

Chad E Niederhuth

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8745609/publications.pdf>

Version: 2024-02-01

19
papers

2,539
citations

567281

15
h-index

794594

19
g-index

28
all docs

28
docs citations

28
times ranked

3841
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome sequences of <i>Arachis duranensis</i> and <i>Arachis ipaensis</i> , the diploid ancestors of cultivated peanut. <i>Nature Genetics</i> , 2016, 48, 438-446.	21.4	761
2	Widespread natural variation of DNA methylation within angiosperms. <i>Genome Biology</i> , 2016, 17, 194.	8.8	436
3	On the origin and evolutionary consequences of gene body DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9111-9116.	7.1	260
4	Single-molecule sequencing and optical mapping yields an improved genome of woodland strawberry (<i>Fragaria vesca</i>) with chromosome-scale contiguity. <i>GigaScience</i> , 2018, 7, 1-7.	6.4	209
5	Putting DNA methylation in context: from genomes to gene expression in plants. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 149-156.	1.9	147
6	The evolution of CHROMOMETHYLASES and gene body DNA methylation in plants. <i>Genome Biology</i> , 2017, 18, 65.	8.8	124
7	A Comparative Analysis of 5-Azacytidine- and Zebularine-Induced DNA Demethylation. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2773-2780.	1.8	104
8	Covering Your Bases: Inheritance of DNA Methylation in Plant Genomes. <i>Molecular Plant</i> , 2014, 7, 472-480.	8.3	80
9	Transcriptional profiling of the <i>Arabidopsis</i> abscission mutant <i>hae hsl2</i> by RNA-Seq. <i>BMC Genomics</i> , 2013, 14, 37.	2.8	78
10	Replaying the evolutionary tape to investigate subgenome dominance in allopolyploid <i>Brassica napus</i> . <i>New Phytologist</i> , 2021, 230, 354-371.	7.3	57
11	Letting Go is Never Easy: Abscission and Receptor-like Protein Kinases. <i>Journal of Integrative Plant Biology</i> , 2013, 55, 1251-1263.	8.5	55
12	Establishment, maintenance, and biological roles of non-CG methylation in plants. <i>Essays in Biochemistry</i> , 2019, 63, 743-755.	4.7	49
13	The Dnmt3L ADD Domain Controls Cytosine Methylation Establishment during Spermatogenesis. <i>Cell Reports</i> , 2015, 10, 944-956.	6.4	39
14	pENCODE: A Plant Encyclopedia of DNA Elements. <i>Annual Review of Genetics</i> , 2014, 48, 49-70.	7.6	38
15	Epigenetics and epigenomics: underlying mechanisms, relevance, and implications in crop improvement. <i>Functional and Integrative Genomics</i> , 2020, 20, 739-761.	3.5	37
16	Intertwined evolution of plant epigenomes and genomes. <i>Current Opinion in Plant Biology</i> , 2021, 61, 101990.	7.1	15
17	From Gigabyte to Kilobyte: A Bioinformatics Protocol for Mining Large RNA-Seq Transcriptomics Data. <i>PLoS ONE</i> , 2015, 10, e0125000.	2.5	7
18	Prenatal testosterone triggers long-term behavioral changes in male zebra finches: unravelling the neurogenomic mechanisms. <i>BMC Genomics</i> , 2021, 22, 158.	2.8	7

#	ARTICLE	IF	CITATIONS
19	Epigenetic Diversity and Application to Breeding. <i>Advances in Botanical Research</i> , 2018, , 49-86.	1.1	5