

Steven R Eichten

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

3,859
citations

230014

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times ranked

5828
citing authors

#	ARTICLE	IF	CITATIONS
1	Extending the Genotype in <i>Brachypodium</i> by Including DNA Methylation Reveals a Joint Contribution with Genetics on Adaptive Traits. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1629-1637.	0.8	3
2	HOME: a histogram based machine learning approach for effective identification of differentially methylated regions. <i>BMC Bioinformatics</i> , 2019, 20, 253.	1.2	45
3	Excess Light Priming in <i>Arabidopsis thaliana</i> Genotypes with Altered DNA Methylomes. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3611-3621.	0.8	9
4	Maintenance of pre-existing DNA methylation states through recurring excess light stress. <i>Plant, Cell and Environment</i> , 2018, 41, 1657-1672.	2.8	33
5	RNA Polymerase II Read-Through Promotes Expression of Neighboring Genes in SAL1-PAP-XRN Retrograde Signaling. <i>Plant Physiology</i> , 2018, 178, 1614-1630.	2.3	23
6	Genomic features shaping the landscape of meiotic double-strand-break hotspots in maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12231-12236.	3.3	91
7	The <i>Arabidopsis</i> DNA Methylome Is Stable under Transgenerational Drought Stress. <i>Plant Physiology</i> , 2017, 175, 1893-1912.	2.3	112
8	Rapid Recovery Gene Downregulation during Excess-Light Stress and Recovery in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2017, 29, 1836-1863.	3.1	90
9	DNA methylation profiles of diverse <i>Brachypodium distachyon</i> align with underlying genetic diversity. <i>Genome Research</i> , 2016, 26, 1520-1531.	2.4	34
10	Twenty-four nucleotide siRNAs produce heritable trans-chromosomal methylation in F1 <i>Arabidopsis</i> hybrids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6895-E6902.	3.3	36
11	Reconsidering plant memory: Intersections between stress recovery, RNA turnover, and epigenetics. <i>Science Advances</i> , 2016, 2, e1501340.	4.7	477
12	Population scale mapping of transposable element diversity reveals links to gene regulation and epigenomic variation. <i>ELife</i> , 2016, 5, .	2.8	181
13	Minimal evidence for consistent changes in maize DNA methylation patterns following environmental stress. <i>Frontiers in Plant Science</i> , 2015, 6, 308.	1.7	82
14	Examining the Causes and Consequences of Context-Specific Differential DNA Methylation in Maize. <i>Plant Physiology</i> , 2015, 168, 1262-1274.	2.3	62
15	Post-conversion targeted capture of modified cytosines in mammalian and plant genomes. <i>Nucleic Acids Research</i> , 2015, 43, e81-e81.	6.5	62
16	Genomic Distribution of H3K9me2 and DNA Methylation in a Maize Genome. <i>PLoS ONE</i> , 2014, 9, e105267.	1.1	137
17	Genetic Perturbation of the Maize Methylome. <i>Plant Cell</i> , 2014, 26, 4602-4616.	3.1	158
18	Genome-wide discovery and characterization of maize long non-coding RNAs. <i>Genome Biology</i> , 2014, 15, R40.	13.9	419

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19	Epigenetics: Beyond Chromatin Modifications and Complex Genetic Regulation. <i>Plant Physiology</i> , 2014, 165, 933-947.	2.3	126
20	Insights into the Effects of Long-Term Artificial Selection on Seed Size in Maize. <i>Genetics</i> , 2014, 198, 409-421.	1.2	38
21	Inheritance Patterns and Stability of DNA Methylation Variation in Maize Near-Isogenic Lines. <i>Genetics</i> , 2014, 196, 667-676.	1.2	58
22	Consistent and Heritable Alterations of DNA Methylation Are Induced by Tissue Culture in Maize. <i>Genetics</i> , 2014, 198, 209-218.	1.2	76
23	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. <i>Genome Biology</i> , 2013, 14, R58.	3.8	125
24	Genomic Distribution of Maize Facultative Heterochromatin Marked by Trimethylation of H3K27. <i>Plant Cell</i> , 2013, 25, 780-793.	3.1	91
25	Epigenetic and Genetic Influences on DNA Methylation Variation in Maize Populations. <i>Plant Cell</i> , 2013, 25, 2783-2797.	3.1	227
26	Comprehensive analysis of imprinted genes in maize reveals allelic variation for imprinting and limited conservation with other species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19639-19644.	3.3	131
27	Variation in DNA Methylation Patterns is More Common among Maize Inbreds than among Tissues. <i>Plant Genome</i> , 2013, 6, plantgenome2012.06.0009.	1.6	28
28	Spreading of Heterochromatin Is Limited to Specific Families of Maize Retrotransposons. <i>PLoS Genetics</i> , 2012, 8, e1003127.	1.5	166
29	B73-Mo17 Near-Isogenic Lines Demonstrate Dispersed Structural Variation in Maize. <i>Plant Physiology</i> , 2011, 156, 1679-1690.	2.3	76
30	Parent-of-Origin Effects on Gene Expression and DNA Methylation in the Maize Endosperm. <i>Plant Cell</i> , 2011, 23, 4221-4233.	3.1	189
31	Heritable Epigenetic Variation among Maize Inbreds. <i>PLoS Genetics</i> , 2011, 7, e1002372.	1.5	150
32	Pervasive gene content variation and copy number variation in maize and its undomesticated progenitor. <i>Genome Research</i> , 2010, 20, 1689-1699.	2.4	309