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List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

1,621
citations

623188

14
h-index

794141

19
g-index

24
all docs

24
docs citations

24
times ranked

2641
citing authors

#	ARTICLE	IF	CITATIONS
1	AGRIS: the Arabidopsis Gene Regulatory Information Server, an update. <i>Nucleic Acids Research</i> , 2011, 39, D1118-D1122.	6.5	289
2	Unraveling the KNOTTED1 regulatory network in maize meristems. <i>Genes and Development</i> , 2012, 26, 1685-1690.	2.7	258
3	Widespread long-range cis-regulatory elements in the maize genome. <i>Nature Plants</i> , 2019, 5, 1237-1249.	4.7	250
4	A Genome-Wide Regulatory Framework Identifies Maize <i>Pericarp Color1</i> Controlled Genes. <i>Plant Cell</i> , 2012, 24, 2745-2764.	3.1	148
5	Evolutionarily informed deep learning methods for predicting relative transcript abundance from DNA sequence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5542-5549.	3.3	121
6	Reconstructing the maize leaf regulatory network using ChIP-seq data of 104 transcription factors. <i>Nature Communications</i> , 2020, 11, 5089.	5.8	111
7	A Maize Gene Regulatory Network for Phenolic Metabolism. <i>Molecular Plant</i> , 2017, 10, 498-515.	3.9	74
8	Core Promoter Plasticity Between Maize Tissues and Genotypes Contrasts with Predominance of Sharp Transcription Initiation Sites. <i>Plant Cell</i> , 2015, 27, 3309-3320.	3.1	65
9	Identification and Characterization of Maize <i>salmon silks</i> Genes Involved in Insecticidal Maysin Biosynthesis. <i>Plant Cell</i> , 2016, 28, 1297-1309.	3.1	64
10	The Maize <i>TFome</i> development of a transcription factor open reading frame collection for functional genomics. <i>Plant Journal</i> , 2014, 80, 356-366.	2.8	55
11	Emergence of Switch-Like Behavior in a Large Family of Simple Biochemical Networks. <i>PLoS Computational Biology</i> , 2011, 7, e1002039.	1.5	41
12	From plant gene regulatory grids to network dynamics. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 454-465.	0.9	41
13	A k-mer grammar analysis to uncover maize regulatory architecture. <i>BMC Plant Biology</i> , 2019, 19, 103.	1.6	35
14	Large-scale transcriptional profiling of lignified tissues in <i>Tectona grandis</i> . <i>BMC Plant Biology</i> , 2015, 15, 221.	1.6	27
15	Assessing the regulatory potential of transposable elements using chromatin accessibility profiles of maize transposons. <i>Genetics</i> , 2021, 217, 1-13.	1.2	14
16	Important biological information uncovered in previously unaligned reads from chromatin immunoprecipitation experiments (ChIP-Seq). <i>Scientific Reports</i> , 2015, 5, 8635.	1.6	5
17	In Silico Identification of Regulatory Elements of GRIN1 Genes. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 106-115.	1.0	3
18	Genomic Resources for Breeding in Alfalfa: Availability, Utility, and Adoption. <i>Compendium of Plant Genomes</i> , 2021, , 177-189.	0.3	2

#	ARTICLE	IF	CITATIONS
19	Genome-Wide TSS Identification in Maize. <i>Methods in Molecular Biology</i> , 2018, 1830, 239-256.	0.4	1