Sebastien Lemieux

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.

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	Monoallelic Deletion Reduces the Requirement for NOTCH1 Hyperactivation in T-Cell Acute Lymphoblastic Leukemia.. *Frontiers in Immunology*, **2022**, 13, 867443	8.4	1
94	CAMAP: Artificial neural networks unveil the role of codon arrangement in modulating MHC-I peptides presentation. *PLoS Computational Biology*, **2021**, 17, e1009482	5	
93	Legal and Ethical Considerations for the Design and Use of Web Portals for Researchers, Clinicians, and Patients: Scoping Literature Review. *Journal of Medical Internet Research*, **2021**, 23, e26450	7.6	0
92	Most non-canonical proteins uniquely populate the proteome or immunopeptidome. *Cell Reports*, **2021**, 34, 108815	10.6	26
91	Atypical acute myeloid leukemia-specific transcripts generate shared and immunogenic MHC class-I-associated epitopes. *Immunity*, **2021**, 54, 737-752.e10	32.3	17
90	UM171-Expanded Cord Blood Transplants Support Robust T Cell Reconstitution with Low Rates of Severe Infections. *Transplantation and Cellular Therapy*, **2021**, 27, 76.e1-76.e9		1
89	p16 Regulates Cellular Senescence in PD-1-Expressing Human T Cells. *Frontiers in Immunology*, **2021** , 12, 698565	8.4	3
88	Single UM171-Expanded Cord Blood Transplants Support Robust T-Cell Reconstitution with Low Rates of Severe Infections. *Stem Cells Translational Medicine*, **2020**, 9, S8	6.9	78
87	High frequency of germline RUNX1 mutations in patients with RUNX1-mutated AML. *Blood*, **2020**, 135, 1882-1886	2.2	19
86	Proteogenomics Uncovers a Vast Repertoire of Shared Tumor-Specific Antigens in Ovarian Cancer. *Cancer Immunology Research*, **2020**, 8, 544-555	12.5	23
85	MAPDP: A Cloud-Based Computational Platform for Immunopeptidomics Analyses. *Journal of Proteome Research*, **2020**, 19, 1873-1881	5.6	7
84	Widespread and tissue-specific expression of endogenous retroelements in human somatic tissues. *Genome Medicine*, **2020**, 12, 40	14.4	14
83	UM171-Expanded Cord Blood Transplants Support Robust T-Cell Reconstitution with Low Rates of Severe Infections. *Blood*, **2020**, 136, 36-37	2.2	1
82	STRIPAK regulates Slik localization to control mitotic morphogenesis and epithelial integrity. *Journal of Cell Biology*, **2020**, 219,	7.3	2
81	Hematopoietic stem cell transplantation using single UM171-expanded cord blood: a single-arm, phase 1-2 safety and feasibility study. *Lancet Haematology,the*, **2020**, 7, e134-e145	14.6	67
80	Factorized embeddings learns rich and biologically meaningful embedding spaces using factorized tensor decomposition. *Bioinformatics*, **2020**, 36, i417-i426	7.2	2
79	Genetic characterization of ABT-199 sensitivity in human AML. *Leukemia*, **2020**, 34, 63-74	10.7	26

78	Hepatic leukemia factor is a novel leukemic stem cell regulator in DNMT3A, NPM1, and FLT3-ITD triple-mutated AML. *Blood*, **2019**, 134, 263-276	2.2	23
77	Qualitative Changes in Cortical Thymic Epithelial Cells Drive Postpartum Thymic Regeneration. *Frontiers in Immunology*, **2019**, 10, 3118	8.4	3
76	Enhancing the drug discovery process: Bayesian inference for the analysis and comparison of dose-response experiments. *Bioinformatics*, **2019**, 35, i464-i473	7.2	5
75	Mubritinib Targets the Electron Transport Chain Complex I and Reveals the Landscape of OXPHOS Dependency in Acute Myeloid Leukemia. *Cancer Cell*, **2019**, 36, 84-99.e8	24.3	75
74	Targeted variant detection using unaligned RNA-Seq reads. *Life Science Alliance*, **2019**, 2,	5.8	5
73	Complex karyotype AML displays G2/M signature and hypersensitivity to PLK1 inhibition. *Blood Advances*, **2019**, 3, 552-563	7.8	14
72	Transcriptomic landscape of acute promyelocytic leukemia reveals aberrant surface expression of the platelet aggregation agonist Podoplanin. *Leukemia*, **2018**, 32, 1349-1357	10.7	17
71	High expression of HMGA2 independently predicts poor clinical outcomes in acute myeloid leukemia. *Blood Cancer Journal*, **2018**, 8, 68	7	23
70	Single UM171 Expanded Cord Blood Permits Transplantation of Better HLA Matched Cords with Excellent Gvhd Relapse Free Survival. *Blood*, **2018**, 132, 4658-4658	2.2	3
69	Chemogenomic Profiling of Complex Karyotype AML Reveals a Novel Susceptibility to G2/M Checkpoint Inhibition Mediated By HMGA2 Overexpression. *Blood*, **2018**, 132, 3925-3925	2.2	1
68	Genetic Characterization of ABT-199 Sensitivity in Human AML. *Blood*, **2018**, 132, 283-283	2.2	1
67	Chemogenomic Approach Unveils the Increased Susceptibility of RUNX1-Mutated AML to Glucocorticoids. *Blood*, **2018**, 132, 4675-4675	2.2	
66	Noncoding regions are the main source of targetable tumor-specific antigens. *Science Translational Medicine*, **2018**, 10,	17.5	199
65	MiSTIC, an integrated platform for the analysis of heterogeneity in large tumour transcriptome datasets. *Nucleic Acids Research*, **2017**, 45, e122	20.1	12
64	Chemogenomic Landscape of -mutated AML Reveals Importance of Allele Dosage in Genetics and Glucocorticoid Sensitivity. *Clinical Cancer Research*, **2017**, 23, 6969-6981	12.9	26
63	Detection of Quiescent Radioresistant Epithelial Progenitors in the Adult Thymus. *Frontiers in Immunology*, **2017**, 8, 1717	8.4	12
62	Single UM171 Expanded Cord Blood Transplant Is Feasible, Safe, and Permits Transplantation of Better HLA Matched Cords with Very Low Transplant Related Mortality. *Blood*, **2017**, 130, 658-658	2.2	2
61	GPR56 identifies primary human acute myeloid leukemia cells with high repopulating potential in vivo. *Blood*, **2016**, 127, 2018-27	2.2	95

60	RNA-sequencing analysis of core binding factor AML identifies recurrent ZBTB7A mutations and defines RUNX1-CBFA2T3 fusion signature. *Blood*, **2016**, 127, 2498-501	2.2	46
59	Chemo-genomic interrogation of CEBPA mutated AML reveals recurrent CSF3R mutations and subgroup sensitivity to JAK inhibitors. *Blood*, **2016**, 127, 3054-61	2.2	55
58	Expression of immunoproteasome genes is regulated by cell-intrinsic and -extrinsic factors in human cancers. *Scientific Reports*, **2016**, 6, 34019	4.9	45
57	Transcriptome analysis of G protein-coupled receptors in distinct genetic subgroups of acute myeloid leukemia: identification of potential disease-specific targets. *Blood Cancer Journal*, **2016**, 6, e431	7	43
56	Identification of MYC mutations in acute myeloid leukemias with NUP98-NSD1 translocations. *Leukemia*, **2016**, 30, 1621-4	10.7	22
55	Proteogenomic-based discovery of minor histocompatibility antigens with suitable features for immunotherapy of hematologic cancers. *Leukemia*, **2016**, 30, 1344-54	10.7	42
54	Chemo-Transcriptomic Analysis of Complex Karyotype AML Reveals Increased Expression of Cell Cycle Components and Exquisite Dependency on Polo-like Kinase 1. *Blood*, **2016**, 128, 769-769	2.2	1
53	pyGeno: A Python package for precision medicine and proteogenomics. *F1000Research*, **2016**, 5, 381	3.6	8
52	pyGeno: A Python package for precision medicine and proteogenomics. *F1000Research*, **2016**, 5, 381	3.6	5
51	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	
50	MHC class I-associated peptides derive from selective regions of the human genome. *Journal of Clinical Investigation*, **2016**, 126, 4690-4701	15.9	123
49	Global proteogenomic analysis of human MHC class I-associated peptides derived from non-canonical reading frames. *Nature Communications*, **2016**, 7, 10238	17.4	127
48	The transcriptomic landscape and directed chemical interrogation of MLL-rearranged acute myeloid leukemias. *Nature Genetics*, **2015**, 47, 1030-7	36.3	95
47	The NMR structure of the II-III-VI three-way junction from the Neurospora VS ribozyme reveals a critical tertiary interaction and provides new insights into the global ribozyme structure. *Rna*, **2015**, 21, 1621-32	5.8	17
46	EVI1-rearranged acute myeloid leukemias are characterized by distinct molecular alterations. *Blood* , **2015**, 125, 140-3	2.2	43
45	Differential Features of AIRE-Induced and AIRE-Independent Promiscuous Gene Expression in Thymic Epithelial Cells. *Journal of Immunology*, **2015**, 195, 498-506	5.3	44
44	Transcriptome Analysis Reveals That G Protein-Coupled Receptors Are Potential Diagnostic Markers or Therapeutic Targets in Acute Myeloid Leukemia. *Blood*, **2015**, 126, 3855-3855	2.2	2
43	Mutational and Transcriptomic Landscape of AML with Core-Binding Factor Rearrangements. *Blood*, **2015**, 126, 802-802	2.2	

42	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	
41	Identification of small molecules that support human leukemia stem cell activity ex vivo. *Nature Methods*, **2014**, 11, 436-42	21.6	86
40	Epigenetic regulation of GATA2 and its impact on normal karyotype acute myeloid leukemia. *Leukemia*, **2014**, 28, 1617-26	10.7	31
39	A functional screen reveals an extensive layer of transcriptional and splicing control underlying RAS/MAPK signaling in Drosophila. *PLoS Biology*, **2014**, 12, e1001809	9.7	46
38	SCL, LMO1 and Notch1 reprogram thymocytes into self-renewing cells. *PLoS Genetics*, **2014**, 10, e1004768	8	46
37	Impact of genomic polymorphisms on the repertoire of human MHC class I-associated peptides. *Nature Communications*, **2014**, 5, 3600	17.4	75
36	The TGF-□Smad3 pathway inhibits CD28-dependent cell growth and proliferation of CD4 T cells. *Genes and Immunity*, **2013**, 14, 115-26	4.4	59
35	Transcriptome sequencing of neonatal thymic epithelial cells. *Scientific Reports*, **2013**, 3, 1860	4.9	53
34	Phosphoproteome dynamics reveal novel ERK1/2 MAP kinase substrates with broad spectrum of functions. *Molecular Systems Biology*, **2013**, 9, 669	12.2	236
33	Harnessing virtual machines to simplify next-generation DNA sequencing analysis. *Bioinformatics*, **2013**, 29, 2075-83	7.2	21
32	Genetic interaction between Kit and Scl. *Blood*, **2013**, 122, 1150-61	2.2	20
31	RNA-Seq reveals spliceosome and proteasome genes as most consistent transcripts in human cancer cells. *PLoS ONE*, **2013**, 8, e72884	3.7	36
30	Correction of spatial bias in oligonucleotide array data. *Advances in Bioinformatics*, **2013**, 2013, 167915	5.5	2
29	NGS-Based Detection Of Multiple RAS-Mutated Clones In MLL-Rearranged Leukemias Suggests Strong Oncogenic Collaboration. *Blood*, **2013**, 122, 744-744	2.2	
28	MHC I-associated peptides preferentially derive from transcripts bearing miRNA response elements. *Blood*, **2012**, 119, e181-91	2.2	53
27	Occurrence and detection of phosphopeptide isomers in large-scale phosphoproteomics experiments. *Journal of Proteome Research*, **2012**, 11, 3753-65	5.6	22
26	A key role for EZH2 and associated genes in mouse and human adult T-cell acute leukemia. *Genes and Development*, **2012**, 26, 651-6	12.6	204
25	Helix-length compensation studies reveal the adaptability of the VS ribozyme architecture. *Nucleic Acids Research*, **2012**, 40, 2284-93	20.1	11

24	ProteoConnections: a bioinformatics platform to facilitate proteome and phosphoproteome analyses. *Proteomics*, **2011**, 11, 2654-71	4.8	20
23	The MHC I immunopeptidome conveys to the cell surface an integrative view of cellular regulation. *Molecular Systems Biology*, **2011**, 7, 533	12.2	80
22	Deletion of immunoproteasome subunits imprints on the transcriptome and has a broad impact on peptides presented by major histocompatibility complex I molecules. *Molecular and Cellular Proteomics*, **2010**, 9, 2034-47	7.6	58
21	A comprehensive map of the mTOR signaling network. *Molecular Systems Biology*, **2010**, 6, 453	12.2	171
20	Depletion of the cullin Cdc53p induces morphogenetic changes in Candida albicans. *Eukaryotic Cell*, **2009**, 8, 756-67		18
19	Structural and electrostatic characterization of pariacoto virus: implications for viral assembly. *Biopolymers*, **2009**, 91, 530-8	2.2	51
18	The phagosomal proteome in interferon-gamma-activated macrophages. *Immunity*, **2009**, 30, 143-54	32.3	177
17	Genomic islands in the pathogenic filamentous fungus Aspergillus fumigatus. *PLoS Genetics*, **2008**, 4, e1000046	6	382
16	Genomewide location analysis of Candida albicans Upc2p, a regulator of sterol metabolism and azole drug resistance. *Eukaryotic Cell*, **2008**, 7, 836-47		89
15	Role of SLV in SLI substrate recognition by the Neurospora VS ribozyme. *Rna*, **2008**, 14, 736-48	5.8	24
14	The MHC class I peptide repertoire is molded by the transcriptome. *Journal of Experimental Medicine*, **2008**, 205, 595-610	16.6	127
13	Quantitative expression profiling guided by common retroviral insertion sites reveals novel and cell type specific cancer genes in leukemia. *Blood*, **2008**, 111, 790-9	2.2	29
12	Essential gene identification and drug target prioritization in Aspergillus fumigatus. *PLoS Pathogens*, **2007**, 3, e24	7.6	178
11	Genome-wide fitness test and mechanism-of-action studies of inhibitory compounds in Candida albicans. *PLoS Pathogens*, **2007**, 3, e92	7.6	178
10	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. *Journal of Biological Chemistry*, **2007**, 282, 31610-20	5.4	68
9	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	
8	Probe-level linear model fitting and mixture modeling results in high accuracy detection of differential gene expression. *BMC Bioinformatics*, **2006**, 7, 391	3.6	10
7	Automated extraction and classification of RNA tertiary structure cyclic motifs. *Nucleic Acids Research*, **2006**, 34, 2340-6	20.1	45

6	Large-scale essential gene identification in Candida albicans and applications to antifungal drug discovery. *Molecular Microbiology*, **2003**, 50, 167-81	4.1	371
5	RNA canonical and non-canonical base pairing types: a recognition method and complete repertoire. *Nucleic Acids Research*, **2002**, 30, 4250-63	20.1	101
4	Quantitative analysis of nucleic acid three-dimensional structures. *Journal of Molecular Biology*, **2001**, 308, 919-36	6.5	129
3	Function of hexameric RNA in packaging of bacteriophage phi 29 DNA in vitro. *Molecular Cell*, **1998**, 2, 141-7	17.6	140
2	Modeling active RNA structures using the intersection of conformational space: application to the lead-activated ribozyme. *Rna*, **1998**, 4, 739-49	5.8	23
1	Target variant detection in leukemia using unaligned RNA-Seq reads		2