

Roger P Wise

List of Publications by Year in Descending Order

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Version: 2024-04-27

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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.

96
papers

7,579
citations

43
h-index

86
g-index

103
ext. papers

8,447
ext. citations

6.4
avg, IF

5.72
L-index

#	Paper	IF	Citations
96	NGPINT: a next-generation protein-protein interaction software. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	3
95	Disruption of barley immunity to powdery mildew by an in-frame Lys-Leu deletion in the essential protein SGT1. <i>Genetics</i> , 2021 , 217,	4	4
94	FINDER: an automated software package to annotate eukaryotic genes from RNA-Seq data and associated protein sequences. <i>BMC Bioinformatics</i> , 2021 , 22, 205	3.6	5
93	Next-generation yeast-two-hybrid analysis with Y2H-SCORES identifies novel interactors of the MLA immune receptor. <i>PLoS Computational Biology</i> , 2021 , 17, e1008890	5	2
92	Small RNA discovery in the interaction between barley and the powdery mildew pathogen. <i>BMC Genomics</i> , 2019 , 20, 610	4.5	17
91	Convergent Evolution of Effector Protease Recognition by and Barley. <i>Molecular Plant-Microbe Interactions</i> , 2019 , 32, 550-565	3.6	23
90	A Genomic View of Biotic Stress Resistance. <i>Compendium of Plant Genomes</i> , 2018 , 233-257	0.8	
89	A Confounding Effect of Bacterial Titer in a Type III Delivery-Based Assay of Eukaryotic Effector Function. <i>Molecular Plant-Microbe Interactions</i> , 2018 , 31, 1115-1116	3.6	1
88	DiffSLC: A graph centrality method to detect essential proteins of a protein-protein interaction network. <i>PLoS ONE</i> , 2017 , 12, e0187091	3.7	26
87	Interchromosomal Transfer of Immune Regulation During Infection of Barley with the Powdery Mildew Pathogen. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 3317-3329	3.2	2
86	Genes and Small RNA Transcripts Exhibit Dosage-Dependent Expression Pattern in Maize Copy-Number Alterations. <i>Genetics</i> , 2016 , 203, 1133-47	4	8
85	Allelic barley MLA immune receptors recognize sequence-unrelated avirulence effectors of the powdery mildew pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E6486-E6495	11.5	89
84	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
83	The knottin-like Blufensin family regulates genes involved in nuclear import and the secretory pathway in barley-powdery mildew interactions. <i>Frontiers in Plant Science</i> , 2015 , 6, 409	6.2	6
82	Broadly Conserved Fungal Effector BEC1019 Suppresses Host Cell Death and Enhances Pathogen Virulence in Powdery Mildew of Barley (<i>Hordeum vulgare</i> L.). <i>Molecular Plant-Microbe Interactions</i> , 2015 , 28, 968-83	3.6	32
81	Mla- and Rom1-mediated control of microRNA398 and chloroplast copper/zinc superoxide dismutase regulates cell death in response to the barley powdery mildew fungus. <i>New Phytologist</i> , 2014 , 201, 1396-1412	9.8	32
80	The miR9863 family regulates distinct Mla alleles in barley to attenuate NLR receptor-triggered disease resistance and cell-death signaling. <i>PLoS Genetics</i> , 2014 , 10, e1004755	6	85

79	Code-assisted discovery of TAL effector targets in bacterial leaf streak of rice reveals contrast with bacterial blight and a novel susceptibility gene. <i>PLoS Pathogens</i> , 2014 , 10, e1003972	7.6	94
78	Flor Revisited (Again): eQTL and Mutational Analysis of NB-LRR Mediated Immunity to Powdery Mildew in Barley. <i>Journal of Integrative Agriculture</i> , 2014 , 13, 237-243	3.2	0
77	TEnest 2.0: computational annotation and visualization of nested transposable elements. <i>Methods in Molecular Biology</i> , 2013 , 1057, 305-19	1.4	3
76	Anchoring and ordering NGS contig assemblies by population sequencing (POPSEQ). <i>Plant Journal</i> , 2013 , 76, 718-27	6.9	219
75	Host-induced gene silencing in barley powdery mildew reveals a class of ribonuclease-like effectors. <i>Molecular Plant-Microbe Interactions</i> , 2013 , 26, 633-42	3.6	136
74	Prospects for advancing defense to cereal rusts through genetical genomics. <i>Frontiers in Plant Science</i> , 2013 , 4, 117	6.2	4
73	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012 , 491, 711-6	50.4	1124
72	Differential accumulation of host mRNAs on polyribosomes during obligate pathogen-plant interactions. <i>Molecular BioSystems</i> , 2012 , 8, 2153-65		23
71	HvWRKY10, HvWRKY19, and HvWRKY28 regulate Mla-triggered immunity and basal defense to barley powdery mildew. <i>Molecular Plant-Microbe Interactions</i> , 2012 , 25, 1492-505	3.6	28
70	The Hordeum Toolbox: The Barley Coordinated Agricultural Project Genotype and Phenotype Resource. <i>Plant Genome</i> , 2012 , 5, 81-91	4.4	29
69	PLEXdb: gene expression resources for plants and plant pathogens. <i>Nucleic Acids Research</i> , 2012 , 40, D1194-201	20.1	215
68	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
67	Rf8-Mediated T-urf13 Transcript Accumulation Coincides with a Pentatricopeptide Repeat Cluster on Maize Chromosome 2L. <i>Plant Genome</i> , 2011 , 4, 283-299	4.4	13
66	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
65	Drought response in the spikes of barley: gene expression in the lemma, palea, awn, and seed. <i>Functional and Integrative Genomics</i> , 2010 , 10, 191-205	3.8	72
64	Comparative Transcriptional Profiling Established the Awn as the Major Photosynthetic Organ of the Barley Spike While the Lemma and the Palea Primarily Protect the Seed. <i>Plant Genome</i> , 2009 , 2,	4.4	17
63	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
62	Blufensin1 negatively impacts basal defense in response to barley powdery mildew. <i>Plant Physiology</i> , 2009 , 149, 271-85	6.6	53

61	The international barley sequencing consortium--at the threshold of efficient access to the barley genome. <i>Plant Physiology</i> , 2009 , 149, 142-7	6.6	163
60	Comparative transcriptomics in the Triticeae. <i>BMC Genomics</i> , 2009 , 10, 285	4.5	59
59	Functional contribution of chorismate synthase, anthranilate synthase, and chorismate mutase to penetration resistance in barley-powdery mildew interactions. <i>Molecular Plant-Microbe Interactions</i> , 2009 , 22, 311-20	3.6	39
58	Computational finishing of large sequence contigs reveals interspersed nested repeats and gene islands in the rf1-associated region of maize. <i>Plant Physiology</i> , 2009 , 151, 483-95	6.6	9
57	A single molecule scaffold for the maize genome. <i>PLoS Genetics</i> , 2009 , 5, e1000711	6	110
56	Genomics of Biotic Interactions in the Triticeae 2009 , 559-589		4
55	Gene expression quantitative trait locus analysis of 16 000 barley genes reveals a complex pattern of genome-wide transcriptional regulation. <i>Plant Journal</i> , 2008 , 53, 90-101	6.9	139
54	Tissue-dependent limited pleiotropy affects gene expression in barley. <i>Plant Journal</i> , 2008 , 56, 287-296	6.9	26
53	TENest: automated chronological annotation and visualization of nested plant transposable elements. <i>Plant Physiology</i> , 2008 , 146, 45-59	6.6	54
52	Exploiting regulatory variation to identify genes underlying quantitative resistance to the wheat stem rust pathogen <i>Puccinia graminis</i> f. sp. <i>tritici</i> in barley. <i>Theoretical and Applied Genetics</i> , 2008 , 117, 261-72	6	41
51	Diversification of Lrk/Tak kinase gene clusters is associated with subfunctionalization and cultivar-specific transcript accumulation in barley. <i>Functional and Integrative Genomics</i> , 2008 , 8, 199-209	3.8	7
50	Towards systems genetic analyses in barley: Integration of phenotypic, expression and genotype data into GeneNetwork. <i>BMC Genomics</i> , 2008 , 9, 73	2.6	22
49	BarleyBase/PLEXdb. <i>Methods in Molecular Biology</i> , 2007 , 406, 347-63	1.4	75
48	SFP genotyping from affymetrix arrays is robust but largely detects cis-acting expression regulators. <i>Genetics</i> , 2007 , 176, 789-800	4	61
47	Transcript profiling in host-pathogen interactions. <i>Annual Review of Phytopathology</i> , 2007 , 45, 329-69	10.8	136
46	Stage-specific suppression of basal defense discriminates barley plants containing fast- and delayed-acting Mla powdery mildew resistance alleles. <i>Molecular Plant-Microbe Interactions</i> , 2006 , 19, 939-47	3.6	71
45	Genetic diversity contribution to errors in short oligonucleotide microarray analysis. <i>Plant Biotechnology Journal</i> , 2006 , 4, 489-98	11.6	25
44	Upstream open reading frames of the barley Mla13 powdery mildew resistance gene function co-operatively to down-regulate translation. <i>Molecular Plant Pathology</i> , 2006 , 7, 167-76	5.7	13

43	Estimating the number of true null hypotheses from a histogram of p values. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2006 , 11, 337-356	1.9	81
42	Mapping multiple disease resistance genes using a barley mapping population evaluated in Peru, Mexico, and the USA. <i>Molecular Breeding</i> , 2006 , 18, 355-366	3.4	25
41	An atlas of gene expression from seed to seed through barley development. <i>Functional and Integrative Genomics</i> , 2006 , 6, 202-11	3.8	126
40	BarleyBase--an expression profiling database for plant genomics. <i>Nucleic Acids Research</i> , 2005 , 33, D614-8	20.1	74
39	Interaction-dependent gene expression in Mla-specified response to barley powdery mildew. <i>Plant Cell</i> , 2004 , 16, 2514-28	11.6	174
38	A new resource for cereal genomics: 22K barley GeneChip comes of age. <i>Plant Physiology</i> , 2004 , 134, 960-8	6.6	266
37	A single-amino acid substitution in the sixth leucine-rich repeat of barley MLA6 and MLA13 alleviates dependence on RAR1 for disease resistance signaling. <i>Plant Journal</i> , 2004 , 38, 215-26	6.9	93
36	Powdery mildew-induced Mla mRNAs are alternatively spliced and contain multiple upstream open reading frames. <i>Plant Physiology</i> , 2003 , 131, 558-67	6.6	117
35	Alternative transcription initiation sites and polyadenylation sites are recruited during Mu suppression at the rf2a locus of maize. <i>Genetics</i> , 2003 , 163, 685-98	4	27
34	Nuclear-mediated mitochondrial gene regulation and male fertility in higher plants: Light at the end of the tunnel?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 10240-2	11.5	53
33	Genome dynamics and evolution of the Mla (powdery mildew) resistance locus in barley. <i>Plant Cell</i> , 2002 , 14, 1903-17	11.6	201
32	The MLA6 coiled-coil, NBS-LRR protein confers AvrMla6-dependent resistance specificity to <i>Blumeria graminis</i> f. sp. <i>hordei</i> in barley and wheat. <i>Plant Journal</i> , 2001 , 25, 335-48	6.9	163
31	Cell-autonomous expression of barley Mla1 confers race-specific resistance to the powdery mildew fungus via a Rar1-independent signaling pathway. <i>Plant Cell</i> , 2001 , 13, 337-50	11.6	188
30	Rds and Rih mediate hypersensitive cell death independent of gene-for-gene resistance to the oat crown rust pathogen <i>Puccinia coronata</i> f. sp. <i>avenae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2001 , 14, 1376-83	2.6	17
29	A bacterial artificial chromosome library for barley (<i>Hordeum vulgare</i> L.) and the identification of clones containing putative resistance genes. <i>Theoretical and Applied Genetics</i> , 2000 , 101, 1093-1099	6	177
28	Disease Resistance: What's Brewing in Barley Genomics. <i>Plant Disease</i> , 2000 , 84, 1160-1170	1.5	19
27	An anchored AFLP- and retrotransposon-based map of diploid <i>Avena</i> . <i>Genome</i> , 2000 , 43, 736-749	2.4	90
26	An anchored AFLP- and retrotransposon-based map of diploid <i>Avena</i> . <i>Genome</i> , 2000 , 43, 736-749	2.4	51

25	Mitochondrial transcript processing and restoration of male fertility in T-cytoplasm maize. <i>Journal of Heredity</i> , 1999 , 90, 380-5	2.4	46
24	The Genetics, Pathology, and Molecular Biology of T-Cytoplasm Male Sterility in Maize. <i>Advances in Agronomy</i> , 1999 , 65, 79-130	7.7	41
23	The Mla (powdery mildew) resistance cluster is associated with three NBS-LRR gene families and suppressed recombination within a 240-kb DNA interval on chromosome 5S (1HS) of barley. <i>Genetics</i> , 1999 , 153, 1929-48	4	196
22	High-resolution mapping adjacent to the Pc71 crown-rust resistance locus in hexaploid oat 1998 , 4, 13-21		32
21	The molecular basis of cytoplasmic male sterility and fertility restoration. <i>Trends in Plant Science</i> , 1998 , 3, 175-180	13.1	594
20	Rf8 and Rf* mediate unique T-urf13-transcript accumulation, revealing a conserved motif associated with RNA processing and restoration of pollen fertility in T-cytoplasm maize. <i>Genetics</i> , 1997 , 147, 1367-79	4	58
19	Crown Rust Resistance Loci on Linkage Groups 4 and 13 in Cultivated Oat. <i>Journal of Heredity</i> , 1996 , 87, 427-432	2.4	34
18	The rf2 nuclear restorer gene of male-sterile T-cytoplasm maize. <i>Science</i> , 1996 , 272, 1334-6	33.3	316
17	Comparative mapping of homoeologous group 1 regions and genes for resistance to obligate biotrophs in Avena, Hordeum, and Zea mays. <i>Genome</i> , 1996 , 39, 155-64	2.4	33
16	Mutator-induced mutations of the rf1 nuclear fertility restorer of T-cytoplasm maize alter the accumulation of T-urf13 mitochondrial transcripts. <i>Genetics</i> , 1996 , 143, 1383-94	4	31
15	Recombination Within a 5-centimorgan Region in Diploid Avena Reveals Multiple Specificities Conferring Resistance to Puccinia coronata. <i>Phytopathology</i> , 1996 , 86, 340	3.8	22
14	Variation in the ratio of physical to genetic distance in intervals adjacent to the. <i>Molecular Genetics and Genomics</i> , 1996 , 251, 472		3
13	Recombination of alleles conferring specific resistance to powdery mildew at the Mla locus in barley. <i>Genome</i> , 1994 , 37, 460-8	2.4	19
12	A linkage map of diploid Avena based on RFLP loci and a locus conferring resistance to nine isolates of Puccinia coronata var. avenae. <i>Theoretical and Applied Genetics</i> , 1994 , 89, 831-7	6	43
11	Linkage of genes conferring specific resistance to oat crown rust in diploid Avena. <i>Genome</i> , 1994 , 37, 92-6	2.4	10
10	Reproducibility of random amplified polymorphic DNA (RAPD) analysis among laboratories. <i>Genome Research</i> , 1993 , 2, 341-5	9.7	251
9	Nucleotide sequence of the Bronze-1 homologous gene from Hordeum vulgare. <i>Plant Molecular Biology</i> , 1990 , 14, 277-9	4.6	39
8	Expression in Saccharomyces cerevisiae of a gene associated with cytoplasmic male sterility from maize: respiratory dysfunction and uncoupling of yeast mitochondria. <i>Molecular Genetics and Genomics</i> , 1990 , 223, 24-32		50

7	Mutation to male fertility and toxin insensitivity in Texas (T)-cytoplasm maize is associated with a frameshift in a mitochondrial open reading frame. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1987 , 84, 2858-62	11.5	110
6	Influence of nuclear background on transcription of a maize mitochondrial region associated with Texas male sterile cytoplasm. <i>Molecular Genetics and Genomics</i> , 1987 , 210, 399-406		46
5	urf13-T of T cytoplasm maize mitochondria encodes a 13 kD polypeptide. <i>Plant Molecular Biology</i> , 1987 , 9, 121-6	4.6	88
4	Fine structure and instability of the Ml-a locus in barley. <i>Genetics</i> , 1985 , 111, 113-30	4	31
3	Y2H-SCORES: A statistical framework to infer protein-protein interactions from next-generation yeast-two-hybrid sequence data		2
2	Convergent evolution of effector protease recognition by Arabidopsis and barley		2
1	FINDER: An automated software package to annotate eukaryotic genes from RNA-Seq data and associated protein sequences		1