Stephane E Castel

List of Publications by Year
in descending order

20 papers	4,109 citations	471509 17 h-index	752698 20 g-index
32 all docs	32 docs citations	32 times ranked	8387 citing authors

#	Article	IF	Citations
1	RNA interference in the nucleus: roles for small RNAs in transcription, epigenetics and beyond. Nature Reviews Genetics, 2013, 14, 100-112.	16.3	871
2	Landscape of X chromosome inactivation across human tissues. Nature, 2017, 550, 244-248.	27.8	764
3	Tools and best practices for data processing in allelic expression analysis. Genome Biology, 2015, 16, 195.	8.8	335
4	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	12.6	329
5	Cell typeâ€“specific genetic regulation of gene expression across human tissues. Science, 2020, 369, .	12.6	210
6	Modified penetrance of coding variants by cis-regulatory variation contributes to disease risk. Nature Genetics, 2018, 50, 1327-1334.	21.4	167
7	Structural basis of the oxidative activation of the carboxysomal Î³-carbonic anhydrase, CcmM. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2455-2460.	7.1	160
8	Genetic regulatory effects modified by immune activation contribute to autoimmune disease associations. Nature Communications, 2017, 8, 266.	12.8	157
9	RNAi promotes heterochromatic silencing through replication-coupled release of RNA Pol II. Nature, 2011, 479, 135-138.	27.8	142
10	Quantifying the regulatory effect size of cis-acting genetic variation using allelic fold change. Genome Research, 2017, 27, 1872-1884.	5.5	114
11	Rare variant phasing and haplotypic expression from RNA sequencing with phASER. Nature Communications, 2016, 7, 12817.	12.8	105
12	Dicer Promotes Transcription Termination at Sites of Replication Stress to Maintain Genome Stability. Cell, 2014, 159, 572-583.	28.9	102
13	Genetic regulatory variation in populations informs transcriptome analysis in rare disease. Science, 2019, 366, 351-356.	12.6	99
14	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	28.9	94
15	Transcriptomic signatures across human tissues identify functional rare genetic variation. Science, 2020, 369, .	12.6	89
16	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	8.8	68
17	Oncogenic transformation of Drosophila somatic cells induces a functional piRNA pathway. Genes and Development, 2016, 30, 1623-1635.	5.9	33
18	Leveraging allelic imbalance to refine fine-mapping for eQTL studies. PLoS Genetics, 2019, 15, e1008481.	3.5	20

#	Article	IF	Citations
19	Mid-pass whole genome sequencing enables biomedical genetic studies of diverse populations. BMC Genomics, 2021, 22, 666.	2.8	5
20	Dicer in action at replication-transcription collisions. Molecular and Cellular Oncology, 2015, 2, e991224.	0.7	2