

Valentine Murigneux

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

876
citations

759233

12
h-index

713466

21
g-index

30
all docs

30
docs citations

30
times ranked

1655
citing authors

#	ARTICLE	IF	CITATIONS
1	EBV-associated primary CNS lymphoma occurring after immunosuppression is a distinct immunobiological entity. <i>Blood</i> , 2021, 137, 1468-1477.	1.4	59
2	MicroPIPE: validating an end-to-end workflow for high-quality complete bacterial genome construction. <i>BMC Genomics</i> , 2021, 22, 474.	2.8	25
3	Subtype-Specific Analyses Reveal Infiltrative Basal Cell Carcinomas Are Highly Interactive with their Environment. <i>Journal of Investigative Dermatology</i> , 2021, 141, 2380-2390.	0.7	13
4	The genome of the endangered <i>Macadamia janseni</i> displays little diversity but represents an important genetic resource for plant breeding. <i>Plant Direct</i> , 2021, 5, e364.	1.9	7
5	Regional Variation in Epidermal Susceptibility to UV-Induced Carcinogenesis Reflects Proliferative Activity of Epidermal Progenitors. <i>Cell Reports</i> , 2020, 31, 107702.	6.4	9
6	Genetic aberrations of NLRC5 are associated with downregulated MHC class II antigen presentation and impaired T cell immunity in follicular lymphoma. <i>EJHaem</i> , 2020, 1, 517-526.	1.0	2
7	Increased lipid metabolism impairs NK cell function and mediates adaptation to the lymphoma environment. <i>Blood</i> , 2020, 136, 3004-3017.	1.4	71
8	Comparison of long-read methods for sequencing and assembly of a plant genome. <i>GigaScience</i> , 2020, 9, .	6.4	62
9	Progression of Disease Within 24 Months in Follicular Lymphoma Is Associated With Reduced Intratumoral Immune Infiltration. <i>Journal of Clinical Oncology</i> , 2019, 37, 3300-3309.	1.6	83
10	457 Cancer associated fibroblast profiling reveals endothelin signalling as a novel mediator of niche to tumour cross-talk in Basal Cell Carcinoma. <i>Journal of Investigative Dermatology</i> , 2019, 139, S293.	0.7	0
11	517 Laser dermabrasion: a potential treatment for non-melanoma skin cancers. <i>Journal of Investigative Dermatology</i> , 2019, 139, S303.	0.7	0
12	Breakage-Fusion-Bridge Events Trigger Complex Genome Rearrangements and Amplifications in Developmentally Arrested T Cell Lymphomas. <i>Cell Reports</i> , 2019, 27, 2847-2858.e4.	6.4	14
13	ALFA: annotation landscape for aligned reads. <i>BMC Genomics</i> , 2019, 20, 250.	2.8	9
14	Endovascular progenitors infiltrate melanomas and differentiate towards a variety of vascular beds promoting tumor metastasis. <i>Nature Communications</i> , 2019, 10, 18.	12.8	41
15	An integrative analysis of non-coding regulatory DNA variations associated with autism spectrum disorder. <i>Molecular Psychiatry</i> , 2019, 24, 1707-1719.	7.9	59
16	B2M Gene Expression Reflects an Immunologically Active Tumor Microenvironment in DLBCL. <i>Blood</i> , 2019, 134, 2778-2778.	1.4	2
17	The Dynamics of Interleukin-10-Afforded Protection during Dextran Sulfate Sodium-Induced Colitis. <i>Frontiers in Immunology</i> , 2018, 9, 400.	4.8	25
18	The Tumor Microenvironment Is Independently Prognostic of Conventional and Clinicogenetic Risk Models in Follicular Lymphoma. <i>Blood</i> , 2017, 130, 728-728.	1.4	2

#	ARTICLE	IF	CITATIONS
19	RAG2 and XLF/Cernunnos interplay reveals a novel role for the RAG complex in DNA repair. <i>Nature Communications</i> , 2016, 7, 10529.	12.8	57
20	Transcriptome-wide modulation of splicing by the exon junction complex. <i>Genome Biology</i> , 2014, 15, 551.	8.8	79
21	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. <i>Journal of Forensic Sciences</i> , 2014, 59, 1074-1079.	1.6	1
22	Transcriptome-wide identification of RNA binding sites by CLIP-seq. <i>Methods</i> , 2013, 63, 32-40.	3.8	28
23	CLIP-seq of eIF4AIII reveals transcriptome-wide mapping of the human exon junction complex. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1124-1131.	8.2	197
24	Improvements in the sequencing and assembly of plant genomes. <i>GigaByte</i> , 0, 2021, 1-10.	0.0	15
25	High-throughput multiplexed tandem repeat genotyping using targeted long-read sequencing. <i>F1000Research</i> , 0, 9, 1084.	1.6	0