Filipe Borges

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5931067/publications.pdf

Version: 2024-02-01

23 papers	4,242 citations	430874 18 h-index	677142 22 g-index
28 all docs	28 docs citations	28 times ranked	4526 citing authors

#	Article	IF	Citations
1	Bypassing reproductive barriers in hybrid seeds using chemically induced epimutagenesis. Plant Cell, 2022, 34, 989-1001.	6.6	16
2	Specificities and Dynamics of Transposable Elements in Land Plants. Biology, 2022, 11, 488.	2.8	20
3	Loss of Small-RNA-Directed DNA Methylation in the Plant Cell Cycle Promotes Germline Reprogramming and Somaclonal Variation. Current Biology, 2021, 31, 591-600.e4.	3.9	36
4	Contrasting epigenetic control of transgenes and endogenous genes promotes post-transcriptional transgene silencing in Arabidopsis. Nature Communications, 2021, 12, 2787.	12.8	5
5	DEFECTIVE EMBRYO AND MERISTEMS genes are required for cell division and gamete viability in Arabidopsis. PLoS Genetics, 2021, 17, e1009561.	3.5	3
6	Male fertility in Arabidopsis requires active DNA demethylation of genes that control pollen tube function. Nature Communications, 2021, 12, 410.	12.8	41
7	Polymerase IV Plays a Crucial Role in Pollen Development in Capsella. Plant Cell, 2020, 32, 950-966.	6.6	46
8	Arabidopsis retrotransposon virus-like particles and their regulation by epigenetically activated small RNA. Genome Research, 2020, 30, 576-588.	5.5	33
9	Small RNA Function in Plants: From Chromatin to the Next Generation. Cold Spring Harbor Symposia on Quantitative Biology, 2019, 84, 133-140.	1.1	0
10	Transposon-derived small RNAs triggered by miR845 mediate genome dosage response in Arabidopsis. Nature Genetics, 2018, 50, 186-192.	21.4	126
11	Epigenetic activation of meiotic recombination near Arabidopsis thaliana centromeres via loss of H3K9me2 and non-CG DNA methylation. Genome Research, 2018, 28, 519-531.	5.5	138
12	The expanding world of small RNAs in plants. Nature Reviews Molecular Cell Biology, 2015, 16, 727-741.	37.0	932
13	miRNAs trigger widespread epigenetically activated siRNAs from transposons in Arabidopsis. Nature, 2014, 508, 411-415.	27.8	331
14	Transcriptional profiling of Arabidopsis root hairs and pollen defines an apical cell growth signature. BMC Plant Biology, 2014, 14, 197.	3.6	49
15	Establishing epigenetic variation during genome reprogramming. RNA Biology, 2013, 10, 490-494.	3.1	23
16	Reprogramming the Epigenome in Arabidopsis Pollen. Cold Spring Harbor Symposia on Quantitative Biology, 2012, 77, 1-5.	1.1	20
17	Reprogramming of DNA Methylation in Pollen Guides Epigenetic Inheritance via Small RNA. Cell, 2012, 151, 194-205.	28.9	506
18	FACS-based purification of Arabidopsis microspores, sperm cells and vegetative nuclei. Plant Methods, 2012, 8, 44.	4.3	76

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19	MicroRNA activity in theArabidopsismale germline. Journal of Experimental Botany, 2011, 62, 1611-1620.	4.8	137
20	Glutamate Receptorâ€“Like Genes Form Ca ²⁺ Channels in Pollen Tubes and Are Regulated by Pistil <scp> d </scp> -Serine. Science, 2011, 332, 434-437.	12.6	372
21	Whole Genome Analysis of Gene Expression Reveals Coordinated Activation of Signaling and Metabolic Pathways during Pollen-Pistil Interactions in Arabidopsis Â Â. Plant Physiology, 2011, 155, 2066-2080.	4.8	78
22	Epigenetic Reprogramming and Small RNA Silencing of Transposable Elements in Pollen. Cell, 2009, 136, 461-472.	28.9	908
23	Comparative Transcriptomics of Arabidopsis Sperm Cells Â. Plant Physiology, 2008, 148, 1168-1181.	4.8	339