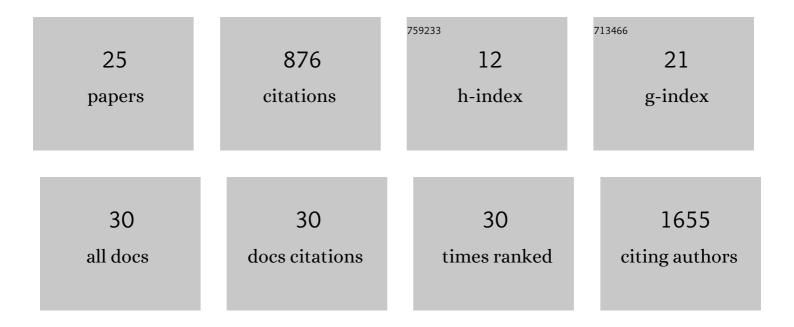
Valentine Murigneux

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	CLIP-seq of eIF4AIII reveals transcriptome-wide mapping of the human exon junction complex. Nature Structural and Molecular Biology, 2012, 19, 1124-1131.	8.2	197
2	Progression of Disease Within 24 Months in Follicular Lymphoma Is Associated With Reduced Intratumoral Immune Infiltration. Journal of Clinical Oncology, 2019, 37, 3300-3309.	1.6	83
3	Transcriptome-wide modulation of splicing by the exon junction complex. Genome Biology, 2014, 15, 551.	8.8	79
4	Increased lipid metabolism impairs NK cell function and mediates adaptation to the lymphoma environment. Blood, 2020, 136, 3004-3017.	1.4	71
5	Comparison of long-read methods for sequencing and assembly of a plant genome. CigaScience, 2020, 9, .	6.4	62
6	An integrative analysis of non-coding regulatory DNA variations associated with autism spectrum disorder. Molecular Psychiatry, 2019, 24, 1707-1719.	7.9	59
7	EBV-associated primary CNS lymphoma occurring after immunosuppression is a distinct immunobiological entity. Blood, 2021, 137, 1468-1477.	1.4	59
8	RAG2 and XLF/Cernunnos interplay reveals a novel role for the RAG complex in DNA repair. Nature Communications, 2016, 7, 10529.	12.8	57
9	Endovascular progenitors infiltrate melanomas and differentiate towards a variety of vascular beds promoting tumor metastasis. Nature Communications, 2019, 10, 18.	12.8	41
10	Transcriptome-wide identification of RNA binding sites by CLIP-seq. Methods, 2013, 63, 32-40.	3.8	28
11	The Dynamics of Interleukin-10-Afforded Protection during Dextran Sulfate Sodium-Induced Colitis. Frontiers in Immunology, 2018, 9, 400.	4.8	25
12	MicroPIPE: validating an end-to-end workflow for high-quality complete bacterial genome construction. BMC Genomics, 2021, 22, 474.	2.8	25
13	Improvements in the sequencing and assembly of plant genomes. GigaByte, 0, 2021, 1-10.	0.0	15
14	Breakage-Fusion-Bridge Events Trigger Complex Genome Rearrangements and Amplifications in Developmentally Arrested T Cell Lymphomas. Cell Reports, 2019, 27, 2847-2858.e4.	6.4	14
15	Subtype-Specific Analyses Reveal Infiltrative Basal Cell Carcinomas Are Highly Interactive with their Environment. Journal of Investigative Dermatology, 2021, 141, 2380-2390.	0.7	13
16	ALFA: annotation landscape for aligned reads. BMC Genomics, 2019, 20, 250.	2.8	9
17	Regional Variation in Epidermal Susceptibility to UV-Induced Carcinogenesis Reflects Proliferative Activity of Epidermal Progenitors. Cell Reports, 2020, 31, 107702.	6.4	9
18	The genome of the endangered <i>Macadamia jansenii</i> displays little diversity but represents an important genetic resource for plant breeding. Plant Direct, 2021, 5, e364.	1.9	7

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#	Article	IF	CITATIONS
19	Genetic aberrations of NLRC5 are associated with downregulated MHCâ€l antigen presentation and impaired Tâ€cell immunity in follicular lymphoma. EJHaem, 2020, 1, 517-526.	1.0	2
20	The Tumor Microenvironment Is Independently Prognostic of Conventional and Clinicogenetic Risk Models in Follicular Lymphoma. Blood, 2017, 130, 728-728.	1.4	2
21	B2M Gene Expression Reflects an Immunologically Active Tumor Microenvironment in DLBCL. Blood, 2019, 134, 2778-2778.	1.4	2
22	Analysis of Positive Control <scp>STR</scp> Experiments Reveals that Results Obtained for <scp>FGA</scp> , D3S1358, and D13S317 Condition the Success Rate of the Analysis of Routine Reference Samples. Journal of Forensic Sciences, 2014, 59, 1074-1079.	1.6	1
23	457 Cancer associated fibroblast profiling reveals endothelin signalling as a novel mediator of niche to tumour cross-talk in Basal Cell Carcinoma. Journal of Investigative Dermatology, 2019, 139, S293.	0.7	Ο
24	517 Laser dermabrasion: a potential treatment for non-melanoma skin cancers. Journal of Investigative Dermatology, 2019, 139, S303.	0.7	0
25	High-throughput multiplexed tandem repeat genotyping using targeted long-read sequencing. F1000Research, 0, 9, 1084.	1.6	Ο