

Marion Leleu

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

4,333
citations

393982

19
h-index

580395

25
g-index

28
all docs

28
docs citations

28
times ranked

7298
citing authors

#	ARTICLE	IF	CITATIONS
1	Multicenter analysis of sputum microbiota in tuberculosis patients. PLoS ONE, 2020, 15, e0240250.	1.1	10
2	Integrated proteogenomic deep sequencing and analytics accurately identify non-canonical peptides in tumor immunopeptidomes. Nature Communications, 2020, 11, 1293.	5.8	196
3	Three-dimensional chromatin interactions remain stable upon CAG/CTG repeat expansion. Science Advances, 2020, 6, eaaz4012.	4.7	16
4	The process of Lewy body formation, rather than simply α -synuclein fibrillization, is one of the major drivers of neurodegeneration. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 4971-4982.	3.3	422
5	AMPK promotes survival of c-Myc-positive melanoma cells by suppressing oxidative stress. EMBO Journal, 2018, 37, .	3.5	34
6	Large scale genomic reorganization of topological domains at the HoxD locus. Genome Biology, 2017, 18, 149.	3.8	31
7	Transcriptome-wide co-expression analysis identifies LRRC2 as a novel mediator of mitochondrial and cardiac function. PLoS ONE, 2017, 12, e0170458.	1.1	11
8	A role for mitotic bookmarking of SOX2 in pluripotency and differentiation. Genes and Development, 2016, 30, 2538-2550.	2.7	133
9	Identification of a RAI1-associated disease network through integration of exome sequencing, transcriptomics, and 3D genomics. Genome Medicine, 2016, 8, 105.	3.6	20
10	Clustering of mammalian <i>Hox</i> genes with other H3K27me3 targets within an active nuclear domain. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4672-4677.	3.3	143
11	Conservation and Divergence of Regulatory Strategies at Hox Loci and the Origin of Tetrapod Digits. PLoS Biology, 2014, 12, e1001773.	2.6	137
12	HTSstation: A Web Application and Open-Access Libraries for High-Throughput Sequencing Data Analysis. PLoS ONE, 2014, 9, e85879.	1.1	93
13	Temporal dynamics and developmental memory of 3D chromatin architecture at Hox gene loci. ELife, 2014, 3, e02557.	2.8	125
14	A Switch Between Topological Domains Underlies <i>HoxD</i> Genes Collinearity in Mouse Limbs. Science, 2013, 340, 1234-1237.	6.0	391
15	Multiple Enhancers Regulate Hoxd Genes and the Hotdog LncRNA during Cecum Budding. Cell Reports, 2013, 5, 137-150.	2.9	70
16	Structural Variation-Associated Expression Changes Are Paralleled by Chromatin Architecture Modifications. PLoS ONE, 2013, 8, e79973.	1.1	27
17	Detecting Long-Range Chromatin Interactions Using the Chromosome Conformation Capture Sequencing (4C-seq) Method. Methods in Molecular Biology, 2012, 786, 211-225.	0.4	43
18	The Dynamic Architecture of <i>Hox</i> Gene Clusters. Science, 2011, 334, 222-225.	6.0	370

#	ARTICLE	IF	CITATIONS
19	Processing and analyzing ChIP-seq data: from short reads to regulatory interactions. Briefings in Functional Genomics, 2010, 9, 466-476.	1.3	15
20	Jarid2 is a PRC2 component in embryonic stem cells required for multi-lineage differentiation and recruitment of PRC1 and RNA Polymerase II to developmental regulators. Nature Cell Biology, 2010, 12, 618-624.	4.6	274
21	Functional Analysis of CTCF During Mammalian Limb Development. Developmental Cell, 2010, 19, 819-830.	3.1	136
22	Runx proteins regulate Foxp3 expression. Journal of Experimental Medicine, 2009, 206, 2329-2337.	4.2	88
23	Runx proteins regulate Foxp3 expression. Journal of Cell Biology, 2009, 187, i3-i3.	2.3	1
24	Cohesins Functionally Associate with CTCF on Mammalian Chromosome Arms. Cell, 2008, 132, 422-433.	13.5	800
25	T cell receptor signaling controls Foxp3 expression via PI3K, Akt, and mTOR. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7797-7802.	3.3	747