

# Genome-wide mapping of transcriptional enhancer can features in maize

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Citation Report

#	ARTICLE	IF	CITATIONS
1	ChIP-ping the branches of the tree: functional genomics and the evolution of eukaryotic gene regulation. <i>Briefings in Functional Genomics</i> , 2018, 17, 116-137.	1.3	5
2	Identification of cis-regulatory elements by chromatin structure. <i>Current Opinion in Plant Biology</i> , 2018, 42, 90-94.	3.5	31
3	Plant Lineage-Specific Amplification of Transcription Factor Binding Motifs by Miniature Inverted-Repeat Transposable Elements (MITEs). <i>Genome Biology and Evolution</i> , 2018, 10, 1210-1220.	1.1	26
4	Adaptation in plant genomes: Bigger is different. <i>American Journal of Botany</i> , 2018, 105, 16-19.	0.8	50
6	Plant Protection by Benzoxazinoids—Recent Insights into Biosynthesis and Function. <i>Agronomy</i> , 2018, 8, 143.	1.3	69
7	Enhancer-Promoter Interaction of <i>SELF PRUNING 5G</i> Shapes Photoperiod Adaptation. <i>Plant Physiology</i> , 2018, 178, 1631-1642.	2.3	34
8	Evolutionary Impacts of Alternative Transposition. , 2018, , 113-130.		6
9	Three-dimensional chromatin packing and positioning of plant genomes. <i>Nature Plants</i> , 2018, 4, 521-529.	4.7	100
10	The bread wheat epigenomic map reveals distinct chromatin architectural and evolutionary features of functional genetic elements. <i>Genome Biology</i> , 2019, 20, 139.	3.8	90
11	Novel mRNAs 3' end-associated cis-regulatory elements with epigenomic signatures of mammalian enhancers in the <i>Arabidopsis</i> genome. <i>Rna</i> , 2019, 25, 1242-1258.	1.6	6
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16	Long-range interactions between proximal and distal regulatory regions in maize. <i>Nature Communications</i> , 2019, 10, 2633.	5.8	79
17	Identification and functional evaluation of accessible chromatin associated with wood formation in <i>Eucalyptus grandis</i> . <i>New Phytologist</i> , 2019, 223, 1937-1951.	3.5	10
18	3D genome organization: a role for phase separation and loop extrusion?. <i>Current Opinion in Plant Biology</i> , 2019, 48, 36-46.	3.5	43
19	Rapid validation of transcriptional enhancers using agrobacterium-mediated transient assay. <i>Plant Methods</i> , 2019, 15, 21.	1.9	13

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20	Dynamic control of enhancer activity drives stage-specific gene expression during flower morphogenesis. <i>Nature Communications</i> , 2019, 10, 1705.	5.8	70
21	Opportunities to Use DNA Methylation to Distil Functional Elements in Large Crop Genomes. <i>Molecular Plant</i> , 2019, 12, 282-284.	3.9	12
22	Dynamic Patterns of Transcript Abundance of Transposable Element Families in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3673-3682.	0.8	32
23	Widespread long-range cis-regulatory elements in the maize genome. <i>Nature Plants</i> , 2019, 5, 1237-1249.	4.7	250
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26	Chromatin domains in space and their functional implications. <i>Current Opinion in Plant Biology</i> , 2020, 54, 1-10.	3.5	26
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33	Evolutionary and functional genomics of DNA methylation in maize domestication and improvement. <i>Nature Communications</i> , 2020, 11, 5539.	5.8	59
34	Stable unmethylated DNA demarcates expressed genes and their cis-regulatory space in plant genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23991-24000.	3.3	67
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37	3D genome architecture coordinates trans and cis regulation of differentially expressed ear and tassel genes in maize. <i>Genome Biology</i> , 2020, 21, 143.	3.8	60

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39	MH-seq for Functional Characterization of Open Chromatin in Plants. <i>Trends in Plant Science</i> , 2020, 25, 618-619.	4.3	6
40	The regulatory landscape of early maize inflorescence development. <i>Genome Biology</i> , 2020, 21, 165.	3.8	32
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43	Considerations in the analysis of plant chromatin accessibility data. <i>Current Opinion in Plant Biology</i> , 2020, 54, 69-78.	3.5	15
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59	A cis-regulatory atlas in maize at single-cell resolution. <i>Cell</i> , 2021, 184, 3041-3055.e21.	13.5	176

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61	Conserved noncoding sequences provide insights into regulatory sequence and loss of gene expression in maize. <i>Genome Research</i> , 2021, 31, 1245-1257.	2.4	29
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