

# Cory D Hirsch

## List of Publications by Year in descending order

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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	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
2	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
3	Opportunities and challenges in phenotyping row crops using drone-based RGB imaging. <i>The Plant Phenome Journal</i> , 2022, 5, .	2.0	9
4	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
5	Single-parent expression drives dynamic gene expression complementation in maize hybrids. <i>Plant Journal</i> , 2021, 105, 93-107.	5.7	16
6	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
7	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
8	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
9	Description and functional analysis of the transcriptome from malting barley. <i>Genomics</i> , 2021, 113, 3310-3324.	2.9	7
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	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
12	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
13	Evaluating and Mapping Grape Color Using Image-Based Phenotyping. <i>Plant Phenomics</i> , 2020, 2020, 8086309.	5.9	15
14	Transposable elements contribute to dynamic genome content in maize. <i>Plant Journal</i> , 2019, 100, 1052-1065.	5.7	76
15	Emergence of the Ug99 lineage of the wheat stem rust pathogen through somatic hybridisation. <i>Nature Communications</i> , 2019, 10, 5068.	12.8	121
16	Classifying cold-stress responses of inbred maize seedlings using RGB imaging. <i>Plant Direct</i> , 2019, 3, e00104.	1.9	34
17	Dynamic Patterns of Transcript Abundance of Transposable Element Families in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3673-3682.	1.8	32
18	Towards Improved Molecular Identification Tools in Fine Fescue ( <i>Festuca</i> L., Poaceae) Turfgrasses: Nuclear Genome Size, Ploidy, and Chloroplast Genome Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 1223.	2.3	14

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19	Detection of Fusarium Head Blight in Wheat Using a Deep Neural Network and Color Imaging. Remote Sensing, 2019, 11, 2658.	4.0	67
20	<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. MBio, 2018, 9, .	4.1	57
21	Transposable element influences on gene expression in plants. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2017, 1860, 157-165.	1.9	188
22	Natural variation for gene expression responses to abiotic stress in maize. Plant Journal, 2017, 89, 706-717.	5.7	145
23	Draft Assembly of Elite Inbred Line PH207 Provides Insights into Genomic and Transcriptome Diversity in Maize. Plant Cell, 2016, 28, 2700-2714.	6.6	183
24	A Toolbox of Potato Genetic and Genomic Resources. American Journal of Potato Research, 2016, 93, 21-32.	0.9	3
25	Genomic limitations to <sc>RNA</sc> sequencing expression profiling. Plant Journal, 2015, 84, 491-503.	5.7	34
26	RNA-directed DNA methylation enforces boundaries between heterochromatin and euchromatin in the maize genome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14728-14733.	7.1	179
27	Spud DB: A Resource for Mining Sequences, Genotypes, and Phenotypes to Accelerate Potato Breeding. Plant Genome, 2014, 7, plantgenome2013.12.0042.	2.8	82
28	Reduced representation approaches to interrogate genome diversity in large repetitive plant genomes. Briefings in Functional Genomics, 2014, 13, 257-267.	2.7	53
29	Retrospective View of North American Potato (<i>Solanum tuberosum</i>L.) Breeding in the 20th and 21st Centuries. G3: Genes, Genomes, Genetics, 2013, 3, 1003-1013.	1.8	171
30	Centromeres: Sequences, Structure, and Biology. , 2012, , 59-70.		5
31	Organization and Evolution of Subtelomeric Satellite Repeats in the Potato Genome. G3: Genes, Genomes, Genetics, 2011, 1, 85-92.	1.8	75
32	Conservation and Purifying Selection of Transcribed Genes Located in a Rice Centromere. Plant Cell, 2011, 23, 2821-2830.	6.6	22
33	Lineage-Specific Adaptive Evolution of the Centromeric Protein CENH3 in Diploid and Allotetraploid Oryza Species. Molecular Biology and Evolution, 2009, 26, 2877-2885.	8.9	59