

Maria ColomÃ©-TatchÃ©

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

2,031
citations

516710

16
h-index

752698

20
g-index

25
all docs

25
docs citations

25
times ranked

3092
citing authors

#	ARTICLE	IF	CITATIONS
1	Region-level epimutation rates in <i>Arabidopsis thaliana</i> . <i>Heredity</i> , 2021, 127, 190-202.	2.6	21
2	ARID1A Controls a Novel Transcriptional Network Regulating FAS in Follicular Lymphoma. <i>Blood</i> , 2021, 138, 3492-3492.	1.4	0
3	A genome assembly and the somatic genetic and epigenetic mutation rate in a wild long-lived perennial <i>Populus trichocarpa</i> . <i>Genome Biology</i> , 2020, 21, 259.	8.8	68
4	AlphaBeta: computational inference of epimutation rates and spectra from high-throughput DNA methylation data in plants. <i>Genome Biology</i> , 2020, 21, 260.	8.8	24
5	Endogenous retroviral insertions drive non-canonical imprinting in extra-embryonic tissues. <i>Genome Biology</i> , 2019, 20, 225.	8.8	67
6	MLL2 conveys transcription-independent H3K4 trimethylation in oocytes. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 73-82.	8.2	127
7	METHimpute: imputation-guided construction of complete methylomes from WGBS data. <i>BMC Genomics</i> , 2018, 19, 444.	2.8	28
8	Ecological plant epigenetics: Evidence from model and non-model species, and the way forward. <i>Ecology Letters</i> , 2017, 20, 1576-1590.	6.4	279
9	Histone propionylation is a mark of active chromatin. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 1048-1056.	8.2	148
10	Genetic sources of population epigenomic variation. <i>Nature Reviews Genetics</i> , 2016, 17, 319-332.	16.3	136
11	Signatures of Dobzhansky's "Muller Incompatibilities in the Genomes of Recombinant Inbred Lines. <i>Genetics</i> , 2016, 202, 825-841.	2.9	12
12	histoneHMM: Differential analysis of histone modifications with broad genomic footprints. <i>BMC Bioinformatics</i> , 2015, 16, 60.	2.6	28
13	Rate, spectrum, and evolutionary dynamics of spontaneous epimutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6676-6681.	7.1	251
14	Mapping the Epigenetic Basis of Complex Traits. <i>Science</i> , 2014, 343, 1145-1148.	12.6	403
15	Natural variation of histone modification and its impact on gene expression in the rat genome. <i>Genome Research</i> , 2014, 24, 942-953.	5.5	53
16	Genome-Wide Analysis of DNA Methylation in <i>Arabidopsis</i> Using MeDIP-Chip. <i>Methods in Molecular Biology</i> , 2014, 1112, 125-149.	0.9	15
17	Evaluation of MeDIP-Chip in the Context of Whole-Genome Bisulfite Sequencing (WGBS-Seq) in <i>Arabidopsis</i> . <i>Methods in Molecular Biology</i> , 2013, 1067, 203-224.	0.9	11
18	Features of the <i>Arabidopsis</i> recombination landscape resulting from the combined loss of sequence variation and DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16240-16245.	7.1	145

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19	Quantitative Epigenetics Through Epigenomic Perturbation of Isogenic Lines. <i>Genetics</i> , 2011, 188, 215-227.	2.9	61
20	Concerning epigenetics and inbreeding. <i>Nature Reviews Genetics</i> , 2011, 12, 376-376.	16.3	6
21	Genome-Wide Epigenetic Perturbation Jump-Starts Patterns of Heritable Variation Found in Nature. <i>Genetics</i> , 2011, 188, 1015-1017.	2.9	109