

Thomas Wicker

List of Publications by Year in descending order

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117
papers

23,500
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22099

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docs citations

127
times ranked

18451
citing authors

#	ARTICLE	IF	CITATIONS
1	Transposable Element Populations Shed Light on the Evolutionary History of Wheat and the Complex Co-evolution of Autonomous and Non-autonomous Retrotransposons. <i>Genetics & Genomics Next</i> , 2022, 3, .	0.8	12
2	De Novo Genome Assembly of the Japanese Wheat Cultivar Norin 61 Highlights Functional Variation in Flowering Time and Fusarium-Resistant Genes in East Asian Genotypes. <i>Plant and Cell Physiology</i> , 2021, 62, 8-27.	1.5	16
3	A membrane-bound ankyrin repeat protein confers race-specific leaf rust disease resistance in wheat. <i>Nature Communications</i> , 2021, 12, 956.	5.8	63
4	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021, 53, 564-573.	9.4	138
5	Defects in Cell Wall Differentiation of the Arabidopsis Mutant rol1-2 Is Dependent on Cyclin-Dependent Kinase CDK8. <i>Cells</i> , 2021, 10, 685.	1.8	3
6	Alleles of a wall-associated kinase gene account for three of the major northern corn leaf blight resistance loci in maize. <i>Plant Journal</i> , 2021, 106, 526-535.	2.8	23
7	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.	3.1	180
8	Wheat Pm4 resistance to powdery mildew is controlled by alternative splice variants encoding chimeric proteins. <i>Nature Plants</i> , 2021, 7, 327-341.	4.7	85
9	Comparative Transcriptome Analysis of Wheat Lines in the Field Reveals Multiple Essential Biochemical Pathways Suppressed by Obligate Pathogens. <i>Frontiers in Plant Science</i> , 2021, 12, 720462.	1.7	14
10	A population-level invasion by transposable elements triggers genome expansion in a fungal pathogen. <i>ELife</i> , 2021, 10, .	2.8	49
11	Domestication of High-Copy Transposons Underlays the Wheat Small RNA Response to an Obligate Pathogen. <i>Molecular Biology and Evolution</i> , 2020, 37, 839-848.	3.5	21
12	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	13.7	513
13	Fonio millet genome unlocks African orphan crop diversity for agriculture in a changing climate. <i>Nature Communications</i> , 2020, 11, 4488.	5.8	63
14	Cross-Kingdom RNAi of Pathogen Effectors Leads to Quantitative Adult Plant Resistance in Wheat. <i>Frontiers in Plant Science</i> , 2020, 11, 253.	1.7	24
15	The AvrPm3-Pm3 effector-NLR interactions control both race-specific resistance and host-specificity of cereal mildews on wheat. <i>Nature Communications</i> , 2019, 10, 2292.	5.8	103
16	The highly divergent Jekyll genes, required for sexual reproduction, are lineage specific for the related grass tribes Triticeae and Bromoae. <i>Plant Journal</i> , 2019, 98, 961-974.	2.8	7
17	The evolution of functional complexity within the Î²-amylase gene family in land plants. <i>BMC Evolutionary Biology</i> , 2019, 19, 66.	3.2	47
18	Mutations in the Arabidopsis ROL17/isopropylmalate synthase 1 locus alter amino acid content, modify the TOR network, and suppress the root hair cell development mutant lrx1. <i>Journal of Experimental Botany</i> , 2019, 70, 2313-2323.	2.4	43

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19	Updated Genome Assembly and Annotation for <i>Metrosideros polymorpha</i> , an Emerging Model Tree Species of Ecological Divergence. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3513-3520.	0.8	4
20	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. <i>Genome Biology</i> , 2019, 20, 284.	3.8	179
21	A chromosome-scale genome assembly reveals a highly dynamic effector repertoire of wheat powdery mildew. <i>New Phytologist</i> , 2019, 221, 2176-2189.	3.5	79
22	Recent Activity in Expanding Populations and Purifying Selection Have Shaped Transposable Element Landscapes across Natural Accessions of the Mediterranean Grass <i>Brachypodium distachyon</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 304-318.	1.1	54
23	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus <i>Oryza</i> . <i>Nature Genetics</i> , 2018, 50, 285-296.	9.4	413
24	Comparative Transcriptomics Reveals How Wheat Responds to Infection by <i>Zymoseptoria tritici</i> . <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 420-431.	1.4	37
25	Non-parent of Origin Expression of Numerous Effector Genes Indicates a Role of Gene Regulation in Host Adaption of the Hybrid Triticale Powdery Mildew Pathogen. <i>Frontiers in Plant Science</i> , 2018, 9, 49.	1.7	33
26	The Repetitive Landscape of the Barley Genome. <i>Compendium of Plant Genomes</i> , 2018, , 123-138.	0.3	6
27	Advances in Wheat and Pathogen Genomics: Implications for Disease Control. <i>Annual Review of Phytopathology</i> , 2018, 56, 67-87.	3.5	66
28	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	6.0	768
29	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	6.0	2,424
30	Impact of transposable elements on genome structure and evolution in bread wheat. <i>Genome Biology</i> , 2018, 19, 103.	3.8	226
31	Chromosome-scale comparative sequence analysis unravels molecular mechanisms of genome dynamics between two wheat cultivars. <i>Genome Biology</i> , 2018, 19, 104.	3.8	54
32	Rapid cloning of genes in hexaploid wheat using cultivar-specific long-range chromosome assembly. <i>Nature Biotechnology</i> , 2017, 35, 793-796.	9.4	218
33	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	13.7	1,365
34	<i>AvrPm2</i> encodes an <i>RNase</i> -like avirulence effector which is conserved in the two different specialized forms of wheat and rye powdery mildew fungus. <i>New Phytologist</i> , 2017, 213, 1301-1314.	3.5	112
35	Rapid Identification of Rust Resistance Genes Through Cultivar-Specific De Novo Chromosome Assemblies. <i>Methods in Molecular Biology</i> , 2017, 1659, 245-255.	0.4	2
36	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017, 551, 498-502.	13.7	563

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37	Letting go: bacterial genome reduction solves the dilemma of adapting to predation mortality in a substrate-restricted environment. <i>ISME Journal</i> , 2017, 11, 2258-2266.	4.4	14
38	Characterization of Lr75: a partial, broad-spectrum leaf rust resistance gene in wheat. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1-12.	1.8	130
39	Fine mapping of the chromosome 5B region carrying closely linked rust resistance genes Yr47 and Lr52 in wheat. <i>Theoretical and Applied Genetics</i> , 2017, 130, 495-504.	1.8	34
40	Rapid turnover of effectors in grass powdery mildew (<i>Blumeria graminis</i>). <i>BMC Evolutionary Biology</i> , 2017, 17, 223.	3.2	52
41	The repetitive landscape of the 5100 Mbp barley genome. <i>Mobile DNA</i> , 2017, 8, 22.	1.3	49
42	Reconstructing the Evolutionary History of Powdery Mildew Lineages (<i>Blumeria graminis</i>) at Different Evolutionary Time Scales with NGS Data. <i>Genome Biology and Evolution</i> , 2017, 9, 446-456.	1.1	34
43	Avirulence Genes in Cereal Powdery Mildews: The Gene-for-Genes Hypothesis 2.0. <i>Frontiers in Plant Science</i> , 2016, 7, 241.	1.7	73
44	Differentiation Among <i>Blumeria graminis</i> f. sp. <i>tritici</i> Isolates Originating from Wild Versus Domesticated <i>Triticum</i> Species in Israel. <i>Phytopathology</i> , 2016, 106, 861-870.	1.1	29
45	Fire blight disease reactome: RNA-seq transcriptional profile of apple host plant defense responses to <i>Erwinia amylovora</i> pathogen infection. <i>Scientific Reports</i> , 2016, 6, 21600.	1.6	38
46	DNA transposon activity is associated with increased mutation rates in genes of rice and other grasses. <i>Nature Communications</i> , 2016, 7, 12790.	5.8	51
47	Rapid gene isolation in barley and wheat by mutant chromosome sequencing. <i>Genome Biology</i> , 2016, 17, 221.	3.8	265
48	Hybridization of powdery mildew strains gives rise to pathogens on novel agricultural crop species. <i>Nature Genetics</i> , 2016, 48, 201-205.	9.4	192
49	Evidence of horizontal gene transfer between obligate leaf nodule symbionts. <i>ISME Journal</i> , 2016, 10, 2092-2105.	4.4	63
50	Marker development, saturation mapping, and high-resolution mapping of the <i>Septoria nodorum</i> blotch susceptibility gene Snn3-B1 in wheat. <i>Molecular Genetics and Genomics</i> , 2016, 291, 107-119.	1.0	41
51	Evolution of the EKA family of powdery mildew avirulence-effector genes from the ORF 1 of a LINE retrotransposon. <i>BMC Genomics</i> , 2015, 16, 917.	1.2	33
52	The making of a genomic parasite - the Mothra family sheds light on the evolution of Helitrons in plants. <i>Mobile DNA</i> , 2015, 6, 23.	1.3	4
53	The wheat resistance gene <i>Lr34</i> results in the constitutive induction of multiple defense pathways in transgenic barley. <i>Plant Journal</i> , 2015, 84, 202-215.	2.8	45
54	Recurrent sequence exchange between homeologous grass chromosomes. <i>Plant Journal</i> , 2015, 84, 747-759.	2.8	5

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55	Genome-wide comparison of Asian and African rice reveals high recent activity of DNA transposons. <i>Mobile DNA</i> , 2015, 6, 8.	1.3	7
56	Evolution of the Grain Dispersal System in Barley. <i>Cell</i> , 2015, 162, 527-539.	13.5	265
57	Fine mapping of powdery mildew resistance genes PmTb7A.1 and PmTb7A.2 in <i>Triticum boeoticum</i> (Boiss.) using the shotgun sequence assembly of chromosome 7AL. <i>Theoretical and Applied Genetics</i> , 2015, 128, 2099-2111.	1.8	11
58	Genetic and molecular characterization of a locus involved in avirulence of <i>Blumeria graminis</i> f. sp. <i>tritici</i> on wheat Pm3 resistance alleles. <i>Fungal Genetics and Biology</i> , 2015, 82, 181-192.	0.9	50
59	The maize disease resistance gene <i>Htn1</i> against northern corn leaf blight encodes a wall-associated receptor-like kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8780-8785.	3.3	302
60	Genomic Approaches Towards Durable Fungal Disease Resistance in Wheat. , 2015, , 369-375.		2
61	Multiple Avirulence Loci and Allele-Specific Effector Recognition Control the Pm3 Race-Specific Resistance of Wheat to Powdery Mildew. <i>Plant Cell</i> , 2015, 27, tpc.15.00171.	3.1	135
62	RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. <i>BMC Genomics</i> , 2015, 16, 538.	1.2	86
63	Analysis of CACTA transposases reveals intron loss as major factor influencing their exon/intron structure in monocotyledonous and eudicotyledonous hosts. <i>Mobile DNA</i> , 2014, 5, 24.	1.3	10
64	Phytochelatins metal(loid) transport into vacuoles shows different substrate preferences in barley and <i>A. rabi</i> . <i>Plant, Cell and Environment</i> , 2014, 37, 1192-1201.	2.8	134
65	Molecular mapping of an adult plant stem rust resistance gene Sr56 in winter wheat cultivar Arina. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1441-1448.	1.8	84
66	High-resolution analysis of a QTL for resistance to <i>Stagonospora nodorum</i> glume blotch in wheat reveals presence of two distinct resistance loci in the target interval. <i>Theoretical and Applied Genetics</i> , 2014, 127, 573-586.	1.8	11
67	The genome sequence of African rice (<i>Oryza glaberrima</i>) and evidence for independent domestication. <i>Nature Genetics</i> , 2014, 46, 982-988.	9.4	342
68	Sequencing of Chloroplast Genomes from Wheat, Barley, Rye and Their Relatives Provides a Detailed Insight into the Evolution of the Triticeae Tribe. <i>PLoS ONE</i> , 2014, 9, e85761.	1.1	190
69	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. <i>Genome Biology</i> , 2013, 14, R58.	3.8	125
70	The wheat powdery mildew genome shows the unique evolution of an obligate biotroph. <i>Nature Genetics</i> , 2013, 45, 1092-1096.	9.4	236
71	Rye <i>Pm8</i> and wheat <i>Pm3</i> are orthologous genes and show evolutionary conservation of resistance function against powdery mildew. <i>Plant Journal</i> , 2013, 76, 957-969.	2.8	178
72	Comparative analysis of genome composition in Triticeae reveals strong variation in transposable element dynamics and nucleotide diversity. <i>Plant Journal</i> , 2013, 73, 347-356.	2.8	43

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73	Genotype-specific SNP map based on whole chromosome 3B sequence information from wheat cultivars Avena and Farino. <i>Plant Biotechnology Journal</i> , 2013, 11, 23-32.	4.1	22
74	<i>Aegilops tauschii</i> draft genome sequence reveals a gene repertoire for wheat adaptation. <i>Nature</i> , 2013, 496, 91-95.	13.7	714
75	High-copy sequences reveal distinct evolution of the rye B chromosome. <i>New Phytologist</i> , 2013, 199, 550-558.	3.5	75
76	Transposons in Cereals: Shaping Genomes and Driving Their Evolution. , 2013, , 127-154.		1
77	Evolutionary Dynamics of Retrotransposons Assessed by High-Throughput Sequencing in Wild Relatives of Wheat. <i>Genome Biology and Evolution</i> , 2013, 5, 1010-1020.	1.1	30
78	Characterization of chromosomal architecture in Arabidopsis by chromosome conformation capture. <i>Genome Biology</i> , 2013, 14, R129.	13.9	79
79	The physical map of wheat chromosome 1BS provides insights into its gene space organization and evolution. <i>Genome Biology</i> , 2013, 14, R138.	13.9	40
80	A Physical Map of the Short Arm of Wheat Chromosome 1A. <i>PLoS ONE</i> , 2013, 8, e80272.	1.1	30
81	Selfish supernumerary chromosome reveals its origin as a mosaic of host genome and organellar sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13343-13346.	3.3	173
82	Computational analysis and characterization of UCE-like elements (ULEs) in plant genomes. <i>Genome Research</i> , 2012, 22, 2455-2466.	2.4	28
83	The banana (<i>Musa acuminata</i>) genome and the evolution of monocotyledonous plants. <i>Nature</i> , 2012, 488, 213-217.	13.7	1,049
84	Interspecies sequence comparison of <i>Brachypodium</i> reveals how transposon activity corrodes genome colinearity. <i>Plant Journal</i> , 2012, 71, 550-563.	2.8	26
85	Frequent Gene Movement and Pseudogene Evolution Is Common to the Large and Complex Genomes of Wheat, Barley, and Their Relatives. <i>Plant Cell</i> , 2011, 23, 1706-1718.	3.1	190
86	Comparative sequence analysis of wheat and barley powdery mildew fungi reveals gene colinearity, dates divergence and indicates host-pathogen co-evolution. <i>Fungal Genetics and Biology</i> , 2011, 48, 327-334.	0.9	33
87	Plant TOR signaling components. <i>Plant Signaling and Behavior</i> , 2011, 6, 1700-1705.	1.2	36
88	Lr34 multi-pathogen resistance ABC transporter: molecular analysis of homoeologous and orthologous genes in hexaploid wheat and other grass species. <i>Plant Journal</i> , 2011, 65, 392-403.	2.8	79
89	A major invasion of transposable elements accounts for the large size of the <i>Blumeria graminis</i> f.sp. <i>tritici</i> genome. <i>Functional and Integrative Genomics</i> , 2011, 11, 671-677.	1.4	50
90	Fine mapping and syntenic integration of the semi-dwarfing gene <i>sdw3</i> of barley. <i>Functional and Integrative Genomics</i> , 2010, 10, 509-521.	1.4	19

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91	Wheat gene bank accessions as a source of new alleles of the powdery mildew resistance gene Pm3: a large scale allele mining project. <i>BMC Plant Biology</i> , 2010, 10, 88.	1.6	115
92	A highly conserved gene island of three genes on chromosome 3B of hexaploid wheat: diverse gene function and genomic structure maintained in a tightly linked block. <i>BMC Plant Biology</i> , 2010, 10, 98.	1.6	16
93	Wheat beta-expansin (EXPB11) genes: Identification of the expressed gene on chromosome 3BS carrying a pollen allergen domain. <i>BMC Plant Biology</i> , 2010, 10, 99.	1.6	17
94	Megabase Level Sequencing Reveals Contrasted Organization and Evolution Patterns of the Wheat Gene and Transposable Element Spaces. <i>Plant Cell</i> , 2010, 22, 1686-1701.	3.1	258
95	Patching gaps in plant genomes results in gene movement and erosion of colinearity. <i>Genome Research</i> , 2010, 20, 1229-1237.	2.4	139
96	Genome Expansion and Gene Loss in Powdery Mildew Fungi Reveal Tradeoffs in Extreme Parasitism. <i>Science</i> , 2010, 330, 1543-1546.	6.0	725
97	Cleistogamous flowering in barley arises from the suppression of microRNA-guided <i>HvAP2</i> mRNA cleavage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 490-495.	3.3	201
98	Gene Content and Virtual Gene Order of Barley Chromosome 1H. <i>Plant Physiology</i> , 2009, 151, 496-505.	2.3	135
99	Fine mapping, physical mapping and development of diagnostic markers for the <i>Rrs2</i> scald resistance gene in barley. <i>Theoretical and Applied Genetics</i> , 2009, 119, 1507-1522.	1.8	40
100	A whole-genome snapshot of 454 sequences exposes the composition of the barley genome and provides evidence for parallel evolution of genome size in wheat and barley. <i>Plant Journal</i> , 2009, 59, 712-722.	2.8	125
101	Two different <i>LRR</i> genes are required for <i>Lr10</i> -mediated leaf rust resistance in tetraploid and hexaploid wheat. <i>Plant Journal</i> , 2009, 60, 1043-1054.	2.8	126
102	The Sorghum bicolor genome and the diversification of grasses. <i>Nature</i> , 2009, 457, 551-556.	13.7	2,642
103	Analysis of Intraspecies Diversity in Wheat and Barley Genomes Identifies Breakpoints of Ancient Haplotypes and Provides Insight into the Structure of Diploid and Hexaploid Triticeae Gene Pools. <i>Plant Physiology</i> , 2009, 149, 258-270.	2.3	38
104	Low-pass shotgun sequencing of the barley genome facilitates rapid identification of genes, conserved non-coding sequences and novel repeats. <i>BMC Genomics</i> , 2008, 9, 518.	1.2	75
105	Contrasting Rates of Evolution in <i>Pm3</i> Loci From Three Wheat Species and Rice. <i>Genetics</i> , 2007, 177, 1207-1216.	1.2	35
106	Six-rowed barley originated from a mutation in a homeodomain-leucine zipper I-class homeobox gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1424-1429.	3.3	563
107	Genome-wide comparative analysis of copia retrotransposons in Triticeae, rice, and Arabidopsis reveals conserved ancient evolutionary lineages and distinct dynamics of individual copia families. <i>Genome Research</i> , 2007, 17, 1072-1081.	2.4	228
108	A unified classification system for eukaryotic transposable elements. <i>Nature Reviews Genetics</i> , 2007, 8, 973-982.	7.7	2,396

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109	Comparison of orthologous loci from small grass genomes Brachypodium and rice: implications for wheat genomics and grass genome annotation. <i>Plant Journal</i> , 2007, 49, 704-717.	2.8	161
110	Illegitimate recombination is a major evolutionary mechanism for initiating size variation in plant resistance genes. <i>Plant Journal</i> , 2007, 51, 631-641.	2.8	89
111	Leaf rust resistance gene Lr1, isolated from bread wheat (<i>Triticum aestivum</i> L.) is a member of the large psr567 gene family. <i>Plant Molecular Biology</i> , 2007, 65, 93-106.	2.0	299
112	454 sequencing put to the test using the complex genome of barley. <i>BMC Genomics</i> , 2006, 7, 275.	1.2	200
113	Updating of transposable element annotations from large wheat genomic sequences reveals diverse activities and gene associations. <i>Molecular Genetics and Genomics</i> , 2005, 274, 119-130.	1.0	82
114	A detailed look at 7 million years of genome evolution in a 439 kb contiguous sequence at the barley Hv-eIF4E locus: recombination, rearrangements and repeats. <i>Plant Journal</i> , 2004, 41, 184-194.	2.8	91
115	CACTA Transposons in Triticeae. A Diverse Family of High-Copy Repetitive Elements. <i>Plant Physiology</i> , 2003, 132, 52-63.	2.3	143
116	Rapid Genome Divergence at Orthologous Low Molecular Weight Glutenin Loci of the A and Am Genomes of Wheat[W]. <i>Plant Cell</i> , 2003, 15, 1186-1197.	3.1	226
117	Analysis of a contiguous 211 kb sequence in diploid wheat (<i>Triticum monococcum</i> L.) reveals multiple mechanisms of genome evolution. <i>Plant Journal</i> , 2001, 26, 307-316.	2.8	213