Ryan R Brinkman

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

8,441 130 45 91 h-index g-index citations papers 6.9 148 5.46 10,130 L-index avg, IF ext. papers ext. citations

#	Paper	IF	Citations
130	Occurrence of T-cell and NK-cell subsets with less well-recognized phenotypes in peripheral blood submitted for routine flow cytometry analysis. <i>Cytometry Part B - Clinical Cytometry</i> , 2021 , 100, 235-239	3.4	2
129	ISAC Probe Tag Dictionary: Standardized Nomenclature for Detection and Visualization Labels Used in Cytometry and Microscopy Imaging. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2021 , 99, 103-106	4.6	3
128	Data File Standard for Flow Cytometry, Version FCS 3.2. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2021 , 99, 100-102	4.6	3
127	Clinical Protocol for a Longitudinal Cohort Study Employing Systems Biology to Identify Markers of Vaccine Immunogenicity in Newborn Infants in The Gambia and Papua New Guinea. <i>Frontiers in Pediatrics</i> , 2020 , 8, 197	3.4	7
126	BCG vaccination-induced emergency granulopoiesis provides rapid protection from neonatal sepsis. <i>Science Translational Medicine</i> , 2020 , 12,	17.5	35
125	The miR-185/PAK6 axis predicts therapy response and regulates survival of drug-resistant leukemic stem cells in CML. <i>Blood</i> , 2020 , 136, 596-609	2.2	12
124	Single Cell Phenotypic Profiling of 27 DLBCL Cases Reveals Marked Intertumoral and Intratumoral Heterogeneity. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2020 , 97, 620-629	4.6	8
123	High-throughput phenotyping reveals expansive genetic and structural underpinnings of immune variation. <i>Nature Immunology</i> , 2020 , 21, 86-100	19.1	15
122	Systems Biology Methods Applied to Blood and Tissue for a Comprehensive Analysis of Immune Response to Hepatitis B Vaccine in Adults. <i>Frontiers in Immunology</i> , 2020 , 11, 580373	8.4	8
121	"Age Related Differences in the Biology of Chronic Graft-Versus-Host Disease After Hematopoietic Stem Cell Transplantation". <i>Frontiers in Immunology</i> , 2020 , 11, 571884	8.4	3
120	Multi-Omic Data Integration Allows Baseline Immune Signatures to Predict Hepatitis B Vaccine Response in a Small Cohort. <i>Frontiers in Immunology</i> , 2020 , 11, 578801	8.4	9
119	Guidelines for the use of flow cytometry and cell sorting in immunological studies (second edition). <i>European Journal of Immunology</i> , 2019 , 49, 1457-1973	6.1	485
118	Flow cytometry data analysis: Recent tools and algorithms. <i>International Journal of Laboratory Hematology</i> , 2019 , 41 Suppl 1, 56-62	2.5	28
117	Data-Driven Flow Cytometry Analysis. <i>Methods in Molecular Biology</i> , 2019 , 1989, 245-265	1.4	4
116	Dynamic molecular changes during the first week of human life follow a robust developmental trajectory. <i>Nature Communications</i> , 2019 , 10, 1092	17.4	79
115	Improving the Quality and Reproducibility of Flow Cytometry in the Lung. An Official American Thoracic Society Workshop Report. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2019 , 61, 150-161	5.7	23
114	Implementation and Validation of an Automated Flow Cytometry Analysis Pipeline for Human Immune Profiling. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2019 , 95, 183-191	4.6	11

113	flowLearn: fast and precise identification and quality checking of cell populations in flow cytometry. <i>Bioinformatics</i> , 2018 , 34, 2245-2253	7.2	22
112	High throughput automated analysis of big flow cytometry data. <i>Methods</i> , 2018 , 134-135, 164-176	4.6	13
111	ddPCRclust: an R package and Shiny app for automated analysis of multiplexed ddPCR data. <i>Bioinformatics</i> , 2018 , 34, 2687-2689	7.2	8
110	Use FlowRepository to share your clinical data upon study publication. <i>Cytometry Part B - Clinical Cytometry</i> , 2018 , 94, 196-198	3.4	5
109	A standardized immune phenotyping and automated data analysis platform for multicenter biomarker studies. <i>JCI Insight</i> , 2018 , 3,	9.9	19
108	Single-Cell Profiling Reveals Distinct Tumor Subtypes and Their Associated T-Cell Environments in Follicular Lymphoma. <i>Blood</i> , 2018 , 132, 1577-1577	2.2	
107	Global Transcriptome Profiling Identifies a Key Mir-185-PAK6 Axis That Promotes Survival of Leukemic Stem Cells and Drug-Insensitive Blasts in BCR-ABL+ Human Leukemia. <i>Blood</i> , 2018 , 132, 931-50.	9 3 1 ²	
106	Methodology for evaluating and comparing flow cytometers: A multisite study of 23 instruments. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2018 , 93, 1087-1091	4.6	8
105	Evaluating flow cytometer performance with weighted quadratic least squares analysis of LED and multi-level bead data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2017 , 91, 232-249	4.6	10
104	Guidelines for the use of flow cytometry and cell sorting in immunological studies. <i>European Journal of Immunology</i> , 2017 , 47, 1584-1797	6.1	359
103	An Early NaWe T Cell Population Lacking PD1 Expression at Day 100 As A Prognostic Biomarker of Chronic GVHD. <i>Transplantation</i> , 2017 , 101, S40	1.8	
102	Standardized Immunophenotyping in the Canadian National Transplant Research Program. <i>Transplantation</i> , 2017 , 101, S62	1.8	
101	T-Cell Phenotypes Predictive of Frailty and Mortality in Elderly Nursing Home Residents. <i>Journal of the American Geriatrics Society</i> , 2017 , 65, 153-159	5.6	22
100	Standardizing Flow Cytometry Immunophenotyping Analysis from the Human ImmunoPhenotyping Consortium. <i>Scientific Reports</i> , 2016 , 6, 20686	4.9	168
99	The Ontology for Biomedical Investigations. <i>PLoS ONE</i> , 2016 , 11, e0154556	3.7	143
98	flowClean: Automated identification and removal of fluorescence anomalies in flow cytometry data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2016 , 89, 461-71	4.6	27
97	A benchmark for evaluation of algorithms for identification of cellular correlates of clinical outcomes. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2016 , 89, 16-21	4.6	51
96	Publishing code is essential for reproducible flow cytometry bioinformatics. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2016 , 89, 10-1	4.6	7

95	Thinking outside the gate: single-cell assessments in multiple dimensions. <i>Immunity</i> , 2015 , 42, 591-2	32.3	51
94	Deep profiling of multitube flow cytometry data. <i>Bioinformatics</i> , 2015 , 31, 1623-31	7.2	10
93	ISACQ classification results file format. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2015 , 87, 86-8	4.6	4
92	flowCL: ontology-based cell population labelling in flow cytometry. <i>Bioinformatics</i> , 2015 , 31, 1337-9	7.2	15
91	A randomized controlled trial on the effects of goal-directed therapy on the inflammatory response open abdominal aortic aneurysm repair. <i>Critical Care</i> , 2015 , 19, 247	10.8	25
90	ISACQ Gating-ML 2.0 data exchange standard for gating description. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2015 , 87, 683-7	4.6	9
89	flowDensity: reproducing manual gating of flow cytometry data by automated density-based cell population identification. <i>Bioinformatics</i> , 2015 , 31, 606-7	7.2	73
88	The core autophagy protein ATG4B is a potential biomarker and therapeutic target in CML stem/progenitor cells. <i>Blood</i> , 2014 , 123, 3622-34	2.2	139
87	The logic of surveillance guidelines: an analysis of vaccine adverse event reports from an ontological perspective. <i>PLoS ONE</i> , 2014 , 9, e92632	3.7	6
86	Enhanced flowType/RchyOptimyx: a BioConductor pipeline for discovery in high-dimensional cytometry data. <i>Bioinformatics</i> , 2014 , 30, 1329-30	7.2	23
85	Bim regulates alloimmune-mediated vascular injury through effects on T-cell activation and death. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2014 , 34, 1290-7	9.4	5
84	Computational analysis optimizes the flow cytometric evaluation for lymphoma. <i>Cytometry Part B - Clinical Cytometry</i> , 2014 , 86, 18-24	3.4	6
83	Computational analysis of high-dimensional flow cytometric data for diagnosis and discovery. <i>Current Topics in Microbiology and Immunology</i> , 2014 , 377, 159-75	3.3	3
82	Identification of New microRNA Biomarkers and Candidate Target Genes in Primitive CML Cells Using Global Comparative RNA analyses. <i>Blood</i> , 2014 , 124, 3133-3133	2.2	2
81	Immune biomarkers predictive of respiratory viral infection in elderly nursing home residents. <i>PLoS ONE</i> , 2014 , 9, e108481	3.7	37
80	GenePattern flow cytometry suite. Source Code for Biology and Medicine, 2013, 8, 14	1.9	14
79	Cerebral oxygen desaturation during one-lung ventilation: correlation with hemodynamic variables. <i>Canadian Journal of Anaesthesia</i> , 2013 , 60, 660-6	3	14
78	Scoring relevancy of features based on combinatorial analysis of Lasso with application to lymphoma diagnosis. <i>BMC Genomics</i> , 2013 , 14 Suppl 1, S14	4.5	18

77	BAIT: Organizing genomes and mapping rearrangements in single cells. <i>Genome Medicine</i> , 2013 , 5, 82	14.4	26
76	Critical assessment of automated flow cytometry data analysis techniques. <i>Nature Methods</i> , 2013 , 10, 228-38	21.6	392
75	The luminal progenitor compartment of the normal human mammary gland constitutes a unique site of telomere dysfunction. <i>Stem Cell Reports</i> , 2013 , 1, 28-37	8	40
74	Flow cytometry bioinformatics. <i>PLoS Computational Biology</i> , 2013 , 9, e1003365	5	63
73	Computational analysis optimizes the flow cytometric evaluation for lymphoma. <i>Cytometry Part B - Clinical Cytometry</i> , 2013 ,	3.4	3
72	Integration of lyoplate based flow cytometry and computational analysis for standardized immunological biomarker discovery. <i>PLoS ONE</i> , 2013 , 8, e65485	3.7	14
71	Distinct but phenotypically heterogeneous human cell populations produce rapid recovery of platelets and neutrophils after transplantation. <i>Blood</i> , 2012 , 119, 3431-9	2.2	18
70	B cells with high side scatter parameter by flow cytometry correlate with inferior survival in diffuse large B-cell lymphoma. <i>American Journal of Clinical Pathology</i> , 2012 , 137, 805-14	1.9	10
69	Early immunologic correlates of HIV protection can be identified from computational analysis of complex multivariate T-cell flow cytometry assays. <i>Bioinformatics</i> , 2012 , 28, 1009-16	7.2	64
68	RchyOptimyx: cellular hierarchy optimization for flow cytometry. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2012 , 81, 1022-30	4.6	46
67	Hematopoietic stem cell subtypes expand differentially during development and display distinct lymphopoietic programs. <i>Cell Stem Cell</i> , 2012 , 10, 273-83	18	220
66	FlowRepository: a resource of annotated flow cytometry datasets associated with peer-reviewed publications. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2012 , 81, 727-31	4.6	109
65	The phenotypic distribution and functional profile of tuberculin-specific CD4 T-cells characterizes different stages of TB infection. <i>Cytometry Part B - Clinical Cytometry</i> , 2012 , 82, 360-8	3.4	15
64	Preparing a Minimum Information about a Flow Cytometry Experiment (MIFlowCyt) compliant manuscript using the International Society for Advancement of Cytometry (ISAC) FCS file repository (FlowRepository.org). <i>Current Protocols in Cytometry</i> , 2012 , Chapter 10, Unit 10.18	3.6	17
63	FCS 3.1 Implementation guidance. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2012 , 81, 523-6	4.6	5
62	Automated analysis of multidimensional flow cytometry data improves diagnostic accuracy between mantle cell lymphoma and small lymphocytic lymphoma. <i>American Journal of Clinical Pathology</i> , 2012 , 137, 75-85	1.9	32
61	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, 2341-2	347	
60	Flow cytometry data standards. <i>BMC Research Notes</i> , 2011 , 4, 50	2.3	11

59	Rapid cell population identification in flow cytometry data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2011 , 79, 6-13	4.6	136
58	Overcoming the ontology enrichment bottleneck with Quick Term Templates. <i>Applied Ontology</i> , 2011 , 6, 13-22	1.4	4
57	MIREOT: The minimum information to reference an external ontology term. <i>Applied Ontology</i> , 2011 , 6, 23-33	1.4	57
56	Per-channel basis normalization methods for flow cytometry data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2010 , 77, 121-31	4.6	55
55	Data File Standard for Flow Cytometry, version FCS 3.1. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2010 , 77, 97-100	4.6	32
54	Properties of CD34+ CML stem/progenitor cells that correlate with different clinical responses to imatinib mesylate. <i>Blood</i> , 2010 , 116, 2112-21	2.2	44
53	Data reduction for spectral clustering to analyze high throughput flow cytometry data. <i>BMC Bioinformatics</i> , 2010 , 11, 403	3.6	107
52	OntoFox: web-based support for ontology reuse. <i>BMC Research Notes</i> , 2010 , 3, 175	2.3	117
51	Modeling biomedical experimental processes with OBI. <i>Journal of Biomedical Semantics</i> , 2010 , 1 Suppl 1, S7	2.2	187
50	Identification of B cells through negative gating-An example of the MIFlowCyt standard applied. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2010, 77, 546-51	4.6	13
49	Correlation analysis of intracellular and secreted cytokines via the generalized integrated mean fluorescence intensity. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2010 , 77, 873-80	4.6	35
48	Analysis of High-Throughput Flow Cytometry Data Using plateCore. <i>Advances in Bioinformatics</i> , 2009 , 356141	5.5	8
47	A survey of flow cytometry data analysis methods. Advances in Bioinformatics, 2009, 584603	5.5	65
46	Recent bioinformatics advances in the analysis of high throughput flow cytometry data. <i>Advances in Bioinformatics</i> , 2009 , 461763	5.5	1
45	Overcoming the Ontology Enrichment Bottleneck with Quick Term Templates. <i>Nature Precedings</i> , 2009 ,		4
44	A pipeline for automated analysis of flow cytometry data: preliminary results on lymphoma sub-type diagnosis. Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference, 2009,	0.9	6
43	A container for the advanced cytometry standard (ACS) 2009 ,		1
42	flowCore: a Bioconductor package for high throughput flow cytometry. <i>BMC Bioinformatics</i> , 2009 , 10, 106	3.6	300

(2007-2009)

41	flowClust: a Bioconductor package for automated gating of flow cytometry data. <i>BMC Bioinformatics</i> , 2009 , 10, 145	3.6	129
40	FuGEFlow: data model and markup language for flow cytometry. <i>BMC Bioinformatics</i> , 2009 , 10, 184	3.6	6
39	Reply to @ eassessing the human mammary stem cell concept by modeling limiting dilution transplantation assays <i>QNature Medicine</i> , 2009 , 15, 604-605	50.5	
38	Cytogenetic and molecular responses to standard-dose imatinib in chronic myeloid leukemia are correlated with Sokal risk scores and duration of therapy but not trough imatinib plasma levels. <i>Leukemia Research</i> , 2009 , 33, 271-5	2.7	63
37	Correlation between trough imatinib plasma concentration and clinical response in chronic myeloid leukemia. <i>Leukemia Research</i> , 2009 , 33, 1149-1150	2.7	
36	Reduction in multi-lineage and erythroid progenitors distinguishes myelodysplastic syndromes from non-malignant cytopenias. <i>Leukemia Research</i> , 2009 , 33, 1636-42	2.7	O
35	Diffuse large B-cell lymphoma: reduced CD20 expression is associated with an inferior survival. <i>Blood</i> , 2009 , 113, 3773-80	2.2	106
34	Merging mixture components for cell population identification in flow cytometry. <i>Advances in Bioinformatics</i> , 2009 , 247646	5.5	72
33	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008 , 26, 889-96	44.5	417
32	Allogeneic SCT for relapsed composite and transformed lymphoma using related and unrelated donors: long-term results. <i>Bone Marrow Transplantation</i> , 2008 , 42, 601-8	4.4	20
31	Automated gating of flow cytometry data via robust model-based clustering. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2008 , 73, 321-32	4.6	185
30	MIFlowCyt: the minimum information about a Flow Cytometry Experiment. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2008 , 73, 926-30	4.6	279
29	Gating-ML: XML-based gating descriptions in flow cytometry. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2008 , 73A, 1151-7	4.6	28
28	Salvage Therapy with Allogeneic Stem Cell Transplantation Results in Better Outcome for Patients with Relapsed/Refractory Follicular Lymphoma Compared to Those with Transformed Non-Hodgkin Lymphoma: A Population-Based Comparative Study <i>Blood</i> , 2008 , 112, 975-975	2.2	4
27	Impact of Comorbidity Index on Outcome with Allogeneic Hematopoetic Stem Cell Transplantation for Chronic Lymphocytic Leukemia. <i>Blood</i> , 2008 , 112, 3305-3305	2.2	
26	Data quality assessment of ungated flow cytometry data in high throughput experiments. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2007, 71, 393-403	4.6	30
25	The relationship between CAG repeat length and age of onset differs for Huntington@ disease patients with juvenile onset or adult onset. <i>Annals of Human Genetics</i> , 2007 , 71, 295-301	2.2	89
24	Long-term propagation of distinct hematopoietic differentiation programs in vivo. <i>Cell Stem Cell</i> , 2007 , 1, 218-29	18	437

23	High-content flow cytometry and temporal data analysis for defining a cellular signature of graft-versus-host disease. <i>Biology of Blood and Marrow Transplantation</i> , 2007 , 13, 691-700	4.7	55
22	Allogeneic Stem Cell Transplant in First Complete Remission Overcomes the Poor Prognosis Associated with the FLT-3 Internal Tandem Duplication in Acute Myeloid Leukemia <i>Blood</i> , 2007 , 110, 3491-3491	2.2	
21	Development of FuGO: an ontology for functional genomics investigations. <i>OMICS A Journal of Integrative Biology</i> , 2006 , 10, 199-204	3.8	45
20	Data standards for flow cytometry. OMICS A Journal of Integrative Biology, 2006, 10, 209-14	3.8	20
19	Human monogenic disorders - a source of novel drug targets. <i>Nature Reviews Genetics</i> , 2006 , 7, 249-60	30.1	69
18	Wrestling with SUMO and bio-ontologies. <i>Nature Biotechnology</i> , 2006 , 24, 21-2; author reply 23	44.5	6
17	Wrestling with SUMO and bio-ontologies. <i>Nature Biotechnology</i> , 2006 , 24, 21; author reply 23	44.5	5
16	Prior Rituximab Reduces Relapse and Improves Survival Following High Dose Chemotherapy and Stem Cell Transplantation for Relapsed Composite Low and Intermediate Grade (Including Transformed) Lymphoma <i>Blood</i> , 2006 , 108, 3662-3662	2.2	0
15	A new model for prediction of the age of onset and penetrance for Huntington@ disease based on CAG length. <i>Clinical Genetics</i> , 2004 , 65, 267-77	4	614
14	Evidence for a modifier of onset age in Huntington disease linked to the HD gene in 4p16. <i>Neurogenetics</i> , 2004 , 5, 109-14	3	63
13	Identification of a novel gene (HSN2) causing hereditary sensory and autonomic neuropathy type II through the Study of Canadian Genetic Isolates. <i>American Journal of Human Genetics</i> , 2004 , 74, 1064-73	11	111
12	Interaction of normal and expanded CAG repeat sizes influences age at onset of Huntington disease 2003 , 119A, 279-82		117
11	Psychological consequences and predictors of adverse events in the first 5 years after predictive testing for Huntington disease. <i>Clinical Genetics</i> , 2003 , 64, 300-9	4	97
10	A genome scan for modifiers of age at onset in Huntington disease: The HD MAPS study. <i>American Journal of Human Genetics</i> , 2003 , 73, 682-7	11	131
9	Familial influence on age of onset among siblings with Huntington disease*. <i>American Journal of Medical Genetics Part A</i> , 2001 , 105, 399-403		75
8	Clinical markers of early disease in persons near onset of Huntington@ disease. <i>Neurology</i> , 2001 , 57, 658	366₹	180
7	A worldwide assessment of the frequency of suicide, suicide attempts, or psychiatric hospitalization after predictive testing for Huntington disease. <i>American Journal of Human Genetics</i> , 1999 , 64, 1293-304	11	214
6	A yeast artificial chromosome-based physical map of the juvenile amyotrophic lateral sclerosis (ALS2) critical region on human chromosome 2q33-q34. <i>Genomics</i> , 1999 , 55, 106-12	4.3	18

LIST OF PUBLICATIONS

5	Representation of cloned genomic sequences in two sequencing vectors: correlation of DNA sequence and subclone distribution. <i>Nucleic Acids Research</i> , 1997 , 25, 2960-6	20.1	16
4	Toward understanding the molecular pathology of Huntington@ disease. <i>Brain Pathology</i> , 1997 , 7, 979-1	l 6 02	68
3	The construction and analysis of M13 libraries prepared from YAC DNA. <i>Nucleic Acids Research</i> , 1995 , 23, 670-4	20.1	23
2	Complete nucleotide sequence of Saccharomyces cerevisiae chromosome VIII. <i>Science</i> , 1994 , 265, 2077-	83 .3	266
1	flowCut IAn R package for precise and accurate automated removal of outlier events and flagging of files based on time versus fluorescence analysis		3