

Ismaël Padioleau

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

4,040
citations

516215

16
h-index

887659

17
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all docs

17
docs citations

17
times ranked

10471
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome and genome sequencing uncovers functional variation in humans. <i>Nature</i> , 2013, 501, 506-511.	13.7	1,857
2	Passive and active DNA methylation and the interplay with genetic variation in gene regulation. <i>ELife</i> , 2013, 2, e00523.	2.8	374
3	Coordinated Effects of Sequence Variation on DNA Binding, Chromatin Structure, and Transcription. <i>Science</i> , 2013, 342, 744-747.	6.0	364
4	Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , 2015, 348, 666-669.	6.0	252
5	Population Variation and Genetic Control of Modular Chromatin Architecture in Humans. <i>Cell</i> , 2015, 162, 1039-1050.	13.5	210
6	Tissue-Specific Effects of Genetic and Epigenetic Variation on Gene Regulation and Splicing. <i>PLoS Genetics</i> , 2015, 11, e1004958.	1.5	185
7	Putative cis-regulatory drivers in colorectal cancer. <i>Nature</i> , 2014, 512, 87-90.	13.7	136
8	Biased Allelic Expression in Human Primary Fibroblast Single Cells. <i>American Journal of Human Genetics</i> , 2015, 96, 70-80.	2.6	117
9	Topoisomerase 1 prevents replication stress at R-loop-enriched transcription termination sites. <i>Nature Communications</i> , 2020, 11, 3940.	5.8	105
10	easyRNASeq: a bioconductor package for processing RNA-Seq data. <i>Bioinformatics</i> , 2012, 28, 2532-2533.	1.8	98
11	The Histone Deacetylases Sir2 and Rpd3 Act on Ribosomal DNA to Control the Replication Program in Budding Yeast. <i>Molecular Cell</i> , 2014, 54, 691-697.	4.5	95
12	Comprehensive Human Virus Screening Using High-Throughput Sequencing with a User-Friendly Representation of Bioinformatics Analysis: a Pilot Study. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3351-3361.	1.8	60
13	Mec1 Is Activated at the Onset of Normal S Phase by Low-dNTP Pools Impeding DNA Replication. <i>Molecular Cell</i> , 2020, 78, 396-410.e4.	4.5	48
14	RAS mutations drive proliferative chronic myelomonocytic leukemia via a KMT2A-PLK1 axis. <i>Nature Communications</i> , 2021, 12, 2901.	5.8	44
15	Celiac disease T-cell epitopes from gamma-gliadins: immunoreactivity depends on the genome of origin, transcript frequency, and flanking protein variation. <i>BMC Genomics</i> , 2012, 13, 277.	1.2	43
16	Comprehensive metagenomic analysis of glioblastoma reveals absence of known virus despite antiviral-like type I interferon gene response. <i>International Journal of Cancer</i> , 2014, 135, 1381-1389.	2.3	35
17	XPC deficiency increases risk of hematologic malignancies through mutator phenotype and characteristic mutational signature. <i>Nature Communications</i> , 2020, 11, 5834.	5.8	17