

# Candice N Hirsch

## List of Publications by Year in descending order

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Version: 2024-02-01

66  
papers

5,010  
citations

136740

32  
h-index

114278

63  
g-index

88  
all docs

88  
docs citations

88  
times ranked

6146  
citing authors

#	ARTICLE	IF	CITATIONS
1	Benchmarking transposable element annotation methods for creation of a streamlined, comprehensive pipeline. <i>Genome Biology</i> , 2019, 20, 275.	3.8	579
2	Insights into the Maize Pan-Genome and Pan-Transcriptome. <i>Plant Cell</i> , 2014, 26, 121-135.	3.1	498
3	Transposable Elements Contribute to Activation of Maize Genes in Response to Abiotic Stress. <i>PLoS Genetics</i> , 2015, 11, e1004915.	1.5	346
4	An Expanded Maize Gene Expression Atlas based on RNA Sequencing and its Use to Explore Root Development. <i>Plant Genome</i> , 2016, 9, plantgenome2015.04.0025.	1.6	289
5	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. <i>Science</i> , 2021, 373, 655-662.	6.0	282
6	Marker Density and Read Depth for Genotyping Populations Using Genotyping-by-Sequencing. <i>Genetics</i> , 2013, 193, 1073-1081.	1.2	206
7	Draft Assembly of Elite Inbred Line PH207 Provides Insights into Genomic and Transcriptome Diversity in Maize. <i>Plant Cell</i> , 2016, 28, 2700-2714.	3.1	183
8	RNA-directed DNA methylation enforces boundaries between heterochromatin and euchromatin in the maize genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14728-14733.	3.3	179
9	Retrospective View of North American Potato ( <i>Solanum tuberosum</i> ) Breeding in the 20th and 21st Centuries. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1003-1013.	0.8	171
10	Maize Gene Atlas Developed by RNA Sequencing and Comparative Evaluation of Transcriptomes Based on RNA Sequencing and Microarrays. <i>PLoS ONE</i> , 2013, 8, e61005.	1.1	152
11	Natural variation for gene expression responses to abiotic stress in maize. <i>Plant Journal</i> , 2017, 89, 706-717.	2.8	145
12	How the pan-genome is changing crop genomics and improvement. <i>Genome Biology</i> , 2021, 22, 3.	3.8	142
13	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017, 8, 1348.	5.8	105
14	Gapless assembly of maize chromosomes using long-read technologies. <i>Genome Biology</i> , 2020, 21, 121.	3.8	101
15	Whole Transcriptome Profiling of Maize during Early Somatic Embryogenesis Reveals Altered Expression of Stress Factors and Embryogenesis-Related Genes. <i>PLoS ONE</i> , 2014, 9, e111407.	1.1	96
16	QTL mapping and phenotypic variation for root architectural traits in maize ( <i>Zea mays</i> L.). <i>Theoretical and Applied Genetics</i> , 2014, 127, 2293-2311.	1.8	90
17	Spud DB: A Resource for Mining Sequences, Genotypes, and Phenotypes to Accelerate Potato Breeding. <i>Plant Genome</i> , 2014, 7, plantgenome2013.12.0042.	1.6	82
18	Genome-wide association analysis of stalk biomass and anatomical traits in maize. <i>BMC Plant Biology</i> , 2019, 19, 45.	1.6	77

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19	Transposable elements contribute to dynamic genome content in maize. <i>Plant Journal</i> , 2019, 100, 1052-1065.	2.8	76
20	Dynamic Patterns of Gene Expression Additivity and Regulatory Variation throughout Maize Development. <i>Molecular Plant</i> , 2019, 12, 410-425.	3.9	69
21	A Genome-Wide Scan for Evidence of Selection in a Maize Population Under Long-Term Artificial Selection for Ear Number. <i>Genetics</i> , 2014, 196, 829-840.	1.2	63
22	Meta Gene Regulatory Networks in Maize Highlight Functionally Relevant Regulatory Interactions. <i>Plant Cell</i> , 2020, 32, 1377-1396.	3.1	60
23	Monitoring the interplay between transposable element families and DNA methylation in maize. <i>PLoS Genetics</i> , 2019, 15, e1008291.	1.5	56
24	Tapping the Promise of Genomics in Species with Complex, Nonmodel Genomes. <i>Annual Review of Plant Biology</i> , 2013, 64, 89-110.	8.6	53
25	Reduced representation approaches to interrogate genome diversity in large repetitive plant genomes. <i>Briefings in Functional Genomics</i> , 2014, 13, 257-267.	1.3	53
26	The importance of dominance and genotype-by-environment interactions on grain yield variation in a large-scale public cooperative maize experiment. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	52
27	Genotype-by-environment interactions affecting heterosis in maize. <i>PLoS ONE</i> , 2018, 13, e0191321.	1.1	51
28	Evidence for maternal control of seed size in maize from phenotypic and transcriptional analysis. <i>Journal of Experimental Botany</i> , 2016, 67, 1907-1917.	2.4	47
29	Utility of Climatic Information via Combining Ability Models to Improve Genomic Prediction for Yield Within the Genomes to Fields Maize Project. <i>Frontiers in Genetics</i> , 2020, 11, 592769.	1.1	44
30	The limited role of differential fractionation in genome content variation and function in maize ( <i>Zea mays</i> L.) inbred lines. <i>Plant Journal</i> , 2018, 93, 131-141.	2.8	42
31	Effect of sequence depth and length in long-read assembly of the maize inbred NC358. <i>Nature Communications</i> , 2020, 11, 2288.	5.8	39
32	Insights into the Effects of Long-Term Artificial Selection on Seed Size in Maize. <i>Genetics</i> , 2014, 198, 409-421.	1.2	38
33	Maize genomes to fields (G2F): 2014–2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. <i>BMC Research Notes</i> , 2020, 13, 71.	0.6	38
34	Phenotypic and Transcriptional Analysis of Divergently Selected Maize Populations Reveals the Role of Developmental Timing in Seed Size Determination. <i>Plant Physiology</i> , 2014, 165, 658-669.	2.3	37
35	Shared Genomic Regions Between Derivatives of a Large Segregating Population of Maize Identified Using Bulk Segregant Analysis Sequencing and Traditional Linkage Analysis. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1593-1602.	0.8	37
36	Maize <i>sugary enhancer1</i> ( <i>se1</i> ) is a gene affecting endosperm starch metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 20776-20785.	3.3	36

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37	Genomic limitations to <i>scRNA-seq</i> sequencing expression profiling. <i>Plant Journal</i> , 2015, 84, 491-503.	2.8	34
38	UAV-based imaging platform for monitoring maize growth throughout development. <i>Plant Direct</i> , 2020, 4, e00230.	0.8	25
39	Development of a Multiparent Population for Genetic Mapping and Allele Discovery in Six-Row Barley. <i>Genetics</i> , 2019, 213, 595-613.	1.2	23
40	Relative utility of agronomic, phenological, and morphological traits for assessing genotype-by-environment interaction in maize inbreds. <i>Crop Science</i> , 2020, 60, 62-81.	0.8	21
41	Utilizing temporal measurements from UAVs to assess root lodging in maize and its impact on productivity. <i>Field Crops Research</i> , 2021, 262, 108014.	2.3	18
42	Genetic Fine-Mapping of a Quantitative Trait Locus (QTL) Associated with Embryogenic Tissue Culture Response and Plant Regeneration Ability in Maize ( <i>Zea mays</i> L.). <i>Plant Genome</i> , 2018, 11, 170111.	1.6	17
43	Single-parent expression drives dynamic gene expression complementation in maize hybrids. <i>Plant Journal</i> , 2021, 105, 93-107.	2.8	16
44	Whole-genome variation of transposable element insertions in a maize diversity panel. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	16
45	Food-Grade Maize Composition, Evaluation, and Genetics for Masa-Based Products. <i>Crop Science</i> , 2019, 59, 1392-1405.	0.8	15
46	Variation and Inheritance of Small RNAs in Maize Inbreds and F1 Hybrids. <i>Plant Physiology</i> , 2020, 182, 318-331.	2.3	14
47	Genomic variation within the maize stiff-stalk heterotic germplasm pool. <i>Plant Genome</i> , 2021, 14, e20114.	1.6	14
48	Assessing the regulatory potential of transposable elements using chromatin accessibility profiles of maize transposons. <i>Genetics</i> , 2021, 217, 1-13.	1.2	14
49	Tandem Duplicate Genes in Maize Are Abundant and Date to Two Distinct Periods of Time. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3049-3058.	0.8	13
50	Using multiple reference genomes to identify and resolve annotation inconsistencies. <i>BMC Genomics</i> , 2020, 21, 281.	1.2	10
51	Opportunities and challenges in phenotyping row crops using drone-based RGB imaging. <i>The Plant Phenome Journal</i> , 2022, 5, .	1.0	9
52	Genetic and Morphometric Analysis of Cob Architecture and Biomass-Related Traits in the Intermated B73 × Mo17 Recombinant Inbred Lines of Maize. <i>Bioenergy Research</i> , 2013, 6, 903-916.	2.2	8
53	The Maize Pan-Genome. <i>Compendium of Plant Genomes</i> , 2018, , 13-29.	0.3	8
54	Multivariate analyses of root phenotype and dynamic transcriptome underscore valuable root traits and water-deficit responsive gene networks in maize. <i>Plant Direct</i> , 2019, 3, e00130.	0.8	8

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55	Genetic control of kernel compositional variation in a maize diversity panel. <i>Plant Genome</i> , 2021, 14, e20115.	1.6	7
56	Whole-genome assembly and annotation of northern wild rice, <i>Zizania palustris</i> L., supports a whole-genome duplication in the <i>Zizania</i> genus. <i>Plant Journal</i> , 2021, 107, 1802-1818.	2.8	7
57	Genome-Wide Association and Gene Co-expression Network Analyses Reveal Complex Genetics of Resistance to Goss's Wilt of Maize. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3139-3152.	0.8	6
58	Generation of Transcript Assemblies and Identification of Single Nucleotide Polymorphisms from Seven Lowland and Upland Cultivars of Switchgrass. <i>Plant Genome</i> , 2014, 7, plantgenome2013.12.0041.	1.6	6
59	Genomic Dissection of Nonhost Resistance to Wheat Stem Rust in <i>Brachypodium distachyon</i> . <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 392-400.	1.4	4
60	A Toolbox of Potato Genetic and Genomic Resources. <i>American Journal of Potato Research</i> , 2016, 93, 21-32.	0.5	3
61	Weeding out bad alleles. <i>Nature Plants</i> , 2018, 4, 193-194.	4.7	3
62	Stability of DNA methylation and chromatin accessibility in structurally diverse maize genomes. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	3
63	Predicting moisture content during maize nixtamalization using machine learning with NIR spectroscopy. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3743-3757.	1.8	3
64	Characterizing introgression-by-environment interactions using maize near isogenic lines. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2761-2773.	1.8	2
65	Genome-wide loss of CHH methylation with limited transcriptome changes in <i>Setaria viridis</i> DOMAINS REARRANGED METHYLTRANSFERASE (DRM) mutants. <i>Plant Journal</i> , 2022, 111, 103-116.	2.8	2
66	Variability in changes of acrylamide precursors during nixtamalization for masa production. <i>LWT - Food Science and Technology</i> , 2022, 161, 113400.	2.5	0