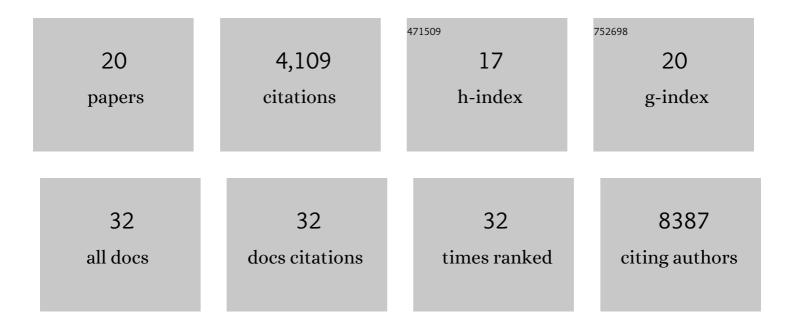
Stephane E Castel

List of Publications by Year in descending order

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STEDHANE F CASTEL

#	Article	IF	CITATIONS
1	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	28.9	94
2	Mid-pass whole genome sequencing enables biomedical genetic studies of diverse populations. BMC Genomics, 2021, 22, 666.	2.8	5
3	Transcriptomic signatures across human tissues identify functional rare genetic variation. Science, 2020, 369, .	12.6	89
4	Cell type–specific genetic regulation of gene expression across human tissues. Science, 2020, 369, .	12.6	210
5	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	12.6	329
6	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	8.8	68
7	Genetic regulatory variation in populations informs transcriptome analysis in rare disease. Science, 2019, 366, 351-356.	12.6	99
8	Leveraging allelic imbalance to refine fine-mapping for eQTL studies. PLoS Genetics, 2019, 15, e1008481.	3.5	20
9	Modified penetrance of coding variants by cis-regulatory variation contributes to disease risk. Nature Genetics, 2018, 50, 1327-1334.	21.4	167
10	Landscape of X chromosome inactivation across human tissues. Nature, 2017, 550, 244-248.	27.8	764
11	Quantifying the regulatory effect size of <i>cis</i> -acting genetic variation using allelic fold change. Genome Research, 2017, 27, 1872-1884.	5.5	114
12	Genetic regulatory effects modified by immune activation contribute to autoimmune disease associations. Nature Communications, 2017, 8, 266.	12.8	157
13	Oncogenic transformation of <i>Drosophila</i> somatic cells induces a functional piRNA pathway. Genes and Development, 2016, 30, 1623-1635.	5.9	33
14	Rare variant phasing and haplotypic expression from RNA sequencing with phASER. Nature Communications, 2016, 7, 12817.	12.8	105
15	Tools and best practices for data processing in allelic expression analysis. Genome Biology, 2015, 16, 195.	8.8	335
16	Dicer in action at replication-transcription collisions. Molecular and Cellular Oncology, 2015, 2, e991224.	0.7	2
17	Dicer Promotes Transcription Termination at Sites of Replication Stress to Maintain Genome Stability. Cell, 2014, 159, 572-583.	28.9	102
18	RNA interference in the nucleus: roles for small RNAs in transcription, epigenetics and beyond. Nature Reviews Genetics, 2013, 14, 100-112.	16.3	871

#	Article	IF	CITATIONS
19	RNAi promotes heterochromatic silencing through replication-coupled release of RNA Pol II. Nature, 2011, 479, 135-138.	27.8	142
20	Structural basis of the oxidative activation of the carboxysomal \hat{I}^3 -carbonic anhydrase, CcmM.	7.1	160

Structural basis of the oxidative activation of the carboxysomal \hat{l}^3 -carbonic anhydrase, CcmM. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2455-2460. 20