts response to anti-PD-1/PD-L1 therapy. Nature Communications, 2016, 7, 10582.	5.8	412
4	Role of glutathione depletion and reactive oxygen species generation in apoptotic signaling in a human B lymphoma cell line. Cell Death and Differentiation, 2002, 9, 252-263.	5.0	410
5	Mutations in early follicular lymphoma progenitors are associated with suppressed antigen presentation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1116-25.	3.3	307
6	Mapping normal and cancer cell signalling networks: towards single-cell proteomics. Nature Reviews Cancer, 2006, 6, 146-155.	12.8	297
7	Analysis of protein phosphorylation and cellular signaling events by flow cytometry: techniques and clinical applications. Clinical Immunology, 2004, 110, 206-221.	1.4	296
8	Hierarchy in somatic mutations arising during genomic evolution and progression of follicular lymphoma. Blood, 2013, 121, 1604-1611.	0.6	279
9	Mitochondrial dysregulation and glycolytic insufficiency functionally impair CD8 T cells infiltrating human renal cell carcinoma. JCI Insight, 2017, 2, .	2.3	257
10	Single-Cell Profiling Identifies Aberrant STAT5 Activation in Myeloid Malignancies with Specific Clinical and Biologic Correlates. Cancer Cell, 2008, 14, 335-343.	7.7	219
11	High PD-1 expression and suppressed cytokine signaling distinguish T cells infiltrating follicular lymphoma tumors from peripheral T cells. Blood, 2013, 121, 1367-1376.	0.6	147
12	B-cell signaling networks reveal a negative prognostic human lymphoma cell subset that emerges during tumor progression. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12747-12754.	3.3	143
13	Methods for discovery and characterization of cell subsets in high dimensional mass cytometry data. Methods, 2015, 82, 55-63.	1.9	133
14	Altered B-cell receptor signaling kinetics distinguish human follicular lymphoma B cells from tumor-infiltrating nonmalignant B cells. Blood, 2006, 108, 3135-3142.	0.6	130
15	Therapeutic effect of CD137 immunomodulation in lymphoma and its enhancement by Treg depletion. Blood, 2009, 114, 3431-3438.	0.6	121
16	Deep phenotyping of Tregs identifies an immune signature for idiopathic aplastic anemia and predicts response to treatment. Blood, 2016, 128, 1193-1205.	0.6	117
17	Kinetics of B Cell Receptor Signaling in Human B Cell Subsets Mapped by Phosphospecific Flow Cytometry. Journal of Immunology, 2006, 177, 1581-1589.	0.4	107
18	K-RasG12D expression induces hyperproliferation and aberrant signaling in primary hematopoietic stem/progenitor cells. Blood, 2007, 109, 3945-3952.	0.6	103

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19	Characterizing cell subsets using marker enrichment modeling. Nature Methods, 2017, 14, 275-278.	9.0	103
20	Single cell analysis of human tissues and solid tumors with mass cytometry. Cytometry Part B - Clinical Cytometry, 2017, 92, 68-78.	0.7	89
21	In Vivo Autofluorescence Imaging of Tumor Heterogeneity in Response to Treatment. Neoplasia, 2015, 17, 862-870.	2.3	82
22	Novel Hybrid Phenotype Revealed in Small Cell Lung Cancer by a Transcription Factor Network Model That Can Explain Tumor Heterogeneity. Cancer Research, 2017, 77, 1063-1074.	0.4	81
23	T Cells Expressing Checkpoint Receptor TIGIT Are Enriched in Follicular Lymphoma Tumors and Characterized by Reversible Suppression of T-cell Receptor Signaling. Clinical Cancer Research, 2018, 24, 870-881.	3.2	75
24	Mass cytometry deep phenotyping of human mononuclear phagocytes and myeloid-derived suppressor cells from human blood and bone marrow. Journal of Leukocyte Biology, 2017, 102, 437-447.	1.5	72
25	Flt3 Y591 duplication and Bcl-2 overexpression are detected in acute myeloid leukemia cells with high levels of phosphorylated wild-type p53. Blood, 2007, 109, 2589-2596.	0.6	69
26	Distinct patterns of B-cell receptor signaling in non-Hodgkin lymphomas identified by single-cell profiling. Blood, 2017, 129, 759-770.	0.6	69
27	Single-cell analysis by mass cytometry reveals metabolic states of early-activated CD8+ TÂcells during the primary immune response. Immunity, 2021, 54, 829-844.e5.	6.6	68
28	Multiparameter analysis of stimulated human peripheral blood mononuclear cells: A comparison of mass and fluorescence cytometry. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2016, 89, 271-280.	1.1	53
29	CD28 costimulation drives tumor-infiltrating T cell glycolysis to promote inflammation. JCI Insight, 2020, 5, .	2.3	52
30	High-Dimensional Analysis of Acute Myeloid Leukemia Reveals Phenotypic Changes in Persistent Cells during Induction Therapy. PLoS ONE, 2016, 11, e0153207.	1.1	50
31	High-Dimensional Single-Cell Cancer Biology. Current Topics in Microbiology and Immunology, 2014, 377, 1-21.	0.7	48
32	Characterizing Phenotypes and Signaling Networks of Single Human Cells by Mass Cytometry. Methods in Molecular Biology, 2015, 1346, 99-113.	0.4	48
33	Preparing Viable Single Cells from Human Tissue and Tumors for Cytomic Analysis. Current Protocols in Molecular Biology, 2017, 118, 25C.1.1-25C.1.23.	2.9	45
34	Machine learning reveals chronic graft-*versus*-host disease phenotypes and stratifies survival after stem cell transplant for hematologic malignancies. Haematologica, 2019, 104, 189-196.	1.7	44
35	Cytometryâ€based singleâ€cell analysis of intact epithelial signaling reveals <scp>MAPK</scp> activation divergent from <scp>TNF</scp>â€‏â€induced apoptosis *inÂvivo*. Molecular Systems Biology, 2015, 11, 835.	3.2	41
36	Joint Modeling and Registration of Cell Populations in Cohorts of High-Dimensional Flow Cytometric Data. PLoS ONE, 2014, 9, e100334.	1.1	41

#	Article	IF	Citations
37	Single Cell Analysis of Human Tissues and Solid Tumors with Mass Cytometry. , 2017, , .		40
38	Beyond the age of cellular discovery. Nature Immunology, 2014, 15, 1095-1097.	7.0	38
39	Systems immune monitoring in cancer therapy. European Journal of Cancer, 2016, 61, 77-84.	1.3	38
40	Cutting Edge: Redox Signaling Hypersensitivity Distinguishes Human Germinal Center B Cells. Journal of Immunology, 2015, 195, 1364-1367.	0.4	34
41	Discovery of human cell selective effector molecules using single cell multiplexed activity metabolomics. Nature Communications, 2018, 9, 39.	5.8	32
42	Two New Neutrophil Subsets Define a Discriminating Sepsis Signature. American Journal of Respiratory and Critical Care Medicine, 2022, 205, 46-59.	2.5	30
43	Single-cell profiling of the antigen-specific response to BNT162b2 SARS-CoV-2 RNA vaccine. Nature Communications, 2022, 13, .	5.8	28
44	Computational Immune Monitoring Reveals Abnormal Double-Negative T Cells Present across Human Tumor Types. Cancer Immunology Research, 2019, 7, 86-99.	1.6	27
45	High‐Dimensional Data Analysis Algorithms Yield Comparable Results for Mass Cytometry and Spectral Flow Cytometry Data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2020, 97, 824-831.	1.1	27
46	Beyond the message: advantages of snapshot proteomics with single‐cell mass cytometry in solid tumors. FEBS Journal, 2019, 286, 1523-1539.	2.2	26
47	Mass Cytometry of Follicular Lymphoma Tumors Reveals Intrinsic Heterogeneity in Proteins Including HLA‐DR and a Deficit in Nonmalignant Plasmablast and Germinal Center B‐Cell Populations. Cytometry Part B - Clinical Cytometry, 2017, 92, 79-87.	0.7	23
48	Genomic Profiling of T-Cell Neoplasms Reveals Frequent *JAK1* and *JAK3* Mutations With Clonal Evasion From Targeted Therapies. JCO Precision Oncology, 2018, 2018, 1-16.	1.5	23
49	Impaired coordination between signaling pathways is revealed in human colorectal cancer using single-cell mass cytometry of archival tissue blocks. Science Signaling, 2016, 9, rs11.	1.6	22
50	Unsupervised machine learning reveals risk stratifying glioblastoma tumor cells. ELife, 2020, 9, .	2.8	21
51	Regulatory myeloid cells: an underexplored continent in B-cell lymphomas. Cancer Immunology, Immunotherapy, 2017, 66, 1103-1111.	2.0	19
52	Phospho-specific flow cytometry identifies aberrant signaling in indolent B-cell lymphoma. BMC Cancer, 2012, 12, 478.	1.1	18
53	Myelodysplastic Syndrome Revealed by Systems Immunology in a Melanoma Patient Undergoing Anti‐PD-1 Therapy. Cancer Immunology Research, 2016, 4, 474-480.	1.6	17
54	Targeting In Vivo Metabolic Vulnerabilities of Th2 and Th17 Cells Reduces Airway Inflammation. Journal of Immunology, 2021, 206, 1127-1139.	0.4	16

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55	CMV exposure drives long-term CD57+ CD4 memory T-cell inflation following allogeneic stem cell transplant. Blood, 2021, 138, 2874-2885.	0.6	16
56	Unsupervised machine learning reveals key immune cell subsets in COVID-19, rhinovirus infection, and cancer therapy. ELife, 2021, 10, .	2.8	16
57	Generating Quantitative Cell Identity Labels with Marker Enrichment Modeling (MEM). Current Protocols in Cytometry, 2018, 83, 10.21.1-10.21.28.	3.7	15
58	Treg sensitivity to FasL and relative IL-2 deprivation drive idiopathic aplastic anemia immune dysfunction. Blood, 2020, 136, 885-897.	0.6	14
59	Mass cytometry defines distinct immune profile in germinal center B-cell lymphomas. Cancer Immunology, Immunotherapy, 2020, 69, 407-420.	2.0	12
60	WebFlow: A Software Package for High-Throughput Analysis of Flow Cytometry Data. Assay and Drug Development Technologies, 2009, 7, 44-55.	0.6	10
61	HLA-DR cancer cells expression correlates with T cell infiltration and is enriched in lung adenocarcinoma with indolent behavior. Scientific Reports, 2021, 11, 14424.	1.6	10
62	Location-dependent maintenance of intrinsic susceptibility to mTORC1-driven tumorigenesis. Life Science Alliance, 2019, 2, e201800218.	1.3	10
63	Characterization of patient specific signaling via augmentation of bayesian networks with disease and patient state nodes. , 2009, 2009, 6624-7.		9
64	<scp>BRAF</scp> and <scp>MEK</scp> inhibitor therapy eliminates Nestinâ€expressing melanoma cells in human tumors. Pigment Cell and Melanoma Research, 2018, 31, 708-719.	1.5	9
65	Human Germinal Center B Cells Differ from NaÃ¯ve and Memory B Cells in CD40 Expression and CD40Lâ€Induced Signaling Response. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2019, 95, 442-449.	1.1	9
66	DebarcodeR increases fluorescent cell barcoding capacity and accuracy. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2021, 99, 946-953.	1.1	8
67	Picturing Polarized Myeloid Phagocytes and Regulatory Cells by Mass Cytometry. Methods in Molecular Biology, 2019, 1989, 217-226.	0.4	7
68	Training Novices in Generation and Analysis of Highâ€Dimensional Human Cell Phosphoâ€Flow Cytometry Data. Current Protocols in Cytometry, 2020, 93, e71.	3.7	7
69	Circulating Myeloid Regulatory Cells: Promising Biomarkers in B-Cell Lymphomas. Frontiers in Immunology, 2020, 11, 623993.	2.2	6
70	Mass Cytometry Reveals PD1 Upregulation Is an Early Step in MDS Disease Progression. Blood, 2016, 128, 4296-4296.	0.6	6
71	Altered <scp>BCR</scp> and <scp>CD</scp>40 signalling are associated with clinical outcome in small lymphocytic lymphoma/chronic lymphocytic leukaemia and marginal zone lymphoma patients. British Journal of Haematology, 2012, 159, 0-0.	1.2	5
72	Nonclassical Monocytes Are Prone to Migrate Into Tumor in Diffuse Large B-Cell Lymphoma. Frontiers in Immunology, 2021, 12, 755623.	2.2	5

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73	Abstract B27: Phenotypic plasticity and heterogeneity in small cell lung cancer (SCLC): Novel molecular subtypes and potential for targeted therapy.. Clinical Cancer Research, 2014, 20, B27-B27.	3.2	4
74	High-Dimensional Analysis Reveals Distinct Endotypes in Patients With Idiopathic Inflammatory Myopathies. Frontiers in Immunology, 2022, 13, 756018.	2.2	4
75	NetworkPainter: dynamic intracellular pathway animation in Cytobank. BMC Bioinformatics, 2015, 16, 172.	1.2	3
76	Dissecting Complex Cellular Systems with High Dimensional Single Cell Mass Cytometry. , 2016, , 15-26.		3
77	A Novel Assay for Juvenile Myelomonocytic Leukemia Based on Aberrant Signaling Networks Measured Via Phospho-Specific Flow Cytometry Reduces Diagnosis Time from Weeks to Days.. Blood, 2007, 110, 546-546.	0.6	3
78	A Cytometrist's Guide to Coordinating and Performing Effective COVID â€19 Research. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2021, 99, 11-18.	1.1	2
79	Selective Inhibition of JAK1 Primes STAT5-Driven Human Leukemia Cells for ATRA-Induced Differentiation. Targeted Oncology, 2021, 16, 663-674.	1.7	2
80	Potentiated B-Cell Antigen Receptor Signaling In Mantle Cell Lymphoma Is Associated With Overexpression Of Surface CD79B and IgM. Blood, 2013, 122, 1768-1768.	0.6	2
81	Mass Cytometry of Acute Myeloid Leukemia Captures Early Therapy Response in Rare Cell Subsets. Blood, 2014, 124, 2381-2381.	0.6	2
82	Systems Immune Monitoring with Mass Cytometry Characterizes Altered Peripheral Immune Cell Environments in Patients with Chronic Graft Versus Host Disease. Blood, 2016, 128, 4572-4572.	0.6	2
83	Targeting metabolic dysregulation of T cells in kidney cancer.. Journal of Clinical Oncology, 2020, 38, 722-722.	0.8	2
84	Potentiated phospho-protein networks in cancer cells. Breast Cancer Research, 2005, 7, 1.	2.2	1
85	Machine Learning Reveals Patient Phenotypes and Stratifies Outcomes in Chronic Graft-Versus Host Disease. Biology of Blood and Marrow Transplantation, 2018, 24, S65.	2.0	1
86	Abstract 364: Mass cytometry of human glioblastoma characterizes more than 99 percent of cells and reveals intratumoral cell subsets defined by contrasting signaling network profiles. Cancer Research, 2017, 77, 364-364.	0.4	1
87	Expression of S100A9 in Bone Marrow Cells Differentiates Refractory Cytopenia with Multilineage Dysplasia (RCMD) from Refractory Anemia with Excess Blasts (RAEB) and Acute Myeloid Leukemia (AML). Blood, 2016, 128, 4303-4303.	0.6	1
88	Identification of Tigit on Intra-Tumor T Cells As a New Target for Immune Checkpoint Blockade in Follicular Lymphoma. Blood, 2016, 128, 917-917.	0.6	1
89	Cytomegalovirus Promotes Aberrant Memory CD4 T Cell Differentiation and Immune Function after Allogeneic Stem Cell Transplantation. Blood, 2020, 136, 15-16.	0.6	1
90	High-Dimensional Single-Cell Monitoring of Circulating Cells in Allergic Asthmatics Infected with Rhinovirus Reveals Dynamic Flux in Diverse Immune Cells. Journal of Allergy and Clinical Immunology, 2015, 135, AB382.	1.5	0

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91	Sa1830 Deciphering Multi-Pathway Signaling Heterogeneity of the Villus Epithelium in Response to TNF-α. Gastroenterology, 2015, 148, S-343.	0.6	0
92	CBIO-19. DISSECTING THE MULTICELLULAR ECOSYSTEM OF HUMAN GLIOBLASTOMA TUMORS USING SINGLE CELL MASS CYTOMETRY. Neuro-Oncology, 2016, 18, vi39-vi39.	0.6	0
93	Single Cell Mass Cytometry Identifies T-Regulatory Cell Subsets Associated with ECP Response in Chronic GVHD. Biology of Blood and Marrow Transplantation, 2016, 22, S400-S401.	2.0	0
94	P-165 Cytometry-Based Single Cell Analysis of Intact Epithelial Signaling Reveals MAPK Activation Divergent from TNF-α-Induced Apoptosis in Vivo. Inflammatory Bowel Diseases, 2016, 22, S59-S60.	0.9	0
95	The use of fluorescently-tagged apoptolidins in cellular uptake and response studies. Journal of Antibiotics, 2016, 69, 327-330.	1.0	0
96	Rhinovirus Infection Induces Dual Amplification of Virus- and Allergen-Specific T Cells with Discrete Phenotypes in Allergic Asthmatics. Journal of Allergy and Clinical Immunology, 2017, 139, AB93.	1.5	0
97	COMP-11. SINGLE CELL MASS CYTOMETRY SIGNALING PROFILES AND A NOVEL COMPUTATIONAL TOOL IDENTIFY HIGH RISK GLIOBLASTOMA CELLS. Neuro-Oncology, 2019, 21, vi63-vi63.	0.6	0
98	IMMU-37. SINGLE-CELL SYSTEMS NEUROIMMUNOLOGY REVEALS IMMUNOSUPPRESSIVE CORRELATES WITH VENTRICULAR STEM CELL NICHE CONTACT IN HUMAN GLIOBLASTOMA. Neuro-Oncology, 2019, 21, vi127-vi127.	0.6	0
99	A Novel System To Explore T-Cell Correlates Of Cross-Protection To Rhinovirus In A Human Sequential Infection Model.. Journal of Allergy and Clinical Immunology, 2020, 145, AB243.	1.5	0
100	Abstract PO014: Early lung adenocarcinoma subtyping based on MHC-I and II immunogenic response. , 2021, , .		0
101	Abstract MP49: Single Cell Multiplex Immunophenotyping Using Mass Cytometry And CITE-Seq Reveals Decreases In Circulating PD-1 $^{+}$ CD8 $^{+}$ Memory T Cells With Features Of Exhaustion In Human Hypertension. Hypertension, 2021, 78, .	1.3	0
102	Signaling Diversity in Human Lymphoma B Cells and in Tumor Infiltrating T Cells Correlates with Follicular Lymphoma Patient Clinical Outcomes. Blood, 2008, 112, 377-377.	0.6	0
103	Clinical Translation of a Prognostic Follicular Lymphoma Signaling Profile. Blood, 2010, 116, 636-636.	0.6	0
104	Hierarchy in Somatic Mutations Arising During Genomic Evolution and Progression of Follicular Lymphoma. Blood, 2012, 120, 148-148.	0.6	0
105	Comprehensive Hybrid Capture-Based Genomic Profiling of T-Cell Leukemias and Lymphomas Reveals Targetable JAK1 and JAK3 Co-Existing Mutations. Blood, 2014, 124, 1672-1672.	0.6	0
106	Abstract 3761: Distinct transcriptional programs drive phenotypic heterogeneity in small cell lung cancer. , 2015, , .		0
107	Dissecting Signaling Network Responses to PAK4 Allosteric Modulators (PAMs) in Cell Subsets within Primary Human Acute Myeloid Leukemia Samples. Blood, 2015, 126, 3686-3686.	0.6	0
108	Abstract B29: Reorganization of signaling modules revealed in human colorectal cancer using single-cell mass cytometry. , 2017, , .		0

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109	Abstract 3726: INCB52793 JAK1 inhibitor synergizes with ATRA to inhibit expansion of AML. , 2017, , .		0
110	Abstract 1772:PIK3CAC2 domain deletions hyperactivate PI3K, generate oncogene dependence and are exquisitely sensitive to PI3KÎ± inhibitors. , 2017, , .		0
111	Abstract 2911: Single cell mass cytometry analysis of human lung adenocarcinoma. , 2017, , .		0
112	Abstract 3935: Dissecting small cell lung carcinoma heterogeneity and chemotherapy resistance with mass cytometry. , 2017, , .		0
113	Abstract 2920: Characterizing human melanoma treatment responsein vivousing single-cell mass cytometry analysis of longitudinal tumor biopsies. , 2017, , .		0
114	Abstract 2180: Investigating lung adenocarcinoma tumor heterogeneity with single-cell mass cytometry. , 2018, , .		0
115	Abstract P157: Immunophenotyping Human Hypertension Using Single Cell Mass Cytometry. Hypertension, 2018, 72, .	1.3	0
116	Abstract 4701: Single cell mass cytometry analysis distinguishes indolent from aggressive lung adenocarcinomas. , 2019, , .		0
117	Abstract 021: Single Cell Multiplex Mass Cytometry Reveals Differential Abundance of Specific Memory and Regulatory T Cell Populations in Human Hypertension. Hypertension, 2019, 74, .	1.3	0
118	Abstract 2692: Novel chemotherapy stable subpopulations are conserved across multiple small cell lung carcinoma patient derived xenograft models. , 2020, , .		0
119	IMMU-16. TWO DISTINCT SUBSETS OF NATURAL KILLER CELLS ARE ENRICHED IN THE TUMOR MICROENVIRONMENT AND CORRELATE WITH SURVIVAL OUTCOME IN HUMAN GLIOBLASTOMA.. Neuro-Oncology, 2020, 22, ii107-ii108.	0.6	0
120	Abstract PO-045: Single cell proteomic analysis of lung adenocarcinoma identifies high HLA-DR expression to be associated with indolent tumor behavior. , 2020, , .		0
121	661â€…Five immunotypic signatures identified in human glioblastoma correlate with tumor contact with the lateral ventricle, immune suppression, and patient outcome. , 2020, , .		0