

# Cory D Hirsch

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4028267/publications.pdf>

Version: 2024-02-01

33  
papers

1,811  
citations

394421

19  
h-index

434195

31  
g-index

40  
all docs

40  
docs citations

40  
times ranked

2931  
citing authors

#	ARTICLE	IF	CITATIONS
1	Transposable element influences on gene expression in plants. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 157-165.	1.9	188
2	Draft Assembly of Elite Inbred Line PH207 Provides Insights into Genomic and Transcriptome Diversity in Maize. <i>Plant Cell</i> , 2016, 28, 2700-2714.	6.6	183
3	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.	7.1	179
4	Retrospective View of North American Potato ( <i>Solanum tuberosum</i> L.) Breeding in the 20th and 21st Centuries. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1003-1013.	1.8	171
5	Natural variation for gene expression responses to abiotic stress in maize. <i>Plant Journal</i> , 2017, 89, 706-717.	5.7	145
6	Emergence of the Ug99 lineage of the wheat stem rust pathogen through somatic hybridisation. <i>Nature Communications</i> , 2019, 10, 5068.	12.8	121
7	Spud DB: A Resource for Mining Sequences, Genotypes, and Phenotypes to Accelerate Potato Breeding. <i>Plant Genome</i> , 2014, 7, plantgenome2013.12.0042.	2.8	82
8	Transposable elements contribute to dynamic genome content in maize. <i>Plant Journal</i> , 2019, 100, 1052-1065.	5.7	76
9	Organization and Evolution of Subtelomeric Satellite Repeats in the Potato Genome. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 85-92.	1.8	75
10	Automatic Evaluation of Wheat Resistance to Fusarium Head Blight Using Dual Mask-RCNN Deep Learning Frameworks in Computer Vision. <i>Remote Sensing</i> , 2021, 13, 26.	4.0	70
11	Detection of Fusarium Head Blight in Wheat Using a Deep Neural Network and Color Imaging. <i>Remote Sensing</i> , 2019, 11, 2658.	4.0	67
12	Lineage-Specific Adaptive Evolution of the Centromeric Protein CENH3 in Diploid and Allotetraploid Oryza Species. <i>Molecular Biology and Evolution</i> , 2009, 26, 2877-2885.	8.9	59
13	<i>De Novo</i> Assembly and Phasing of Dikaryotic Genomes from Two Isolates of <i>Puccinia coronata</i> f. sp. <i>avenae</i> , the Causal Agent of Oat Crown Rust. <i>MBio</i> , 2018, 9, .	4.1	57
14	Reduced representation approaches to interrogate genome diversity in large repetitive plant genomes. <i>Briefings in Functional Genomics</i> , 2014, 13, 257-267.	2.7	53
15	Hyperspectral imaging and improved feature variable selection for automated determination of deoxynivalenol in various genetic lines of barley kernels for resistance screening. <i>Food Chemistry</i> , 2021, 343, 128507.	8.2	38
16	Genomic limitations to <i>RNA</i> sequencing expression profiling. <i>Plant Journal</i> , 2015, 84, 491-503.	5.7	34
17	Classifying cold stress responses of inbred maize seedlings using <i>RGB</i> imaging. <i>Plant Direct</i> , 2019, 3, e00104.	1.9	34
18	Dynamic Patterns of Transcript Abundance of Transposable Element Families in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3673-3682.	1.8	32

#	ARTICLE	IF	CITATIONS
19	Conservation and Purifying Selection of Transcribed Genes Located in a Rice Centromere. <i>Plant Cell</i> , 2011, 23, 2821-2830.	6.6	22
20	Localized Genetic and Phenotypic Diversity of <i>Xanthomonas translucens</i> Associated With Bacterial Leaf Streak on Wheat and Barley in Minnesota. <i>Phytopathology</i> , 2020, 110, 257-266.	2.2	18
21	Single-parent expression drives dynamic gene expression complementation in maize hybrids. <i>Plant Journal</i> , 2021, 105, 93-107.	5.7	16
22	Evaluating and Mapping Grape Color Using Image-Based Phenotyping. <i>Plant Phenomics</i> , 2020, 2020, 8086309.	5.9	15
23	Towards Improved Molecular Identification Tools in Fine Fescue ( <i>Festuca L.</i> , Poaceae) Turfgrasses: Nuclear Genome Size, Ploidy, and Chloroplast Genome Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 1223.	2.3	14
24	Identification of Candidate Susceptibility Genes to <i>Puccinia graminis</i> f. sp. <i>tritici</i> in Wheat. <i>Frontiers in Plant Science</i> , 2021, 12, 657796.	3.6	10
25	Opportunities and challenges in phenotyping row crops using drone-based RGB imaging. <i>The Plant Phenome Journal</i> , 2022, 5, .	2.0	9
26	Description and functional analysis of the transcriptome from malting barley. <i>Genomics</i> , 2021, 113, 3310-3324.	2.9	7
27	Centromeres: Sequences, Structure, and Biology. , 2012, , 59-70.		5
28	Wheat-Net: An Automatic Dense Wheat Spike Segmentation Method Based on an Optimized Hybrid Task Cascade Model. <i>Frontiers in Plant Science</i> , 2022, 13, 834938.	3.6	5
29	Genetic diversity and phylogeny of strains of <i>Clavibacter nebraskensis</i> associated with recent and historic Goss's wilt epidemics in the north Central USA. <i>Plant Pathology</i> , 2020, 69, 990-1002.	2.4	4
30	A Toolbox of Potato Genetic and Genomic Resources. <i>American Journal of Potato Research</i> , 2016, 93, 21-32.	0.9	3
31	Building a reference transcriptome for the hexaploid hard fescue turfgrass ( <i>Festuca brevipila</i> ) using a combination of PacBio Isoseq and Illumina sequencing. <i>Crop Science</i> , 2021, 61, 2798-2811.	1.8	3
32	Wheat-Net: An Automatic Dense Wheat Spike Segmentation Method Based on an Optimized Hybrid Task Cascade Model. <i>Smart Agriculture</i> , 2022, , 87-106.	0.4	1
33	A Reference Genome Sequence Resource for the Sugar Beet Root Rot Pathogen <i>Aphanomyces cochlioides</i> . <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 706-710.	2.6	0