

Thomas Wicker

List of Publications by Year in descending order

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Version: 2024-02-01

117
papers

23,500
citations

22099

59
h-index

20307

116
g-index

127
all docs

127
docs citations

127
times ranked

18451
citing authors

#	ARTICLE	IF	CITATIONS
1	The Sorghum bicolor genome and the diversification of grasses. Nature, 2009, 457, 551-556.	13.7	2,642
2	Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science, 2018, 361, .	6.0	2,424
3	A unified classification system for eukaryotic transposable elements. Nature Reviews Genetics, 2007, 8, 973-982.	7.7	2,396
4	A chromosome conformation capture ordered sequence of the barley genome. Nature, 2017, 544, 427-433.	13.7	1,365
5	The banana (<i>Musa acuminata</i>) genome and the evolution of monocotyledonous plants. Nature, 2012, 488, 213-217.	13.7	1,049
6	The transcriptional landscape of polyploid wheat. Science, 2018, 361, .	6.0	768
7	Genome Expansion and Gene Loss in Powdery Mildew Fungi Reveal Tradeoffs in Extreme Parasitism. Science, 2010, 330, 1543-1546.	6.0	725
8	<i>Aegilops tauschii</i> draft genome sequence reveals a gene repertoire for wheat adaptation. Nature, 2013, 496, 91-95.	13.7	714
9	Six-rowed barley originated from a mutation in a homeodomain-leucine zipper I-class homeobox gene. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1424-1429.	3.3	563
10	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . Nature, 2017, 551, 498-502.	13.7	563
11	Multiple wheat genomes reveal global variation in modern breeding. Nature, 2020, 588, 277-283.	13.7	513
12	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus <i>Oryza</i> . Nature Genetics, 2018, 50, 285-296.	9.4	413
13	The genome sequence of African rice (<i>Oryza glaberrima</i>) and evidence for independent domestication. Nature Genetics, 2014, 46, 982-988.	9.4	342
14	The maize disease resistance gene <i>Htn1</i> against northern corn leaf blight encodes a wall-associated receptor-like kinase. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 8780-8785.	3.3	302
15	Leaf rust resistance gene <i>Lr1</i> , isolated from bread wheat (<i>Triticum aestivum</i> L.) is a member of the large <i>psr567</i> gene family. Plant Molecular Biology, 2007, 65, 93-106.	2.0	299
16	Evolution of the Grain Dispersal System in Barley. Cell, 2015, 162, 527-539.	13.5	265
17	Rapid gene isolation in barley and wheat by mutant chromosome sequencing. Genome Biology, 2016, 17, 221.	3.8	265
18	Megabase Level Sequencing Reveals Contrasted Organization and Evolution Patterns of the Wheat Gene and Transposable Element Spaces. Plant Cell, 2010, 22, 1686-1701.	3.1	258

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19	The wheat powdery mildew genome shows the unique evolution of an obligate biotroph. <i>Nature Genetics</i> , 2013, 45, 1092-1096.	9.4	236
20	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
21	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
22	Impact of transposable elements on genome structure and evolution in bread wheat. <i>Genome Biology</i> , 2018, 19, 103.	3.8	226
23	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
24	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
25	Cleistogamous flowering in barley arises from the suppression of microRNA-guided HvAP2 mRNA cleavage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 490-495.	3.3	201
26	454 sequencing put to the test using the complex genome of barley. <i>BMC Genomics</i> , 2006, 7, 275.	1.2	200
27	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
28	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
29	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
30	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.	3.1	180
31	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. <i>Genome Biology</i> , 2019, 20, 284.	3.8	179
32	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
33	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
34	Comparison of orthologous loci from small grass genomes <i>Brachypodium</i> and rice: implications for wheat genomics and grass genome annotation. <i>Plant Journal</i> , 2007, 49, 704-717.	2.8	161
35	CACTA Transposons in Triticeae. A Diverse Family of High-Copy Repetitive Elements. <i>Plant Physiology</i> , 2003, 132, 52-63.	2.3	143
36	Patching gaps in plant genomes results in gene movement and erosion of colinearity. <i>Genome Research</i> , 2010, 20, 1229-1237.	2.4	139

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37	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021, 53, 564-573.	9.4	138
38	Gene Content and Virtual Gene Order of Barley Chromosome 1H. <i>Plant Physiology</i> , 2009, 151, 496-505.	2.3	135
39	Multiple Avirulence Loci and Allele-Specific Effector Recognition Control the <i>Pm3</i> Race-Specific Resistance of Wheat to Powdery Mildew. <i>Plant Cell</i> , 2015, 27, tpc.15.00171.	3.1	135
40	Phytochelatins—metal(loid) transport into vacuoles shows different substrate preferences in barley and <i>rabidopsis</i> . <i>Plant, Cell and Environment</i> , 2014, 37, 1192-1201.	2.8	134
41	Characterization of <i>Lr75</i> : a partial, broad-spectrum leaf rust resistance gene in wheat. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1-12.	1.8	130
42	Two different CC-NBS-LRR 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
43	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
44	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. <i>Genome Biology</i> , 2013, 14, R58.	3.8	125
45	Wheat gene bank accessions as a source of new alleles of the powdery mildew resistance gene <i>Pm3</i> : a large scale allele mining project. <i>BMC Plant Biology</i> , 2010, 10, 88.	1.6	115
46	<i>AvrPm2</i> encodes an RNase-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
47	The <i>AvrPm3</i> - <i>Pm3</i> 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
48	A detailed look at 7-million years of genome evolution in a 439-kb contiguous sequence at the barley <i>Hv-eIF4E</i> locus: recombination, rearrangements and repeats. <i>Plant Journal</i> , 2004, 41, 184-194.	2.8	91
49	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
50	RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. <i>BMC Genomics</i> , 2015, 16, 538.	1.2	86
51	Wheat <i>Pm4</i> resistance to powdery mildew is controlled by alternative splice variants encoding chimeric proteins. <i>Nature Plants</i> , 2021, 7, 327-341.	4.7	85
52	Molecular mapping of an adult plant stem rust resistance gene <i>Sr56</i> in winter wheat cultivar Arina. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1441-1448.	1.8	84
53	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
54	<i>Lr34</i> 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

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55	Characterization of chromosomal architecture in Arabidopsis by chromosome conformation capture. <i>Genome Biology</i> , 2013, 14, R129.	13.9	79
56	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
57	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
58	High-copy sequences reveal distinct evolution of the rye B chromosome. <i>New Phytologist</i> , 2013, 199, 550-558.	3.5	75
59	Avirulence Genes in Cereal Powdery Mildews: The Gene-for-Gene Hypothesis 2.0. <i>Frontiers in Plant Science</i> , 2016, 7, 241.	1.7	73
60	Advances in Wheat and Pathogen Genomics: Implications for Disease Control. <i>Annual Review of Phytopathology</i> , 2018, 56, 67-87.	3.5	66
61	Evidence of horizontal gene transfer between obligate leaf nodule symbionts. <i>ISME Journal</i> , 2016, 10, 2092-2105.	4.4	63
62	Fonio millet genome unlocks African orphan crop diversity for agriculture in a changing climate. <i>Nature Communications</i> , 2020, 11, 4488.	5.8	63
63	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
64	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
65	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
66	Rapid turnover of effectors in grass powdery mildew (<i>Blumeria graminis</i>). <i>BMC Evolutionary Biology</i> , 2017, 17, 223.	3.2	52
67	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
68	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
69	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
70	The repetitive landscape of the 5100 Mbp barley genome. <i>Mobile DNA</i> , 2017, 8, 22.	1.3	49
71	A population-level invasion by transposable elements triggers genome expansion in a fungal pathogen. <i>ELife</i> , 2021, 10, .	2.8	49
72	The evolution of functional complexity within the α -amylase gene family in land plants. <i>BMC Evolutionary Biology</i> , 2019, 19, 66.	3.2	47

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73	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
74	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
75	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 <i>lrx1</i> . <i>Journal of Experimental Botany</i> , 2019, 70, 2313-2323.	2.4	43
76	Marker development, saturation mapping, and high-resolution mapping of the <i>Septoria nodorum</i> blotch susceptibility gene <i>Snn3-B1</i> in wheat. <i>Molecular Genetics and Genomics</i> , 2016, 291, 107-119.	1.0	41
77	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
78	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
79	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
80	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
81	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
82	Plant TOR signaling components. <i>Plant Signaling and Behavior</i> , 2011, 6, 1700-1705.	1.2	36
83	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
84	Fine mapping of the chromosome 5B region carrying closely linked rust resistance genes <i>Yr47</i> and <i>Lr52</i> in wheat. <i>Theoretical and Applied Genetics</i> , 2017, 130, 495-504.	1.8	34
85	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
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	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
88	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
89	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
90	A Physical Map of the Short Arm of Wheat Chromosome 1A. <i>PLoS ONE</i> , 2013, 8, e80272.	1.1	30

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91	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
92	Computational analysis and characterization of UCE-like elements (ULEs) in plant genomes. <i>Genome Research</i> , 2012, 22, 2455-2466.	2.4	28
93	Inter-species sequence comparison of <i>Brachypodium</i> reveals how transposon activity corrodes genome colinearity. <i>Plant Journal</i> , 2012, 71, 550-563.	2.8	26
94	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
95	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
96	Genotype-specific SNP map based on whole chromosome 3B sequence information from wheat cultivars Arina and Forno. <i>Plant Biotechnology Journal</i> , 2013, 11, 23-32.	4.1	22
97	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
98	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
99	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
100	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
101	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
102	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
103	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
104	Transposable Element Populations Shed Light on the Evolutionary History of Wheat and the Complex Evolution of Autonomous and Non-Autonomous Retrotransposons. <i>Genetics & Genomics Next</i> , 2022, 3, .	0.8	12
105	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
106	Fine mapping of powdery mildew resistance genes <i>PmTb7A.1</i> and <i>PmTb7A.2</i> 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
107	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
108	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

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109	The highly divergent Jekyll genes, required for sexual reproduction, are lineage specific for the related grass tribes Triticeae and Bromaeae. <i>Plant Journal</i> , 2019, 98, 961-974.	2.8	7
110	The Repetitive Landscape of the Barley Genome. <i>Compendium of Plant Genomes</i> , 2018, , 123-138.	0.3	6
111	Recurrent sequence exchange between homeologous grass chromosomes. <i>Plant Journal</i> , 2015, 84, 747-759.	2.8	5
112	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
113	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
114	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
115	Genomic Approaches Towards Durable Fungal Disease Resistance in Wheat. , 2015, , 369-375.		2
116	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
117	Transposons in Cereals: Shaping Genomes and Driving Their Evolution. , 2013, , 127-154.		1