

# Sebastien Lemieux

## 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.

95  
papers

4,994  
citations

40  
h-index

70  
g-index

103  
ext. papers

6,238  
ext. citations

8.3  
avg, IF

5.14  
L-index

#	Paper	IF	Citations
95	Genomic islands in the pathogenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>PLoS Genetics</i> , <b>2008</b> , 4, e1000046	6	382
94	Large-scale essential gene identification in <i>Candida albicans</i> and applications to antifungal drug discovery. <i>Molecular Microbiology</i> , <b>2003</b> , 50, 167-81	4.1	371
93	Phosphoproteome dynamics reveal novel ERK1/2 MAP kinase substrates with broad spectrum of functions. <i>Molecular Systems Biology</i> , <b>2013</b> , 9, 669	12.2	236
92	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
91	Noncoding regions are the main source of targetable tumor-specific antigens. <i>Science Translational Medicine</i> , <b>2018</b> , 10,	17.5	199
90	Essential gene identification and drug target prioritization in <i>Aspergillus fumigatus</i> . <i>PLoS Pathogens</i> , <b>2007</b> , 3, e24	7.6	178
89	Genome-wide fitness test and mechanism-of-action studies of inhibitory compounds in <i>Candida albicans</i> . <i>PLoS Pathogens</i> , <b>2007</b> , 3, e92	7.6	178
88	The phagosomal proteome in interferon-gamma-activated macrophages. <i>Immunity</i> , <b>2009</b> , 30, 143-54	32.3	177
87	A comprehensive map of the mTOR signaling network. <i>Molecular Systems Biology</i> , <b>2010</b> , 6, 453	12.2	171
86	Function of hexameric RNA in packaging of bacteriophage phi 29 DNA in vitro. <i>Molecular Cell</i> , <b>1998</b> , 2, 141-7	17.6	140
85	Quantitative analysis of nucleic acid three-dimensional structures. <i>Journal of Molecular Biology</i> , <b>2001</b> , 308, 919-36	6.5	129
84	The MHC class I peptide repertoire is molded by the transcriptome. <i>Journal of Experimental Medicine</i> , <b>2008</b> , 205, 595-610	16.6	127
83	Global proteogenomic analysis of human MHC class I-associated peptides derived from non-canonical reading frames. <i>Nature Communications</i> , <b>2016</b> , 7, 10238	17.4	127
82	MHC class I-associated peptides derive from selective regions of the human genome. <i>Journal of Clinical Investigation</i> , <b>2016</b> , 126, 4690-4701	15.9	123
81	RNA canonical and non-canonical base pairing types: a recognition method and complete repertoire. <i>Nucleic Acids Research</i> , <b>2002</b> , 30, 4250-63	20.1	101
80	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
79	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

78	Genomewide location analysis of <i>Candida albicans</i> Upc2p, a regulator of sterol metabolism and azole drug resistance. <i>Eukaryotic Cell</i> , <b>2008</b> , 7, 836-47		89
77	Identification of small molecules that support human leukemia stem cell activity <i>ex vivo</i> . <i>Nature Methods</i> , <b>2014</b> , 11, 436-42	21.6	86
76	The MHC I immunopeptidome conveys to the cell surface an integrative view of cellular regulation. <i>Molecular Systems Biology</i> , <b>2011</b> , 7, 533	12.2	80
75	Single UM171-Expanded Cord Blood Transplants Support Robust T-Cell Reconstitution with Low Rates of Severe Infections. <i>Stem Cells Translational Medicine</i> , <b>2020</b> , 9, S8	6.9	78
74	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
73	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
72	Functional calcitonin gene-related peptide receptors are formed by the asymmetric assembly of a calcitonin receptor-like receptor homo-oligomer and a monomer of receptor activity-modifying protein-1. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 31610-20	5.4	68
71	Hematopoietic stem cell transplantation using single UM171-expanded cord blood: a single-arm, phase 1-2 safety and feasibility study. <i>Lancet Haematology</i> , <b>2020</b> , 7, e134-e145	14.6	67
70	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
69	Deletion of immunoproteasome subunits imprints on the transcriptome and has a broad impact on peptides presented by major histocompatibility complex I molecules. <i>Molecular and Cellular Proteomics</i> , <b>2010</b> , 9, 2034-47	7.6	58
68	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
67	MHC I-associated peptides preferentially derive from transcripts bearing miRNA response elements. <i>Blood</i> , <b>2012</b> , 119, e181-91	2.2	53
66	Transcriptome sequencing of neonatal thymic epithelial cells. <i>Scientific Reports</i> , <b>2013</b> , 3, 1860	4.9	53
65	Structural and electrostatic characterization of pariacoto virus: implications for viral assembly. <i>Biopolymers</i> , <b>2009</b> , 91, 530-8	2.2	51
64	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
63	A functional screen reveals an extensive layer of transcriptional and splicing control underlying RAS/MAPK signaling in <i>Drosophila</i> . <i>PLoS Biology</i> , <b>2014</b> , 12, e1001809	9.7	46
62	SCL, LMO1 and Notch1 reprogram thymocytes into self-renewing cells. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004768		46
61	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

60	Automated extraction and classification of RNA tertiary structure cyclic motifs. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, 2340-6	20.1	45
59	Differential Features of AIRE-Induced and AIRE-Independent Promiscuous Gene Expression in Thymic Epithelial Cells. <i>Journal of Immunology</i> , <b>2015</b> , 195, 498-506	5.3	44
58	Transcriptome analysis of G protein-coupled receptors in distinct genetic subgroups of acute myeloid leukemia: identification of potential disease-specific targets. <i>Blood Cancer Journal</i> , <b>2016</b> , 6, e4317	4.7	43
57	EVI1-rearranged acute myeloid leukemias are characterized by distinct molecular alterations. <i>Blood</i> , <b>2015</b> , 125, 140-3	2.2	43
56	Proteogenomic-based discovery of minor histocompatibility antigens with suitable features for immunotherapy of hematologic cancers. <i>Leukemia</i> , <b>2016</b> , 30, 1344-54	10.7	42
55	RNA-Seq reveals spliceosome and proteasome genes as most consistent transcripts in human cancer cells. <i>PLoS ONE</i> , <b>2013</b> , 8, e72884	3.7	36
54	Epigenetic regulation of GATA2 and its impact on normal karyotype acute myeloid leukemia. <i>Leukemia</i> , <b>2014</b> , 28, 1617-26	10.7	31
53	Quantitative expression profiling guided by common retroviral insertion sites reveals novel and cell type specific cancer genes in leukemia. <i>Blood</i> , <b>2008</b> , 111, 790-9	2.2	29
52	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
51	Most non-canonical proteins uniquely populate the proteome or immunopeptidome. <i>Cell Reports</i> , <b>2021</b> , 34, 108815	10.6	26
50	Genetic characterization of ABT-199 sensitivity in human AML. <i>Leukemia</i> , <b>2020</b> , 34, 63-74	10.7	26
49	Role of SLV in SLI substrate recognition by the Neurospora VS ribozyme. <i>Rna</i> , <b>2008</b> , 14, 736-48	5.8	24
48	Hepatic leukemia factor is a novel leukemic stem cell regulator in DNMT3A, NPM1, and FLT3-ITD triple-mutated AML. <i>Blood</i> , <b>2019</b> , 134, 263-276	2.2	23
47	Proteogenomics Uncovers a Vast Repertoire of Shared Tumor-Specific Antigens in Ovarian Cancer. <i>Cancer Immunology Research</i> , <b>2020</b> , 8, 544-555	12.5	23
46	High expression of HMGA2 independently predicts poor clinical outcomes in acute myeloid leukemia. <i>Blood Cancer Journal</i> , <b>2018</b> , 8, 68	7	23
45	Modeling active RNA structures using the intersection of conformational space: application to the lead-activated ribozyme. <i>Rna</i> , <b>1998</b> , 4, 739-49	5.8	23
44	Identification of MYC mutations in acute myeloid leukemias with NUP98-NSD1 translocations. <i>Leukemia</i> , <b>2016</b> , 30, 1621-4	10.7	22
43	Occurrence and detection of phosphopeptide isomers in large-scale phosphoproteomics experiments. <i>Journal of Proteome Research</i> , <b>2012</b> , 11, 3753-65	5.6	22

42	Harnessing virtual machines to simplify next-generation DNA sequencing analysis. <i>Bioinformatics</i> , <b>2013</b> , 29, 2075-83	7.2	21
41	Genetic interaction between Kit and Scl. <i>Blood</i> , <b>2013</b> , 122, 1150-61	2.2	20
40	ProteoConnections: a bioinformatics platform to facilitate proteome and phosphoproteome analyses. <i>Proteomics</i> , <b>2011</b> , 11, 2654-71	4.8	20
39	High frequency of germline RUNX1 mutations in patients with RUNX1-mutated AML. <i>Blood</i> , <b>2020</b> , 135, 1882-1886	2.2	19
38	Depletion of the cullin Cdc53p induces morphogenetic changes in <i>Candida albicans</i> . <i>Eukaryotic Cell</i> , <b>2009</b> , 8, 756-67		18
37	The NMR structure of the II-III-VI three-way junction from the <i>Neurospora VS</i> ribozyme reveals a critical tertiary interaction and provides new insights into the global ribozyme structure. <i>Rna</i> , <b>2015</b> , 21, 1621-32	5.8	17
36	Transcriptomic landscape of acute promyelocytic leukemia reveals aberrant surface expression of the platelet aggregation agonist Podoplanin. <i>Leukemia</i> , <b>2018</b> , 32, 1349-1357	10.7	17
35	Atypical acute myeloid leukemia-specific transcripts generate shared and immunogenic MHC class-I-associated epitopes. <i>Immunity</i> , <b>2021</b> , 54, 737-752.e10	32.3	17
34	Widespread and tissue-specific expression of endogenous retroelements in human somatic tissues. <i>Genome Medicine</i> , <b>2020</b> , 12, 40	14.4	14
33	Complex karyotype AML displays G2/M signature and hypersensitivity to PLK1 inhibition. <i>Blood Advances</i> , <b>2019</b> , 3, 552-563	7.8	14
32	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
31	Detection of Quiescent Radioresistant Epithelial Progenitors in the Adult Thymus. <i>Frontiers in Immunology</i> , <b>2017</b> , 8, 1717	8.4	12
30	Helix-length compensation studies reveal the adaptability of the VS ribozyme architecture. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, 2284-93	20.1	11
29	Probe-level linear model fitting and mixture modeling results in high accuracy detection of differential gene expression. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 391	3.6	10
28	pyGeno: A Python package for precision medicine and proteogenomics. <i>F1000Research</i> , <b>2016</b> , 5, 381	3.6	8
27	MAPDP: A Cloud-Based Computational Platform for Immunopeptidomics Analyses. <i>Journal of Proteome Research</i> , <b>2020</b> , 19, 1873-1881	5.6	7
26	Enhancing the drug discovery process: Bayesian inference for the analysis and comparison of dose-response experiments. <i>Bioinformatics</i> , <b>2019</b> , 35, i464-i473	7.2	5
25	pyGeno: A Python package for precision medicine and proteogenomics. <i>F1000Research</i> , <b>2016</b> , 5, 381	3.6	5

24	Targeted variant detection using unaligned RNA-Seq reads. <i>Life Science Alliance</i> , <b>2019</b> , 2,	5.8	5
23	Qualitative Changes in Cortical Thymic Epithelial Cells Drive Postpartum Thymic Regeneration. <i>Frontiers in Immunology</i> , <b>2019</b> , 10, 3118	8.4	3
22	Single UM171 Expanded Cord Blood Permits Transplantation of Better HLA Matched Cords with Excellent Gvhd Relapse Free Survival. <i>Blood</i> , <b>2018</b> , 132, 4658-4658	2.2	3
21	p16 Regulates Cellular Senescence in PD-1-Expressing Human T Cells. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 698565	8.4	3
20	Correction of spatial bias in oligonucleotide array data. <i>Advances in Bioinformatics</i> , <b>2013</b> , 2013, 167915	5.5	2
19	Transcriptome Analysis Reveals That G Protein-Coupled Receptors Are Potential Diagnostic Markers or Therapeutic Targets in Acute Myeloid Leukemia. <i>Blood</i> , <b>2015</b> , 126, 3855-3855	2.2	2
18	Single UM171 Expanded Cord Blood Transplant Is Feasible, Safe, and Permits Transplantation of Better HLA Matched Cords with Very Low Transplant Related Mortality. <i>Blood</i> , <b>2017</b> , 130, 658-658	2.2	2
17	Target variant detection in leukemia using unaligned RNA-Seq reads		2
16	STRIPAK regulates Slik localization to control mitotic morphogenesis and epithelial integrity. <i>Journal of Cell Biology</i> , <b>2020</b> , 219,	7.3	2
15	Factorized embeddings learns rich and biologically meaningful embedding spaces using factorized tensor decomposition. <i>Bioinformatics</i> , <b>2020</b> , 36, i417-i426	7.2	2
14	UM171-Expanded Cord Blood Transplants Support Robust T-Cell Reconstitution with Low Rates of Severe Infections. <i>Blood</i> , <b>2020</b> , 136, 36-37	2.2	1
13	Chemogenomic Profiling of Complex Karyotype AML Reveals a Novel Susceptibility to G2/M Checkpoint Inhibition Mediated By HMGA2 Overexpression. <i>Blood</i> , <b>2018</b> , 132, 3925-3925	2.2	1
12	Genetic Characterization of ABT-199 Sensitivity in Human AML. <i>Blood</i> , <b>2018</b> , 132, 283-283	2.2	1
11	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
10	UM171-Expanded Cord Blood Transplants Support Robust T Cell Reconstitution with Low Rates of Severe Infections. <i>Transplantation and Cellular Therapy</i> , <b>2021</b> , 27, 76.e1-76.e9		1
9	Monoallelic Deletion Reduces the Requirement for NOTCH1 Hyperactivation in T-Cell Acute Lymphoblastic Leukemia.. <i>Frontiers in Immunology</i> , <b>2022</b> , 13, 867443	8.4	1
8	Legal and Ethical Considerations for the Design and Use of Web Portals for Researchers, Clinicians, and Patients: Scoping Literature Review. <i>Journal of Medical Internet Research</i> , <b>2021</b> , 23, e26450	7.6	0
7	CAMAP: Artificial neural networks unveil the role of codon arrangement in modulating MHC-I peptides presentation. <i>PLoS Computational Biology</i> , <b>2021</b> , 17, e1009482	5	

- 6 Identification of SCL and LMO Oncogenes as Transcriptional Repressors of HEB/E2A in the Thymus through Functional Genomic/Genetic Approaches.. *Blood*, **2007**, 110, 2649-2649 2.2
- 5 Chemogenomic Approach Unveils the Increased Susceptibility of RUNX1-Mutated AML to Glucocorticoids. *Blood*, **2018**, 132, 4675-4675 2.2
- 4 Mutational and Transcriptomic Landscape of AML with Core-Binding Factor Rearrangements. *Blood*, **2015**, 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