

Matthew E Hudson

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4663476/publications.pdf>

Version: 2024-02-01

80
papers

7,449
citations

76326

40
h-index

62596

80
g-index

85
all docs

85
docs citations

85
times ranked

10106
citing authors

#	ARTICLE	IF	CITATIONS
1	W12<i>_{Rhg1}</i> interacts with DELLAs and mediates soybean cyst nematode resistance through hormone pathways. <i>Plant Biotechnology Journal</i> , 2022, 20, 283-296.	8.3	17
2	Fine mapping and cloning of the major seed protein quantitative trait loci on soybean chromosome 20. <i>Plant Journal</i> , 2022, 110, 114-128.	5.7	36
3	CROPSR: an automated platform for complex genome-wide CRISPR gRNA design and validation. <i>BMC Bioinformatics</i> , 2022, 23, 74.	2.6	12
4	Impact of multiple selective breeding programs on genetic diversity in soybean germplasm. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1591-1602.	3.6	7
5	Genetic Variation for Seed Oil Biosynthesis in Soybean. <i>Plant Molecular Biology Reporter</i> , 2021, 39, 700-709.	1.8	5
6	Impact of variant-level batch effects on identification of genetic risk factors in large sequencing studies. <i>PLoS ONE</i> , 2021, 16, e0249305.	2.5	5
7	A chromosomal assembly of the soybean cyst nematode genome. <i>Molecular Ecology Resources</i> , 2021, 21, 2407-2422.	4.8	10
8	Soybean Cyst Nematode Resistance Quantitative Trait Locus <i>cqSCN-006</i> Alters the Expression of a β -SNAP Protein. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1433-1445.	2.6	10
9	Design considerations for workflow management systems use in production genomics research and the clinic. <i>Scientific Reports</i> , 2021, 11, 21680.	3.3	7
10	Early transcriptional responses to soybean cyst nematode HG Type 0 show genetic differences among resistant and susceptible soybeans. <i>Theoretical and Applied Genetics</i> , 2020, 133, 87-102.	3.6	17
11	Bacterial steroid-17,20-desmolase is a taxonomically rare enzymatic pathway that converts prednisone to 1,4-androstenediene-3,11,17-trione, a metabolite that causes proliferation of prostate cancer cells. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2020, 199, 105567.	2.5	28
12	tâ€SNAREs bind the Rhg1 Î±â€SNAP and mediate soybean cyst nematode resistance. <i>Plant Journal</i> , 2020, 104, 318-331.	5.7	24
13	Genome biology of the paleotetraploid perennial biomass crop <i>Miscanthus</i> . <i>Nature Communications</i> , 2020, 11, 5442.	12.8	67
14	Genomic regions influencing aggressive behavior in honey bees are defined by colony allele frequencies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17135-17141.	7.1	24
15	Sentieon DNaseq Variant Calling Workflow Demonstrates Strong Computational Performance and Accuracy. <i>Frontiers in Genetics</i> , 2019, 10, 736.	2.3	131
16	The genome of the soybean cyst nematode (<i>Heterodera glycines</i>) reveals complex patterns of duplications involved in the evolution of parasitism genes. <i>BMC Genomics</i> , 2019, 20, 119.	2.8	55
17	Mapping of new quantitative trait loci for sudden death syndrome and soybean cyst nematode resistance in two soybean populations. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1047-1062.	3.6	13
18	Genome Sequence of the Soybean Cyst Nematode (<i>Heterodera glycines</i>) Endosymbiont â€œCandidatus <i>Cardinium hertigi</i> â€•Strain cHgTN10. <i>Genome Announcements</i> , 2018, 6, .	0.8	6

#	ARTICLE	IF	CITATIONS
19	Allele-defined genome of the autopolyploid sugarcane <i>Saccharum spontaneum</i> L.. <i>Nature Genetics</i> , 2018, 50, 1565-1573.	21.4	463
20	Identification of missing variants by combining multiple analytic pipelines. <i>BMC Bioinformatics</i> , 2018, 19, 139.	2.6	10
21	A soft selective sweep during rapid evolution of gentle behaviour in an Africanized honeybee. <i>Nature Communications</i> , 2017, 8, 1550.	12.8	33
22	Genome-wide association mapping of resistance to a Brazilian isolate of <i>Sclerotinia sclerotiorum</i> in soybean genotypes mostly from Brazil. <i>BMC Genomics</i> , 2017, 18, 849.	2.8	52
23	A comparison of genotyping-by-sequencing analysis methods on low-coverage crop datasets shows advantages of a new workflow, GB-eaSy. <i>BMC Bioinformatics</i> , 2017, 18, 586.	2.6	80
24	An efficient method for measuring copy number variation applied to improvement of nematode resistance in soybean. <i>Plant Journal</i> , 2016, 88, 143-153.	5.7	31
25	Impact of <i>Rhg1</i> copy number, type, and interaction with <i>Rhg4</i> on resistance to <i>Heterodera glycines</i> in soybean. <i>Theoretical and Applied Genetics</i> , 2016, 129, 2403-2412.	3.6	32
26	Identification of Multiple Phytotoxins Produced by <i>Fusarium virguliforme</i> Including a Phytotoxic Effector (FvNIS1) Associated With Sudden Death Syndrome Foliar Symptoms. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 96-108.	2.6	53
27	Evolutionary divergence of phytochrome protein function in <i>Zea mays</i> PIF3 signaling. <i>Journal of Experimental Botany</i> , 2016, 67, 4231-4240.	4.8	34
28	Simulating Next-Generation Sequencing Datasets from Empirical Mutation and Sequencing Models. <i>PLoS ONE</i> , 2016, 11, e0167047.	2.5	59
29	A Classification of Basic Helix-Loop-Helix Transcription Factors of Soybean. <i>International Journal of Genomics</i> , 2015, 2015, 1-10.	1.6	40
30	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015, 16, 76.	8.8	330
31	Genomic signatures of evolutionary transitions from solitary to group living. <i>Science</i> , 2015, 348, 1139-1143.	12.6	357
32	From association to prediction: statistical methods for the dissection and selection of complex traits in plants. <i>Current Opinion in Plant Biology</i> , 2015, 24, 110-118.	7.1	166
33	Evolution and selection of <i>Rhg1</i> , a copy number variant nematode resistance locus. <i>Molecular Ecology</i> , 2015, 24, 1774-1791.	3.9	66
34	Transposable elements, mRNA expression level and strand-specificity of small RNAs are associated with non-additive inheritance of gene expression in hybrid plants. <i>BMC Plant Biology</i> , 2015, 15, 168.	3.6	17
35	Effects of Selective Genetic Introgression from Wild Soybean to Soybean. <i>Crop Science</i> , 2014, 54, 2683-2695.	1.8	14
36	A survey of the small RNA population during far-red light-induced apical hook opening. <i>Frontiers in Plant Science</i> , 2014, 5, 156.	3.6	18

#	ARTICLE	IF	CITATIONS
37	Finding the missing honey bee genes: lessons learned from a genome upgrade. BMC Genomics, 2014, 15, 86.	2.8	375
38	The Basic Helix-Loop-Helix Transcription Factor Family in the Sacred Lotus, <i>Nelumbo Nucifera</i> . Tropical Plant Biology, 2014, 7, 65-70.	1.9	11
39	Intronic Non-CG DNA hydroxymethylation and alternative mRNA splicing in honey bees. BMC Genomics, 2013, 14, 666.	2.8	62
40	Genome of the long-living sacred lotus (<i>Nelumbo nucifera</i> Gaertn.). Genome Biology, 2013, 14, R41.	9.6	329
41	A detailed gene expression study of the <i>Miscanthus</i> genus reveals changes in the transcriptome associated with the rejuvenation of spring rhizomes. BMC Genomics, 2013, 14, 864.	2.8	27
42	Repeat associated small RNAs vary among parents and following hybridization in maize. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10444-10449.	7.1	139
43	Development of microsatellite markers in autopolyploid sugarcane and comparative analysis of conserved microsatellites in sorghum and sugarcane. Molecular Breeding, 2012, 30, 661-669.	2.1	18
44	Copy Number Variation of Multiple Genes at <i>Rhg1</i> Mediates Nematode Resistance in Soybean. Science, 2012, 338, 1206-1209.	12.6	535
45	A framework genetic map for <i>Miscanthus sinensis</i> from RNAseq-based markers shows recent tetraploidy. BMC Genomics, 2012, 13, 142.	2.8	87
46	Divergent patterns of endogenous small RNA populations from seed and vegetative tissues of <i>Glycine max</i> . BMC Plant Biology, 2012, 12, 177.	3.6	30
47	The Inheritance Pattern of 24 nt siRNA Clusters in <i>Arabidopsis</i> Hybrids Is Influenced by Proximity to Transposable Elements. PLoS ONE, 2012, 7, e47043.	2.5	43
48	Rapid Genotyping of Soybean Cultivars Using High Throughput Sequencing. PLoS ONE, 2011, 6, e24811.	2.5	25
49	Genes involved in convergent evolution of eusociality in bees. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7472-7477.	7.1	199
50	Rapid, Organ-Specific Transcriptional Responses to Light Regulate Photomorphogenic Development in Dicot Seedlings. Plant Physiology, 2011, 156, 2124-2140.	4.8	18
51	Human cell toxicogenomic analysis of bromoacetic acid: A regulated drinking water disinfection by-product. Environmental and Molecular Mutagenesis, 2010, 51, 205-214.	2.2	31
52	Fine mapping the soybean aphid resistance gene <i>Rag1</i> in soybean. Theoretical and Applied Genetics, 2010, 120, 1063-1071.	3.6	87
53	Fine mapping of the soybean aphid-resistance gene <i>Rag2</i> in soybean PI 200538. Theoretical and Applied Genetics, 2010, 121, 599-610.	3.6	76
54	Microcollinearity between autopolyploid sugarcane and diploid sorghum genomes. BMC Genomics, 2010, 11, 261.	2.8	175

#	ARTICLE	IF	CITATIONS
55	Brain transcriptomic analysis in paper wasps identifies genes associated with behaviour across social insect lineages. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2010, 277, 2139-2148.	2.6	121
56	A Fluorescence <i>in Situ</i> Hybridization System for Karyotyping Soybean. <i>Genetics</i> , 2010, 185, 727-744.	2.9	70
57	Genomic and small RNA sequencing of <i>Miscanthus Ã— giganteus</i> shows the utility of sorghum as a reference genome sequence for Andropogoneae grasses. <i>Genome Biology</i> , 2010, 11, R12.	9.6	93
58	Endogenous, Tissue-Specific Short Interfering RNAs Silence the Chalcone Synthase Gene Family in <i>Glycine max</i> Seed Coats. <i>Plant Cell</i> , 2009, 21, 3063-3077.	6.6	126
59	Residues Clustered in the Light-Sensing Knot of Phytochrome B are Necessary for Conformer-Specific Binding to Signaling Partner PIF3. <i>PLoS Genetics</i> , 2009, 5, e1000352.	3.5	58
60	Sympatric ecological speciation meets pyrosequencing: sampling the transcriptome of the apple maggot <i>Rhagoletis pomonella</i> . <i>BMC Genomics</i> , 2009, 10, 633.	2.8	81
61	Plant genomes do a balancing act. <i>Molecular Ecology</i> , 2009, 18, 2743-2745.	3.9	3
62	Cytochrome P450 Monooxygenases as Reporters for Circadian-Regulated Pathways. <i>Plant Physiology</i> , 2009, 150, 858-878.	4.8	75
63	Sequencing breakthroughs for genomic ecology and evolutionary biology. <i>Molecular Ecology Resources</i> , 2008, 8, 3-17.	4.8	326
64	A genomic analysis of the archaeal system <i>Ignicoccus hospitalis</i> - <i>Nanoarchaeum equitans</i> . <i>Genome Biology</i> , 2008, 9, R158.	8.8	104
65	Analysis of a Horizontally Transferred Pathway Involved in Vitamin B6 Biosynthesis from the Soybean Cyst Nematode <i>Heterodera glycines</i> . <i>Molecular Biology and Evolution</i> , 2008, 25, 2085-2098.	8.9	42
66	Microarray-Based Genetic Mapping Using Soybean Near-Isogenic Lines and Generation of SNP Markers in the <i>Rag1</i> Aphid-Resistance Interval. <i>Plant Genome</i> , 2008, 1, .	2.8	23
67	Mechanical Stress Induces Biotic and Abiotic Stress Responses via a Novel cis-Element. <i>PLoS Genetics</i> , 2007, 3, e172.	3.5	205
68	Analysis of Gene Expression during Brassica Seed Germination Using a Cross-Species Microarray Platform. <i>Crop Science</i> , 2007, 47, S-96.	1.8	11
69	Global repeat discovery and estimation of genomic copy number in a large, complex genome using a high-throughput 454 sequence survey. <i>BMC Genomics</i> , 2007, 8, 132.	2.8	84
70	Wasp Gene Expression Supports an Evolutionary Link Between Maternal Behavior and Eusociality. <i>Science</i> , 2007, 318, 441-444.	12.6	251
71	Contribution of transcriptional regulation to natural variations in <i>Arabidopsis</i> . <i>Genome Biology</i> , 2005, 6, R32.	9.6	47
72	Expression profiling of phyB mutant demonstrates substantial contribution of other phytochromes to red-light-regulated gene expression during seedling de-etiolation. <i>Plant Journal</i> , 2004, 38, 725-739.	5.7	210

#	ARTICLE	IF	CITATIONS
73	PHYTOCHROME-INTERACTING FACTOR 1 Is a Critical bHLH Regulator of Chlorophyll Biosynthesis. <i>Science</i> , 2004, 305, 1937-1941.	12.6	434
74	Identification of nutrient partitioning genes participating in rice grain filling by singular value decomposition (SVD) of genome expression data. <i>BMC Genomics</i> , 2003, 4, 26.	2.8	13
75	The FHY3 and FAR1 genes encode transposase-related proteins involved in regulation of gene expression by the phytochrome A-signaling pathway. <i>Plant Journal</i> , 2003, 34, 453-471.	5.7	179
76	Identification of Promoter Motifs Involved in the Network of Phytochrome A-Regulated Gene Expression by Combined Analysis of Genomic Sequence and Microarray Data. <i>Plant Physiology</i> , 2003, 133, 1605-1616.	4.8	218
77	The genetics of phytochrome signalling in Arabidopsis. <i>Seminars in Cell and Developmental Biology</i> , 2000, 11, 475-483.	5.0	33
78	The phytochrome B encoded by the HLG locus of <i>Nicotiana plumbaginifolia</i> is required for detection of photoperiod: hlg mutants show altered regulation of flowering and circadian movement. <i>Plant Journal</i> , 1998, 15, 281-287.	5.7	11
79	<i>Nicotiana plumbaginifolia</i> hlg mutants have a mutation in a PHYB-type phytochrome gene: they have elongated hypocotyls in red light, but are not elongated as adult plants. <i>Plant Journal</i> , 1997, 12, 1091-1101.	5.7	12
80	Photoreceptor Biotechnology. , 0, , 267-289.		1