

# Genevive Boucher

## List of Publications by Citations

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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.

38  
papers

3,327  
citations

23  
h-index

43  
g-index

43  
ext. papers

3,967  
ext. citations

9.2  
avg, IF

4.2  
L-index

#	Paper	IF	Citations
38	HIV reservoir size and persistence are driven by T cell survival and homeostatic proliferation. <i>Nature Medicine</i> , <b>2009</b> , 15, 893-900	50.5	1219
37	Yellow fever vaccine induces integrated multilineage and polyfunctional immune responses. <i>Journal of Experimental Medicine</i> , <b>2008</b> , 205, 3119-31	16.6	454
36	A key role for EZH2 and associated genes in mouse and human adult T-cell acute leukemia. <i>Genes and Development</i> , <b>2012</b> , 26, 651-6	12.6	204
35	Establishment of HIV-1 latency in resting CD4+ T cells depends on chemokine-induced changes in the actin cytoskeleton. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 16934-9	11.5	174
34	Transcription factor FOXO3a controls the persistence of memory CD4(+) T cells during HIV infection. <i>Nature Medicine</i> , <b>2008</b> , 14, 266-74	50.5	123
33	The transcriptomic landscape and directed chemical interrogation of MLL-rearranged acute myeloid leukemias. <i>Nature Genetics</i> , <b>2015</b> , 47, 1030-7	36.3	95
32	GPR56 identifies primary human acute myeloid leukemia cells with high repopulating potential in vivo. <i>Blood</i> , <b>2016</b> , 127, 2018-27	2.2	95
31	Identification of small molecules that support human leukemia stem cell activity ex vivo. <i>Nature Methods</i> , <b>2014</b> , 11, 436-42	21.6	86
30	Regulation of efflux pump expression and drug resistance by the transcription factors Mrr1, Upc2, and Cap1 in <i>Candida albicans</i> . <i>Antimicrobial Agents and Chemotherapy</i> , <b>2011</b> , 55, 2212-23	5.9	84
29	Identification of the <i>Candida albicans</i> Cap1p regulon. <i>Eukaryotic Cell</i> , <b>2009</b> , 8, 806-20		79
28	Mubritinib Targets the Electron Transport Chain Complex I and Reveals the Landscape of OXPHOS Dependency in Acute Myeloid Leukemia. <i>Cancer Cell</i> , <b>2019</b> , 36, 84-99.e8	24.3	75
27	Impact of genomic polymorphisms on the repertoire of human MHC class I-associated peptides. <i>Nature Communications</i> , <b>2014</b> , 5, 3600	17.4	75
26	The TGF- $\beta$ /Smad3 pathway inhibits CD28-dependent cell growth and proliferation of CD4 T cells. <i>Genes and Immunity</i> , <b>2013</b> , 14, 115-26	4.4	59
25	Following the aggregation of amyloid-forming peptides by computer simulations. <i>Journal of Chemical Physics</i> , <b>2005</b> , 122, 174904	3.9	57
24	Chemo-genomic interrogation of CEBPA mutated AML reveals recurrent CSF3R mutations and subgroup sensitivity to JAK inhibitors. <i>Blood</i> , <b>2016</b> , 127, 3054-61	2.2	55
23	RNA-sequencing analysis of core binding factor AML identifies recurrent ZBTB7A mutations and defines RUNX1-CBFA2T3 fusion signature. <i>Blood</i> , <b>2016</b> , 127, 2498-501	2.2	46
22	RNA-seq analysis of 2 closely related leukemia clones that differ in their self-renewal capacity. <i>Blood</i> , <b>2011</b> , 117, e27-38	2.2	46

21	Expression of immunoproteasome genes is regulated by cell-intrinsic and -extrinsic factors in human cancers. <i>Scientific Reports</i> , <b>2016</b> , 6, 34019	4.9	45
20	Microarray analysis of HIV resistant female sex workers reveal a gene expression signature pattern reminiscent of a lowered immune activation state. <i>PLoS ONE</i> , <b>2012</b> , 7, e30048	3.7	43
19	Chemogenomic Landscape of -mutated AML Reveals Importance of Allele Dosage in Genetics and Glucocorticoid Sensitivity. <i>Clinical Cancer Research</i> , <b>2017</b> , 23, 6969-6981	12.9	26
18	Redefining interferon-producing killer dendritic cells as a novel intermediate in NK-cell differentiation. <i>Blood</i> , <b>2012</b> , 119, 4349-57	2.2	26
17	Genetic characterization of ABT-199 sensitivity in human AML. <i>Leukemia</i> , <b>2020</b> , 34, 63-74	10.7	26
16	Distinct antiviral signaling pathways in primary human hepatocytes and their differential disruption by HCV NS3 protease. <i>Journal of Hepatology</i> , <b>2010</b> , 52, 167-75	13.4	23
15	Identification of MYC mutations in acute myeloid leukemias with NUP98-NSD1 translocations. <i>Leukemia</i> , <b>2016</b> , 30, 1621-4	10.7	22
14	Aggregating the amyloid Abeta(11-25) peptide into a four-stranded beta-sheet structure. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2006</b> , 65, 877-88	4.2	21
13	High frequency of germline RUNX1 mutations in patients with RUNX1-mutated AML. <i>Blood</i> , <b>2020</b> , 135, 1882-1886	2.2	19
12	MiSTIC, an integrated platform for the analysis of heterogeneity in large tumour transcriptome datasets. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e122	20.1	12
11	is amplified in a large subset of human lung adenocarcinoma and is critical for epithelial lung cell identity and tumor metastasis. <i>FASEB Journal</i> , <b>2017</b> , 31, 5012-5018	0.9	11
10	Gene expression profile in long-term non progressor HIV infected patients: in search of potential resistance factors. <i>Molecular Immunology</i> , <b>2014</b> , 62, 63-70	4.3	10
9	A novel approach for the identification of efficient combination therapies in primary human acute myeloid leukemia specimens. <i>Blood Cancer Journal</i> , <b>2017</b> , 7, e529	7	8
8	A comparative analysis of gene expression patterns and cell phenotypes between cervical and peripheral blood mononuclear cells. <i>PLoS ONE</i> , <b>2009</b> , 4, e8293	3.7	6
7	Genetic Characterization of ABT-199 Sensitivity in Human AML. <i>Blood</i> , <b>2018</b> , 132, 283-283	2.2	1
6	Chemo-Transcriptomic Analysis of Complex Karyotype AML Reveals Increased Expression of Cell Cycle Components and Exquisite Dependency on Polo-like Kinase 1. <i>Blood</i> , <b>2016</b> , 128, 769-769	2.2	1
5	Chemogenomic Approach Unveils the Increased Susceptibility of RUNX1-Mutated AML to Glucocorticoids. <i>Blood</i> , <b>2018</b> , 132, 4675-4675	2.2	
4	Mutational and Transcriptomic Landscape of AML with Core-Binding Factor Rearrangements. <i>Blood</i> , <b>2015</b> , 126, 802-802	2.2	

- 3 The Novel Leukemia Stem Cell Marker GPR56 Discriminates Leukemic Subclones with Divergent Stem Cell Properties in Human Acute Myeloid Leukemia. *Blood*, **2015**, 126, 1859-1859 2.2
- 2 Transcriptional Landscape of APL Identifies Aberrant Podoplanin Expression As a Defining Feature and Missing Link for the Bleeding Disorder of This Disease. *Blood*, **2016**, 128, 1075-1075 2.2
- 1 NGS-Based Detection Of Multiple RAS-Mutated Clones In MLL-Rearranged Leukemias Suggests Strong Oncogenic Collaboration. *Blood*, **2013**, 122, 744-744 2.2