Matthew E Hudson

List of Publications by Year
in descending order

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	Copy Number Variation of Multiple Genes at Rhg1 Mediates Nematode Resistance in Soybean. Science, 2012, 338, 1206-1209.	12.6	535
2	Allele-defined genome of the autopolyploid sugarcane Saccharum spontaneum L.. Nature Genetics, 2018, 50, 1565-1573.	21.4	463
3	PHYTOCHROME-INTERACTING FACTOR 1 Is a Critical bHLH Regulator of Chlorophyll Biosynthesis. Science, 2004, 305, 1937-1941.	12.6	434
4	Finding the missing honey bee genes: lessons learned from a genome upgrade. BMC Genomics, 2014, 15, 86.	2.8	375
5	Genomic signatures of evolutionary transitions from solitary to group living. Science, 2015, 348, 1139-1143.	12.6	357
6	The genomes of two key bumblebee species with primitive eusocial organization. Genome Biology, 2015, 16, 76.	8.8	330
7	Genome of the long-living sacred lotus (Nelumbo nucifera Gaertn.). Genome Biology, 2013, 14, R41.	9.6	329
8	Sequencing breakthroughs for genomic ecology and evolutionary biology. Molecular Ecology Resources, 2008, 8, 3-17.	4.8	326
9	Wasp Gene Expression Supports an Evolutionary Link Between Maternal Behavior and Eusociality. Science, 2007, 318, 441-444.	12.6	251
10	Identification of Promoter Motifs Involved in the Network of Phytochrome A-Regulated Gene Expression by Combined Analysis of Genomic Sequence and Microarray Data Â. Plant Physiology, 2003, 133, 1605-1616.	4.8	218
11	Expression profiling ofphyBmutant demonstrates substantial contribution of other phytochromes to red-light-regulated gene expression during seedling de-etiolation. Plant Journal, 2004, 38, 725-739.	5.7	210
12	Mechanical Stress Induces Biotic and Abiotic Stress Responses via a Novel cis-Element. PLoS Genetics, 2007, 3, e172.	3.5	205
13	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
14	The FHY3 and FAR1 genes encode transposase-related proteins involved in regulation of gene expression by the phytochrome A-signaling pathway. Plant Journal, 2003, 34, 453-471.	5.7	179
15	Microcollinearity between autopolyploid sugarcane and diploid sorghum genomes. BMC Genomics, 2010, 11, 261.	2.8	175
16	From association to prediction: statistical methods for the dissection and selection of complex traits in plants. Current Opinion in Plant Biology, 2015, 24, 110-118.	7.1	166
17	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
18	Sentieon DNASeq Variant Calling Workflow Demonstrates Strong Computational Performance and Accuracy. Frontiers in Genetics, 2019, 10, 736.	2.3	131

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19	Endogenous, Tissue-Specific Short Interfering RNAs Silence the Chalcone Synthase Gene Family inGlycine maxSeed Coats Â. Plant Cell, 2009, 21, 3063-3077.	6.6	126
20	Brain transcriptomic analysis in paper wasps identifies genes associated with behaviour across social insect lineages. Proceedings of the Royal Society B: Biological Sciences, 2010, 277, 2139-2148.	2.6	121
21	A genomic analysis of the archaeal system Ignicoccus hospitalis-Nanoarchaeum equitans. Genome Biology, 2008, 9, R158.	8.8	104
22	Genomic and small RNA sequencing of Miscanthus Ã— giganteus shows the utility of sorghum as a reference genome sequence for Andropogoneae grasses. Genome Biology, 2010, 11, R12.	9.6	93
23	Fine mapping the soybean aphid resistance gene Rag1 in soybean. Theoretical and Applied Genetics, 2010, 120, 1063-1071.	3.6	87
24	A framework genetic map for Miscanthus sinensis from RNAseq-based markers shows recent tetraploidy. BMC Genomics, 2012, 13, 142.	2.8	87
25	Global repeat discovery and estimation of genomic copy number in a large, complex genome using a high-throughput 454 sequence survey. BMC Genomics, 2007, 8, 132.	2.8	84
26	Sympatric ecological speciation meets pyrosequencing: sampling the transcriptome of the apple maggot Rhagoletis pomonella. BMC Genomics, 2009, 10, 633.	2.8	81
27	A comparison of genotyping-by-sequencing analysis methods on low-coverage crop datasets shows advantages of a new workflow, GB-eaSy. BMC Bioinformatics, 2017, 18, 586.	2.6	80
28	Fine mapping of the soybean aphid-resistance gene Rag2 in soybean PI 200538. Theoretical and Applied Genetics, 2010, 121, 599-610.	3.6	76
29	Cytochrome P450 Monooxygenases as Reporters for Circadian-Regulated Pathways Â Â Â. Plant Physiology, 2009, 150, 858-878.	4.8	75
30	A Fluorescence in Situ Hybridization System for Karyotyping Soybean. Genetics, 2010, 185, 727-744.	2.9	70
31	Genome biology of the paleotetraploid perennial biomass crop Miscanthus. Nature Communications, 2020, 11, 5442.	12.8	67
32	Evolution and selection of <scp>R</scp>hg1, a copyâ€number variant nematodeâ€resistance locus. Molecular Ecology, 2015, 24, 1774-1791.	3.9	66
33	Intronic Non-CG DNA hydroxymethylation and alternative mRNA splicing in honey bees. BMC Genomics, 2013, 14, 666.	2.8	62
34	Simulating Next-Generation Sequencing Datasets from Empirical Mutation and Sequencing Models. PLoS ONE, 2016, 11, e0167047.	2.5	59
35	Residues Clustered in the Light-Sensing Knot of Phytochrome B are Necessary for Conformer-Specific Binding to Signaling Partner PIF3. PLoS Genetics, 2009, 5, e1000352.	3.5	58
36	The genome of the soybean cyst nematode (Heterodera glycines) reveals complex patterns of duplications involved in the evolution of parasitism genes. BMC Genomics, 2019, 20, 119.	2.8	55

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37	Identification of Multiple Phytotoxins Produced by Fusarium virguliforme Including a Phytotoxic Effector (FvNIS1) Associated With Sudden Death Syndrome Foliar Symptoms. Molecular Plant-Microbe Interactions, 2016, 29, 96-108.	2.6	53
38	Genome-wide association mapping of resistance to a Brazilian isolate of Sclerotinia sclerotiorum in soybean genotypes mostly from Brazil. BMC Genomics, 2017, 18, 849.	2.8	52
39	Contribution of transcriptional regulation to natural variations in Arabidopsis. Genome Biology, 2005, 6, R32.	9.6	47
40	The Inheritance Pattern of 24 nt siRNA Clusters in Arabidopsis Hybrids Is Influenced by Proximity to Transposable Elements. PLoS ONE, 2012, 7, e47043.	2.5	43
41	Analysis of a Horizontally Transferred Pathway Involved in Vitamin B6 Biosynthesis from the Soybean Cyst Nematode Heterodera glycines. Molecular Biology and Evolution, 2008, 25, 2085-2098.	8.9	42
42	A Classification of Basic Helix-Loop-Helix Transcription Factors of Soybean. International Journal of Genomics, 2015, 2015, 1-10.	1.6	40
43	Fine mapping and cloning of the major seed protein quantitative trait loci on soybean chromosome 20. Plant Journal, 2022, 110, 114-128.	5.7	36
44	Evolutionary divergence of phytochrome protein function inZea maysPIF3 signaling. Journal of Experimental Botany, 2016, 67, 4231-4240.	4.8	34
45	The genetics of phytochrome signalling in Arabidopsis. Seminars in Cell and Developmental Biology, 2000, 11, 475-483.	5.0	33
46	A soft selective sweep during rapid evolution of gentle behaviour in an Africanized honeybee. Nature Communications, 2017, 8, 1550.	12.8	33
47	Impact of Rhg1 copy number, type, and interaction with Rhg4 on resistance to Heterodera glycines in soybean. Theoretical and Applied Genetics, 2016, 129, 2403-2412.	3.6	32
48	Human cell toxicogenomic analysis of bromoacetic acid: A regulated drinking water disinfection byâ€product. Environmental and Molecular Mutagenesis, 2010, 51, 205-214.	2.2	31
49	An efficient method for measuring copy number variation applied to improvement of nematode resistance in soybean. Plant Journal, 2016, 88, 143-153.	5.7	31
50	Divergent patterns of endogenous small RNA populations from seed and vegetative tissues of Glycine max. BMC Plant Biology, 2012, 12, 177.	3.6	30
51	Bacterial steroid-17,20-desmolase is a taxonomically rare enzymatic pathway that converts prednisone to 1,4-androstanediene-3,11,17-trione, a metabolite that causes proliferation of prostate cancer cells. Journal of Steroid Biochemistry and Molecular Biology, 2020, 199, 105567.	2.5	28
52	A detailed gene expression study of the Miscanthusgenus reveals changes in the transcriptome associated with the rejuvenation of spring rhizomes. BMC Genomics, 2013, 14, 864.	2.8	27
53	Rapid Genotyping of Soybean Cultivars Using High Throughput Sequencing. PLoS ONE, 2011, 6, e24811.	2.5	25
54	tâ€SNAREs bind the Rhg1 Î±â€SNAP and mediate soybean cyst nematode resistance. Plant Journal, 2020, 104, 318-331.	5.7	24

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55	Genomic regions influencing aggressive behavior in honey bees are defined by colony allele frequencies. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 17135-17141.	7.1	24
56	Microarrayâ€Based Genetic Mapping Using Soybean Nearâ€Isogenic Lines and Generation of SNP Markers in the Rag1 Aphidâ€Resistance Interval. Plant Genome, 2008, 1, .	2.8	23
57	Rapid, Organ-Specific Transcriptional Responses to Light Regulate Photomorphogenic Development in Dicot Seedlings Â Â Â. Plant Physiology, 2011, 156, 2124-2140.	4.8	18
58	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
59	A survey of the small RNA population during far-red light-induced apical hook opening. Frontiers in Plant Science, 2014, 5, 156.	3.6	18
60	Transposable elements, mRNA expression level and strand-specificity of small RNAs are associated with non-additive inheritance of gene expression in hybrid plants. BMC Plant Biology, 2015, 15, 168.	3.6	17
61	Early transcriptional responses to soybean cyst nematode HG Type 0 show genetic differences among resistant and susceptible soybeans. Theoretical and Applied Genetics, 2020, 133, 87-102.	3.6	17
62	WI12_{Rhg1} interacts with DELLAs and mediates soybean cyst nematode resistance through hormone pathways. Plant Biotechnology Journal, 2022, 20, 283-296.	8.3	17
63	Effects of Selective Genetic Introgression from Wild Soybean to Soybean. Crop Science, 2014, 54, 2683-2695.	1.8	14
64	Identification of nutrient partitioning genes participating in rice grain filling by singular value decomposition (SVD) of genome expression data. BMC Genomics, 2003, 4, 26.	2.8	13
65	Mapping of new quantitative trait loci for sudden death syndrome and soybean cyst nematode resistance in two soybean populations. Theoretical and Applied Genetics, 2018, 131, 1047-1062.	3.6	13
66	Nicotiana plumbaginifolia 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. Plant Journal, 1997, 12, 1091-1101.	5.7	12
67	CROPSR: an automated platform for complex genome-wide CRISPR gRNA design and validation. BMC Bioinformatics, 2022, 23, 74.	2.6	12
68	The phytochrome B encoded by the HLG locus of Nicotiana plumbaginifolia is required for detection of photoperiod: hlg mutants show altered regulation of flowering and circadian movement. Plant Journal, 1998, 15, 281-287.	5.7	11
69	Analysis of Gene Expression during Brassica Seed Germination Using a Crossâ€Species Microarray Platform. Crop Science, 2007, 47, S-96.	1.8	11
70	The Basic Helix-Loop-Helix Transcription Factor Family in the Sacred Lotus, Nelumbo Nucifera. Tropical Plant Biology, 2014, 7, 65-70.	1.9	11
71	Identification of missing variants by combining multiple analytic pipelines. BMC Bioinformatics, 2018, 19, 139.	2.6	10
72	A chromosomal assembly of the soybean cyst nematode genome. Molecular Ecology Resources, 2021, 21, 2407-2422.	4.8	10

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73	Soybean Cyst Nematode Resistance Quantitative Trait Locus cqSCN-006 Alters the Expression of a Î³-SNAP Protein. Molecular Plant-Microbe Interactions, 2021, 34, 1433-1445.	2.6	10
74	Design considerations for workflow management systems use in production genomics research and the clinic. Scientific Reports, 2021, 11, 21680.	3.3	7
75	Impact of multiple selective breeding programs on genetic diversity in soybean germplasm. Theoretical and Applied Genetics, 2022, 135, 1591-1602.	3.6	7
76	Genome Sequence of the Soybean Cyst Nematode (Heterodera glycines) Endosymbiont â€œCandidatus Cardinium hertigiiâ€•Strain cHgTN10. Genome Announcements, 2018, 6, .	0.8	6
77	Genetic Variation for Seed Oil Biosynthesis in Soybean. Plant Molecular Biology Reporter, 2021, 39, 700-709.	1.8	5
78	Impact of variant-level batch effects on identification of genetic risk factors in large sequencing studies. PLoS ONE, 2021, 16, e0249305.	2.5	5
79	Plant genomes do a balancing act. Molecular Ecology, 2009, 18, 2743-2745.	3.9	3
80	Photoreceptor Biotechnology. , 0, , 267-289.		1