

Matthew J Moscou

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

46
papers

3,260
citations

21
h-index

54
g-index

54
ext. papers

4,088
ext. citations

8
avg, IF

5.52
L-index

#	Paper	IF	Citations
46	Aegilops sharonensis genome-assisted identification of stem rust resistance gene Sr62.. <i>Nature Communications</i> , 2022 , 13, 1607	17.4	2
45	Cloning the barley nec3 disease lesion mimic mutant using complementation by sequencing.. <i>Plant Genome</i> , 2022 , e20187	4.4	
44	The TCP transcription factor HvTB2 heterodimerizes with VRS5 and controls spike architecture in barley.. <i>Plant Reproduction</i> , 2022 , 1	3.9	1
43	The barley leaf rust resistance gene Rph3 encodes a predicted membrane protein and is induced upon infection by avirulent pathotypes of Puccinia hordei.. <i>Nature Communications</i> , 2022 , 13, 2386	17.4	0
42	The barley immune receptor Mla recognizes multiple pathogens and contributes to host range dynamics. <i>Nature Communications</i> , 2021 , 12, 6915	17.4	2
41	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021 , 33, 1888-1906	11.6	26
40	Two NLR immune receptors acquired high-affinity binding to a fungal effector through convergent evolution of their integrated domain. <i>ELife</i> , 2021 , 10,	8.9	6
39	Identification of a Locus Conferring Dominant Susceptibility to in Barley. <i>Frontiers in Plant Science</i> , 2020 , 11, 158	6.2	0
38	Stem rust resistance in wheat is suppressed by a subunit of the mediator complex. <i>Nature Communications</i> , 2020 , 11, 1123	17.4	18
37	Genome assembly and characterization of a complex zFBED-NLR gene-containing disease resistance locus in Carolina Gold Select rice with Nanopore sequencing. <i>PLoS Genetics</i> , 2020 , 16, e1008571	6	30
36	Cloning of the Rice Resistance Gene and Interaction of the Xo1 Protein with the Defense-Suppressing Effector Tal2h. <i>Molecular Plant-Microbe Interactions</i> , 2020 , 33, 1189-1195	3.6	9
35	What is the Molecular Basis of Nonhost Resistance?. <i>Molecular Plant-Microbe Interactions</i> , 2020 , 33, 1253-1264	3.6	17
34	Dominant integration locus drives continuous diversification of plant immune receptors with exogenous domain fusions. <i>Genome Biology</i> , 2018 , 19, 23	18.3	61
33	Speed breeding in growth chambers and glasshouses for crop breeding and model plant research. <i>Nature Protocols</i> , 2018 , 13, 2944-2963	18.8	168
32	Components of Brachypodium distachyon resistance to nonadapted wheat stripe rust pathogens are simply inherited. <i>PLoS Genetics</i> , 2018 , 14, e1007636	6	10
31	The genetic architecture of colonization resistance in Brachypodium distachyon to non-adapted stripe rust (Puccinia striiformis) isolates. <i>PLoS Genetics</i> , 2018 , 14, e1007637	6	9
30	Detection of Race-Specific Resistance Against Puccinia coronata f. sp. avenae in Brachypodium Species. <i>Phytopathology</i> , 2018 , 108, 1443-1454	3.8	3

29	Selection of transformation-efficient barley genotypes based on TFA (transformation amenability) haplotype and higher resolution mapping of the TFA loci. <i>Plant Cell Reports</i> , 2017 , 36, 611-620	5.1	12
28	Effects of Barley (<i>Hordeum Vulgare</i> L.) Variety and Growing Environment on Beer Flavor. <i>Journal of the American Society of Brewing Chemists</i> , 2017 , 75, 345-353	1.9	21
27	Discovery and characterization of two new stem rust resistance genes in <i>Aegilops sharonensis</i> . <i>Theoretical and Applied Genetics</i> , 2017 , 130, 1207-1222	6	22
26	Natural Variation in <i>Brachypodium</i> Links Vernalization and Flowering Time Loci as Major Flowering Determinants. <i>Plant Physiology</i> , 2017 , 173, 256-268	6.6	21
25	Colonization of Barley by the Broad-Host Hemibiotrophic Pathogen <i>Phytophthora palmivora</i> Uncovers a Leaf Development-Dependent Involvement of Mlo. <i>Molecular Plant-Microbe Interactions</i> , 2016 , 29, 385-95	3.6	30
24	Isolation and fine mapping of Rps6: an intermediate host resistance gene in barley to wheat stripe rust. <i>Theoretical and Applied Genetics</i> , 2016 , 129, 831-843	6	30
23	Mapping the Breaker element of the gametocidal locus proximal to a block of sub-telomeric heterochromatin on the long arm of chromosome 4S(sh) of <i>Aegilops sharonensis</i> . <i>Theoretical and Applied Genetics</i> , 2015 , 128, 1049-59	6	11
22	Sequencing of 15622 gene-bearing BACs clarifies the gene-dense regions of the barley genome. <i>Plant Journal</i> , 2015 , 84, 216-27	6.9	31
21	The development of quick, robust, quantitative phenotypic assays for describing the host-nonhost landscape to stripe rust. <i>Frontiers in Plant Science</i> , 2015 , 6, 876	6.2	15
20	Nonhost resistance to rust pathogens - a continuation of continua. <i>Frontiers in Plant Science</i> , 2014 , 5, 664	6.2	60
19	Strategies for transferring resistance into wheat: from wide crosses to GM cassettes. <i>Frontiers in Plant Science</i> , 2014 , 5, 692	6.2	131
18	Engineering plant disease resistance based on TAL effectors. <i>Annual Review of Phytopathology</i> , 2013 , 51, 383-406	10.8	77
17	Infection of <i>Brachypodium distachyon</i> with selected grass rust pathogens. <i>Molecular Plant-Microbe Interactions</i> , 2013 , 26, 946-57	3.6	41
16	Characterisation and analysis of the <i>Aegilops sharonensis</i> transcriptome, a wild relative of wheat in the <i>Sitopsis</i> section. <i>PLoS ONE</i> , 2013 , 8, e72782	3.7	10
15	Differential accumulation of host mRNAs on polyribosomes during obligate pathogen-plant interactions. <i>Molecular BioSystems</i> , 2012 , 8, 2153-65		23
14	An Improved Consensus Linkage Map of Barley Based on Flow-Sorted Chromosomes and Single Nucleotide Polymorphism Markers. <i>Plant Genome</i> , 2011 , 4, 238-249	4.4	111
13	Quantitative and temporal definition of the Mla transcriptional regulon during barley-powdery mildew interactions. <i>Molecular Plant-Microbe Interactions</i> , 2011 , 24, 694-705	3.6	22
12	Quantitative and qualitative stem rust resistance factors in barley are associated with transcriptional suppression of defense regulons. <i>PLoS Genetics</i> , 2011 , 7, e1002208	6	45

11	Transcript-based cloning of RRP46, a regulator of rRNA processing and R gene-independent cell death in barley-powdery mildew interactions. <i>Plant Cell</i> , 2009 , 21, 3280-95	11.6	21
10	Blufensin1 negatively impacts basal defense in response to barley powdery mildew. <i>Plant Physiology</i> , 2009 , 149, 271-85	6.6	53
9	Development and implementation of high-throughput SNP genotyping in barley. <i>BMC Genomics</i> , 2009 , 10, 582	4.5	477
8	A simple cipher governs DNA recognition by TAL effectors. <i>Science</i> , 2009 , 326, 1501	33.3	1443
7	Tissue-dependent limited pleiotropy affects gene expression in barley. <i>Plant Journal</i> , 2008 , 56, 287-296	6.9	26
6	Quantitative Genetic Dissection of Shoot Architecture Traits in Maize: Towards a Functional Genomics Approach. <i>Plant Genome</i> , 2008 , 1,	4.4	14
5	Transcript profiling in host-pathogen interactions. <i>Annual Review of Phytopathology</i> , 2007 , 45, 329-69	10.8	136
4	An ancient integration in a plant NLR is maintained as a trans-species polymorphism		4
3	The TCP transcription factor HvTB2 heterodimerizes with VRS5(HvTB1) and controls spike architecture in barley		1
2	Two NLR immune receptors acquired high-affinity binding to a fungal effector through convergent evolution of their integrated domain		3
1	Reference genome-assisted identification of stem rust resistance gene Sr62 encoding a tandem kinase		4