Ryan R Brinkman

List of Publications by Year
in descending order

139 papers	11,211 citations	47006 47 h-index	32842 100 g-index
148 all docs	148 docs citations	148 times ranked	16743 citing authors

#	Article	IF	Citations
1	Guidelines for the use of flow cytometry and cell sorting in immunological studies (second edition). European Journal of Immunology, 2019, 49, 1457-1973.	2.9	766
2	A new model for prediction of the age of onset and penetrance for Huntington's disease based on CAG length. Clinical Genetics, 2004, 65, 267-277.	2.0	738
3	Long-Term Propagation of Distinct Hematopoietic Differentiation Programs In Vivo. Cell Stem Cell, 2007, 1, 218-229.	11.1	520
4	Critical assessment of automated flow cytometry data analysis techniques. Nature Methods, 2013, 10, 228-238.	19.0	509
5	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. Nature Biotechnology, 2008, 26, 889-896.	17.5	506
6	Guidelines for the use of flow cytometry and cell sorting in immunological studies[*]. European Journal of Immunology, 2017, 47, 1584-1797.	2.9	505
7	flowCore: a Bioconductor package for high throughput flow cytometry. BMC Bioinformatics, 2009, 10, 106.	2.6	484
8	MIFlowCyt: The minimum information about a flow cytometry experiment. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2008, 73A, 926-930.	1.5	381
9	Complete nucleotide sequence of Saccharomyces cerevisiae chromosome VIII. Science, 1994, 265, 2077-2082.	12.6	303
10	Hematopoietic Stem Cell Subtypes Expand Differentially during Development and Display Distinct Lymphopoietic Programs. Cell Stem Cell, 2012, 10, 273-283.	11.1	277
11	A Worldwide Assessment of the Frequency of Suicide, Suicide Attempts, or Psychiatric Hospitalization after Predictive Testing for Huntington Disease. American Journal of Human Genetics, 1999, 64, 1293-1304.	6.2	271
12	Standardizing Flow Cytometry Immunophenotyping Analysis from the Human ImmunoPhenotyping Consortium. Scientific Reports, 2016, 6, 20686.	3.3	240
13	Automated gating of flow cytometry data via robust model‐based clustering. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2008, 73A, 321-332.	1.5	224
14	The Ontology for Biomedical Investigations. PLoS ONE, 2016, 11, e0154556.	2.5	217
15	Modeling biomedical experimental processes with OBI. Journal of Biomedical Semantics, 2010, 1, S7.	1.6	207
16	Clinical markers of early disease in persons near onset of Huntington's disease. Neurology, 2001, 57, 658-662.	1.1	197
17	Rapid cell population identification in flow cytometry data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2011, 79A, 6-13.	1.5	183
18	The core autophagy protein ATG4B is a potential biomarker and therapeutic target in CML stem/progenitor cells. Blood, 2014, 123, 3622-3634.	1.4	177

#	ARTICLE	IF	CITATIONS
19	flowClust: a Bioconductor package for automated gating of flow cytometry data. BMC Bioinformatics, 2009, 10, 145.	2.6	171
20	FlowRepository: A resource of annotated flow cytometry datasets associated with peerâ€reviewed publications. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2012, 81A, 727-731.	1.5	159
21	Dynamic molecular changes during the first week of human life follow a robust developmental trajectory. Nature Communications, 2019, 10, 1092.	12.8	151
22	A Genome Scan for Modifiers of Age at Onset in Huntington Disease: The HD MAPS Study. American Journal of Human Genetics, 2003, 73, 682-687.	6.2	148
23	Interaction of normal and expanded CAG repeat sizes influences age at onset of Huntington disease. , 2003, 119A, 279-282.		146
24	OntoFox: web-based support for ontology reuse. BMC Research Notes, 2010, 3, 175.	1.4	145
25	Data reduction for spectral clustering to analyze high throughput flow cytometry data. BMC Bioinformatics, 2010, 11, 403.	2.6	139
26	Identification of a Novel Gene (HSN2) Causing Hereditary Sensory and Autonomic Neuropathy Type II through the Study of Canadian Genetic Isolates. American Journal of Human Genetics, 2004, 74, 1064-1073.	6.2	133
27	Diffuse large B-cell lymphoma: reduced CD20 expression is associated with an inferior survival. Blood, 2009, 113, 3773-3780.	1.4	133
28	The Relationship Between CAG Repeat Length and Age of Onset Differs for Huntington's Disease Patients with Juvenile Onset or Adult Onset. Annals of Human Genetics, 2007, 71, 295-301.	0.8	110
29	Psychological consequences and predictors of adverse events in the first 5 years after predictive testing for Huntington's disease. Clinical Genetics, 2003, 64, 300-309.	2.0	107
30	flowDensity: reproducing manual gating of flow cytometry data by automated density-based cell population identification. Bioinformatics, 2015, 31, 606-607.	4.1	105
31	Familial influence on age of onset among siblings with Huntington disease. American Journal of Medical Genetics Part A, 2001, 105, 399-403.	2.4	92
32	Merging Mixture Components for Cell Population Identification in Flow Cytometry. Advances in Bioinformatics, 2009, 2009, 1-12.	5.7	92
33	A Survey of Flow Cytometry Data Analysis Methods. Advances in Bioinformatics, 2009, 2009, 1-19.	5.7	84
34	Human monogenic disorders â€" a source of novel drug targets. Nature Reviews Genetics, 2006, 7, 249-260.	16.3	81
35	Perâ€channel basis normalization methods for flow cytometry data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2010, 77A, 121-131.	1.5	79
36	Flow Cytometry Bioinformatics. PLoS Computational Biology, 2013, 9, e1003365.	3.2	79

#	Article	IF	Citations
37	MIREOT: The minimum information to reference an external ontology term. Applied Ontology, 2011, 6, 23-33.	2.0	78
38	BCG vaccinationâ€"induced emergency granulopoiesis provides rapid protection from neonatal sepsis. Science Translational Medicine, 2020, 12, .	12.4	76
39	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. Leukemia Research, 2009, 33, 271-275.	0.8	74
40	Early immunologic correlates of HIV protection can be identified from computational analysis of complex multivariate T-cell flow cytometry assays. Bioinformatics, 2012, 28, 1009-1016.	4.1	70
41	Toward Understanding the Molecular Pathology of Huntington's Disease. Brain Pathology, 1997, 7, 979-1002.	4.1	69
42	Evidence for a modifier of onset age in Huntington disease linked to the HD gene in 4p16. Neurogenetics, 2004, 5, 109-114.	1.4	67
43	High-Content Flow Cytometry and Temporal Data Analysis for Defining a Cellular Signature of Graft-Versus-Host Disease. Biology of Blood and Marrow Transplantation, 2007, 13, 691-700.	2.0	67
44	Thinking Outside the Gate: Single-Cell Assessments in Multiple Dimensions. Immunity, 2015, 42, 591-592.	14.3	67
45	A benchmark for evaluation of algorithms for identification of cellular correlates of clinical outcomes. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2016, 89, 16-21.	1.5	65
46	Development of FuGO: An Ontology for Functional Genomics Investigations. OMICS A Journal of Integrative Biology, 2006, 10, 199-204.	2.0	56
47	Properties of CD34+ CML stem/progenitor cells that correlate with different clinical responses to imatinib mesylate. Blood, 2010, 116, 2112-2121.	1.4	56
48	RchyOptimyx: Cellular hierarchy optimization for flow cytometry. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2012, 81A, 1022-1030.	1.5	53
49	Flow cytometry data analysis: Recent tools and algorithms. International Journal of Laboratory Hematology, 2019, 41, 56-62.	1.3	53
50	flow<scp>C</scp>lean: Automated identification and removal of fluorescence anomalies in flow cytometry data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2016, 89, 461-471.	1.5	52
51	Correlation analysis of intracellular and secreted cytokines via the generalized integrated mean fluorescence intensity. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2010, 77A, 873-880.	1.5	50
52	The Luminal Progenitor Compartment of the Normal Human Mammary Gland Constitutes a Unique Site of Telomere Dysfunction. Stem Cell Reports, 2013, 1, 28-37.	4.8	50
53	Data File Standard for Flow Cytometry, version FCS 3.1. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2010, 77A, 97-100.	1.5	49
54	Improving the Quality and Reproducibility of Flow Cytometry in the Lung. An Official American Thoracic Society Workshop Report. American Journal of Respiratory Cell and Molecular Biology, 2019, 61, 150-161.	2.9	49

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55	T‑Cell Phenotypes Predictive of Frailty and Mortality in Elderly Nursing Home Residents. Journal of the American Geriatrics Society, 2017, 65, 153-159.	2.6	46
56	Immune Biomarkers Predictive of Respiratory Viral Infection in Elderly Nursing Home Residents. PLoS ONE, 2014, 9, e108481.	2.5	43
57	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, 71A, 393-403.	1.5	38
58	flowLearn: fast and precise identification and quality checking of cell populations in flow cytometry. Bioinformatics, 2018, 34, 2245-2253.	4.1	37
59	Gating‑ML: XML‑based gating descriptions in flow cytometry. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2008, 73A, 1151-1157.	1.5	36
60	Automated Analysis of Multidimensional Flow Cytometry Data Improves Diagnostic Accuracy Between Mantle Cell Lymphoma and Small Lymphocytic Lymphoma. American Journal of Clinical Pathology, 2012, 137, 75-85.	0.7	36
61	Enhanced flowType/RchyOptimyx: a Bioconductor pipeline for discovery in high-dimensional cytometry data. Bioinformatics, 2014, 30, 1329-1330.	4.1	33
62	BAIT: Organizing genomes and mapping rearrangements in single cells. Genome Medicine, 2013, 5, 82.	8.2	32
63	High-throughput phenotyping reveals expansive genetic and structural underpinnings of immune variation. Nature Immunology, 2020, 21, 86-100.	14.5	32
64	The miR-185/PAK6 axis predicts therapy response and regulates survival of drug-resistant leukemic stem cells in CML. Blood, 2020, 136, 596-609.	1.4	30
65	A standardized immune phenotyping and automated data analysis platform for multicenter biomarker studies. JCI Insight, 2018, 3, .	5.0	29
66	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.. Blood, 2008, 112, 975-975.	1.4	29
67	A randomized controlled trial on the effects of goal-directed therapy on the inflammatory response open abdominal aortic aneurysm repair. Critical Care, 2015, 19, 247.	5.8	28
68	Systems Biology Methods Applied to Blood and Tissue for a Comprehensive Analysis of Immune Response to Hepatitis B Vaccine in Adults. Frontiers in Immunology, 2020, 11, 580373.	4.8	28
69	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). Current Protocols in Cytometry, 2012, 61, Unit 10.18.	3.7	27
70	The construction and analysis of M13 libraries prepared from YAC DNA. Nucleic Acids Research, 1995, 23, 670-674.	14.5	25
71	flowCL: ontology-based cell population labelling in flow cytometry. Bioinformatics, 2015, 31, 1337-1339.	4.1	25
72	High throughput automated analysis of big flow cytometry data. Methods, 2018, 134-135, 164-176.	3.8	25

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73	Data Standards for Flow Cytometry. OMICS A Journal of Integrative Biology, 2006, 10, 209-214.	2.0	23
74	Distinct but phenotypically heterogeneous human cell populations produce rapid recovery of platelets and neutrophils after transplantation. Blood, 2012, 119, 3431-3439.	1.4	23
75	Automated analysis of flow cytometry data comes of age. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2016, 89, 13-15.	1.5	23
76	Scoring relevancy of features based on combinatorial analysis of Lasso with application to lymphoma diagnosis. BMC Genomics, 2013, 14, S14.	2.8	22
77	Allogeneic SCT for relapsed composite and transformed lymphoma using related and unrelated donors: long-term results. Bone Marrow Transplantation, 2008, 42, 601-608.	2.4	21
78	Cerebral oxygen desaturation during one-lung ventilation: correlation with hemodynamic variables. Canadian Journal of Anaesthesia, 2013, 60, 660-666.	1.6	21
79	Multi-Omic Data Integration Allows Baseline Immune Signatures to Predict Hepatitis B Vaccine Response in a Small Cohort. Frontiers in Immunology, 2020, 11, 578801.	4.8	20
80	Representation of cloned genomic sequences in two sequencing vectors: correlation of DNA sequence and subclone distribution. Nucleic Acids Research, 1997, 25, 2960-2966.	14.5	19
81	A Yeast Artificial Chromosome-Based Physical Map of the Juvenile Amyotrophic Lateral Sclerosis (ALS2) Critical Region on Human Chromosome 2q33â€"q34. Genomics, 1999, 55, 106-112.	2.9	18
82	Evaluating flow cytometer performance with weighted quadratic least squares analysis of L<scp>ED</scp> and multiâ€level bead data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2017, 91, 232-249.	1.5	18
83	Implementation and Validation of an Automated Flow Cytometry Analysis Pipeline for Human Immune Profiling. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2019, 95, 183-191.	1.5	18
84	Identification of B cells through negative gatingâ€"An example of the MIFlowCyt standard applied. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2010, 77A, 546-551.	1.5	17
85	The phenotypic distribution and functional profile of tuberculinâ€specific CD4 Tâ€cells characterizes different stages of TB infection. Cytometry Part B - Clinical Cytometry, 2012, 82B, 360-368.	1.5	17
86	Improving the Rigor and Reproducibility of Flow Cytometryâ€Based Clinical Research and Trials Through Automated Data Analysis. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2020, 97, 107-112.	1.5	17
87	GenePattern flow cytometry suite. Source Code for Biology and Medicine, 2013, 8, 14.	1.7	16
88	Integration of Lyoplate Based Flow Cytometry and Computational Analysis for Standardized Immunological Biomarker Discovery. PLoS ONE, 2013, 8, e65485.	2.5	16
89	â€œAge Related Differences in the Biology of Chronic Graft-Versus-Host Disease After Hematopoietic Stem Cell Transplantationâ€. Frontiers in Immunology, 2020, 11, 571884.	4.8	16
90	ddPCRclust: an R package and Shiny app for automated analysis of multiplexed ddPCR data. Bioinformatics, 2018, 34, 2687-2689.	4.1	14

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91	Methodology for evaluating and comparing flow cytometers: A multisite study of 23 instruments. , 2018, 93, 1087-1091.		14
92	<scp>flowCut:</scp> An R package for automated removal of outlier events and flagging of files based on time versus fluorescence analysis. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2023, 103, 71-81.	1.5	14
93	Stateâ€ofâ€theâ€Art in the Computational Analysis of Cytometry Data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2015, 87, 591-593.	1.5	13
94	<scp>ISAC</scp>'s <scp>G</scp>atingâ€<scp>ML</scp> 2.0 data exchange standard for gating description. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2015, 87, 683-687.	1.5	13
95	Deep profiling of multitube flow cytometry data. Bioinformatics, 2015, 31, 1623-1631.	4.1	13
96	Flow cytometry data standards. BMC Research Notes, 2011, 4, 50.	1.4	12
97	B Cells With High Side Scatter Parameter by Flow Cytometry Correlate With Inferior Survival in Diffuse Large B-Cell Lymphoma. American Journal of Clinical Pathology, 2012, 137, 805-814.	0.7	12
98	Single Cell Phenotypic Profiling of 27 DLBCL Cases Reveals Marked Intertumoral and Intratumoral Heterogeneity. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2020, 97, 620-629.	1.5	12
99	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. Frontiers in Pediatrics, 2020, 8, 197.	1.9	12
100	The Logic of Surveillance Guidelines: An Analysis of Vaccine Adverse Event Reports from an Ontological Perspective. PLoS ONE, 2014, 9, e92632.	2.5	10
101	Publishing code is essential for reproducible flow cytometry bioinformatics. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2016, 89, 10-11.	1.5	10
102	Use FlowRepository to share your clinical data upon study publication. Cytometry Part B - Clinical Cytometry, 2018, 94, 196-198.	1.5	10
103	Analysis of High-Throughput Flow Cytometry Data Using plateCore. Advances in Bioinformatics, 2009, 2009, 1-10.	5.7	9
104	Data-Driven Flow Cytometry Analysis. Methods in Molecular Biology, 2019, 1989, 245-265.	0.9	9
105	Wrestling with SUMO and bio-ontologies. Nature Biotechnology, 2006, 24, 21-21.	17.5	8
106	A Pipeline for automated analysis of flow cytometry data: Preliminary results on lymphoma sub-type diagnosis. , 2009, 2009, 4945-8.		8
107	FCS 3.1 Implementation Guidance. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2012, 81A, 523-526.	1.5	8
108	Bim Regulates Alloimmune-Mediated Vascular Injury Through Effects on T-Cell Activation and Death. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 1290-1297.	2.4	8

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109	Overcoming the ontology enrichment bottleneck with Quick Term Templates. Applied Ontology, 2011, 6, 13-22.	2.0	7
110	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.. Blood, 2006, 108, 3662-3662.	1.4	7
111	Overcoming the Ontology Enrichment Bottleneck with Quick Term Templates. Nature Precedings, 0, , .	0.1	6
112	FuGEFlow: data model and markup language for flow cytometry. BMC Bioinformatics, 2009, 10, 184.	2.6	6
113	Computational analysis optimizes the flow cytometric evaluation for lymphoma. , 2014, 86, 18-24.		6
114	Data File Standard for Flow Cytometry, Version <scp>FCS</scp> 3.2. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2021, 99, 100-102.	1.5	6
115	Wrestling with SUMO and bio-ontologies. Nature Biotechnology, 2006, 24, 21-22.	17.5	5
116	A container for the advanced cytometry standard (ACS). Proceedings of SPIE, 2009, , .	0.8	4
117	Computational analysis optimizes the flow cytometric evaluation for lymphoma. , 2013, , n/a-n/a.		4
118	ISAC's classification results file format. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2015, 87, 86-88.	1.5	4
119	Occurrence of Tâ€cell and <scp>NK</scp>â€cell subsets with less wellâ€recognized phenotypes in peripheral blood submitted for routine flow cytometry analysis. Cytometry Part B - Clinical Cytometry, 2021, 100, 235-239.	1.5	4
120	Cytometry standards continuum. Proceedings of SPIE, 2008, , .	0.8	3
121	Computational Analysis of High-Dimensional Flow Cytometric Data for Diagnosis and Discovery. Current Topics in Microbiology and Immunology, 2013, 377, 159-175.	1.1	3
122	ISAC Probe Tag Dictionary: Standardized Nomenclature for Detection and Visualization Labels Used in Cytometry and Microscopy Imaging. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2021, 99, 103-106.	1.5	3
123	Reduction in multi-lineage and erythroid progenitors distinguishes myelodysplastic syndromes from non-malignant cytopenias. Leukemia Research, 2009, 33, 1636-1642.	0.8	2
124	Automated identification of maximal differential cell populations in flow cytometry data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2022, 101, 177-184.	1.5	2
125	Identification of New microRNA Biomarkers and Candidate Target Genes in Primitive CML Cells Using Global Comparative RNA analyses. Blood, 2014, 124, 3133-3133.	1.4	2
126	Recent Bioinformatics Advances in the Analysis of High Throughput Flow Cytometry Data. Advances in Bioinformatics, 2009, 2009, 1-2.	5.7	1

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127	Reply to 'Reassessing the human mammary stem cell concept by modeling limiting dilution transplantation assays'. Nature Medicine, 2009, 15, 604-605.	30.7	0
128	Correlation between trough imatinib plasma concentration and clinical response in chronic myeloid leukemia. Leukemia Research, 2009, 33, 1149-1150.	0.8	0
129	Comparative RNA-seq analyses identify new microRNA biomarkers and candidate target genes in patientsâ€™ drug-resistant CD34+ CML stem/progenitor cells. Experimental Hematology, 2015, 43, S63.	0.4	0
130	An Early NaÃ¯ve T Cell Population Lacking PD1 Expression at Day 100 As A Prognostic Biomarker of Chronic GVHD. Transplantation, 2017, 101, S40.	1.0	0
131	Standardized Immunophenotyping in the Canadian National Transplant Research Program. Transplantation, 2017, 101, S62.	1.0	0
132	Long Term Results of Myeloablative Allogeneic Stem Cell Transplantation Using Related and Unrelated Donors in Patients with Relapsed Composite Low and Intermediate Grade (Including Transformed) Lymphoma.. Blood, 2006, 108, 3139-3139.	1.4	0
133	Induction Therapy with High-Dose Dex Alone in Newly Diagnosed Myeloma Patients Produces a 57% Partial Response and Is Predictive of Progression Free Survival.. Blood, 2006, 108, 3098-3098.	1.4	0
134	Allogeneic Stem Cell Transplant in First Complete Remission Overcomes the Poor Prognosis Associated with the FLT-3 Internal Tandem Duplication in Acute Myeloid Leukemia.. Blood, 2007, 110, 3491-3491.	1.4	0
135	Impact of Comorbidity Index on Outcome with Allogeneic Hematopoetic Stem Cell Transplantation for Chronic Lymphocytic Leukemia. Blood, 2008, 112, 3305-3305.	1.4	0
136	Short Term Signalling Responses of the Most Primitive Subsets of Human Hematopoietic Cells Stimulated in Vitro Correlate with Their Subsequent Self-Renewal Behaviour.. Blood, 2012, 120, 2341-2341.	1.4	0
137	MIFlowCyt. , 2013, , 1358-1360.		0
138	Single-Cell Profiling Reveals Distinct Tumor Subtypes and Their Associated T-Cell Environments in Follicular Lymphoma. Blood, 2018, 132, 1577-1577.	1.4	0
139	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. Blood, 2018, 132, 931-931.	1.4	0