Roger P Wise

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	SGT1-Specific Domain Mutations Impair Interactions with the Barley MLA6 Immune Receptor in Association with Loss of NLR Protein. Molecular Plant-Microbe Interactions, 2022, 35, 274-289.	2.6	4
2	An interolog-based barley interactome as an integration framework for immune signaling. Genetics, 2022, 221, .	2.9	3
3	FINDER: an automated software package to annotate eukaryotic genes from RNA-Seq data and associated protein sequences. BMC Bioinformatics, 2021, 22, 205.	2.6	17
4	Next-generation yeast-two-hybrid analysis with Y2H-SCORES identifies novel interactors of the MLA immune receptor. PLoS Computational Biology, 2021, 17, e1008890.	3.2	14
5	NGPINT: a next-generation protein–protein interaction software. Briefings in Bioinformatics, 2021, 22, .	6.5	12
6	Disruption of barley immunity to powdery mildew by an in-frame Lys-Leu deletion in the essential protein SGT1. Genetics, 2021, 217, .	2.9	11
7	Small RNA discovery in the interaction between barley and the powdery mildew pathogen. BMC Genomics, 2019, 20, 610.	2.8	37
8	Convergent Evolution of Effector Protease Recognition by <i>Arabidopsis</i> and Barley. Molecular Plant-Microbe Interactions, 2019, 32, 550-565.	2.6	47
9	A Confounding Effect of Bacterial Titer in a Type III Delivery–Based Assay of Eukaryotic Effector Function. Molecular Plant-Microbe Interactions, 2018, 31, 1115-1116.	2.6	1
10	A Genomic View of Biotic Stress Resistance. Compendium of Plant Genomes, 2018, , 233-257.	0.5	0
11	Interchromosomal Transfer of Immune Regulation During Infection of Barley with the Powdery Mildew Pathogen. G3: Genes, Genomes, Genetics, 2017, 7, 3317-3329.	1.8	6
12	DiffSLC: A graph centrality method to detect essential proteins of a protein-protein interaction network. PLoS ONE, 2017, 12, e0187091.	2.5	43
13	Allelic barley MLA immune receptors recognize sequence-unrelated avirulence effectors of the powdery mildew pathogen. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6486-E6495.	7.1	162
14	Genes and Small RNA Transcripts Exhibit Dosage-Dependent Expression Pattern in Maize Copy-Number Alterations. Genetics, 2016, 203, 1133-1147.	2.9	12
15	The knottin-like Blufensin family regulates genes involved in nuclear import and the secretory pathway in barley-powdery mildew interactions. Frontiers in Plant Science, 2015, 6, 409.	3.6	14
16	Broadly Conserved Fungal Effector BEC1019 Suppresses Host Cell Death and Enhances Pathogen Virulence in Powdery Mildew of Barley (<i>Hordeum vulgare</i> L.) (Retracted). Molecular Plant-Microbe Interactions, 2015, 28, 968-983.	2.6	33
17	Sequencing of 15Â622 geneâ€bearing BAC s clarifies the geneâ€dense regions of the barley genome. Plant Journal, 2015, 84, 216-227.	5.7	36
18	The miR9863 Family Regulates Distinct Mla Alleles in Barley to Attenuate NLR Receptor-Triggered Disease Resistance and Cell-Death Signaling. PLoS Genetics, 2014, 10, e1004755.	3.5	121

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19	Code-Assisted Discovery of TAL Effector Targets in Bacterial Leaf Streak of Rice Reveals Contrast with Bacterial Blight and a Novel Susceptibility Gene. PLoS Pathogens, 2014, 10, e1003972.	4.7	137
20	Flor Revisited (Again): eQTL and Mutational Analysis of NB-LRR Mediated Immunity to Powdery Mildew in Barley. Journal of Integrative Agriculture, 2014, 13, 237-243.	3.5	1
21	<i>Mlaâ€</i> and <i>Rom1</i> â€mediated control of microRNA398 and chloroplast copper/zinc superoxide dismutase regulates cell death in response to the barley powdery mildew fungus. New Phytologist, 2014, 201, 1396-1412.	7.3	62
22	TEnest 2.0: Computational Annotation and Visualization of Nested Transposable Elements. Methods in Molecular Biology, 2013, 1057, 305-319.	0.9	4
23	Anchoring and ordering <scp>NCS</scp> contig assemblies by population sequencing (<scp>POPSEQ</scp>). Plant Journal, 2013, 76, 718-727.	5.7	264
24	Host-Induced Gene Silencing in Barley Powdery Mildew Reveals a Class of Ribonuclease-Like Effectors. Molecular Plant-Microbe Interactions, 2013, 26, 633-642.	2.6	190
25	Prospects for advancing defense to cereal rusts through genetical genomics. Frontiers in Plant Science, 2013, 4, 117.	3.6	5
26	PLEXdb: gene expression resources for plants and plant pathogens. Nucleic Acids Research, 2012, 40, D1194-D1201.	14.5	244
27	A physical, genetic and functional sequence assembly of the barley genome. Nature, 2012, 491, 711-716.	27.8	1,416
28	Differential accumulation of host mRNAs on polyribosomes during obligate pathogen-plant interactions. Molecular BioSystems, 2012, 8, 2153.	2.9	31
29	HvWRKY10, HvWRKY19, and HvWRKY28 Regulate <i>Mla</i> -Triggered Immunity and Basal Defense to Barley Powdery Mildew. Molecular Plant-Microbe Interactions, 2012, 25, 1492-1505.	2.6	31
30	The Hordeum Toolbox: The Barley Coordinated Agricultural Project Genotype and Phenotype Resource. Plant Genome, 2012, 5, 81-91.	2.8	35
31	Quantitative and Temporal Definition of the <i>Mla</i> Transcriptional Regulon During Barley–Powdery Mildew Interactions. Molecular Plant-Microbe Interactions, 2011, 24, 694-705.	2.6	24
32	<i>Rf8</i> -Mediated T- <i>urf13</i> Transcript Accumulation Coincides with a Pentatricopeptide Repeat Cluster on Maize Chromosome 2L. Plant Genome, 2011, 4, 283-299.	2.8	15
33	Quantitative and Qualitative Stem Rust Resistance Factors in Barley Are Associated with Transcriptional Suppression of Defense Regulons. PLoS Genetics, 2011, 7, e1002208.	3.5	56
34	Drought response in the spikes of barley: gene expression in the lemma, palea, awn, and seed. Functional and Integrative Genomics, 2010, 10, 191-205.	3.5	93
35	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. Plant Genome, 2009, 2, .	2.8	27
36	Transcript-Based Cloning of <i>RRP46</i> , a Regulator of rRNA Processing and <i>R</i> Gene–Independent Cell Death in Barley–Powdery Mildew Interactions Â. Plant Cell, 2009, 21, 3280-3295.	6.6	26

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37	<i>Blufensin1</i> Negatively Impacts Basal Defense in Response to Barley Powdery Mildew Â. Plant Physiology, 2009, 149, 271-285.	4.8	66
38	The International Barley Sequencing Consortium—At the Threshold of Efficient Access to the Barley Genome Â. Plant Physiology, 2009, 149, 142-147.	4.8	195
39	Comparative transcriptomics in the Triticeae. BMC Genomics, 2009, 10, 285.	2.8	62
40	Functional Contribution of Chorismate Synthase, Anthranilate Synthase, and Chorismate Mutase to Penetration Resistance in Barley–Powdery Mildew Interactions. Molecular Plant-Microbe Interactions, 2009, 22, 311-320.	2.6	58
41	Computational Finishing of Large Sequence Contigs Reveals Interspersed Nested Repeats and Gene Islands in the <i>rf1</i> -Associated Region of Maize Â. Plant Physiology, 2009, 151, 483-495.	4.8	9
42	Genomics of Biotic Interactions in the Triticeae. , 2009, , 559-589.		5
43	A Single Molecule Scaffold for the Maize Genome. PLoS Genetics, 2009, 5, e1000711.	3.5	122
44	Exploiting regulatory variation to identify genes underlying quantitative resistance to the wheat stem rust pathogen Puccinia graminis f. sp. tritici in barley. Theoretical and Applied Genetics, 2008, 117, 261-272.	3.6	43
45	Diversification of Lrk/Tak kinase gene clusters is associated with subfunctionalization and cultivar-specific transcript accumulation in barley. Functional and Integrative Genomics, 2008, 8, 199-209.	3.5	7
46	Towards systems genetic analyses in barley: Integration of phenotypic, expression and genotype data into GeneNetwork. BMC Genetics, 2008, 9, 73.	2.7	26
47	Gene expression quantitative trait locus analysis of 16 000 barley genes reveals a complex pattern of genomeâ€wide transcriptional regulation. Plant Journal, 2008, 53, 90-101.	5.7	158
48	Tissueâ€dependent limited pleiotropy affects gene expression in barley. Plant Journal, 2008, 56, 287-296.	5.7	26
49	TEnest: Automated Chronological Annotation and Visualization of Nested Plant Transposable Elements. Plant Physiology, 2008, 146, 45-59.	4.8	61
50	SFP Genotyping From Affymetrix Arrays Is Robust But Largely Detects Cis-acting Expression Regulators. Genetics, 2007, 176, 789-800.	2.9	69
51	Transcript Profiling in Host–Pathogen Interactions. Annual Review of Phytopathology, 2007, 45, 329-369.	7.8	155
52	BarleyBase/PLEXdb. , 2007, 406, 347-363.		76
53	Stage-Specific Suppression of Basal Defense Discriminates Barley Plants Containing Fast- and Delayed-Acting Mla Powdery Mildew Resistance Alleles. Molecular Plant-Microbe Interactions, 2006, 19, 939-947.	2.6	88
54	Genetic diversity contribution to errors in short oligonucleotide microarray analysis. Plant Biotechnology Journal, 2006, 4, 060615010054001-???.	8.3	26

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55	Upstream open reading frames of the barley Mla13 powdery mildew resistance gene function co-operatively to down-regulate translation. Molecular Plant Pathology, 2006, 7, 167-176.	4.2	16
56	Estimating the number of true null hypotheses from a histogram of p values. Journal of Agricultural, Biological, and Environmental Statistics, 2006, 11, 337-356.	1.4	107
57	Mapping multiple disease resistance genes using a barley mapping population evaluated in Peru, Mexico, and the USA. Molecular Breeding, 2006, 18, 355-366.	2.1	27
58	An atlas of gene expression from seed to seed through barley development. Functional and Integrative Genomics, 2006, 6, 202-211.	3.5	138
59	Interaction-Dependent Gene Expression in Mla-Specified Response to Barley Powdery Mildew[W]. Plant Cell, 2004, 16, 2514-2528.	6.6	204
60	BarleyBase–an expression profiling database for plant genomics. Nucleic Acids Research, 2004, 33, D614-D618.	14.5	86
61	A New Resource for Cereal Genomics: 22K Barley GeneChip Comes of Age. Plant Physiology, 2004, 134, 960-968.	4.8	287
62	A single-amino acid substitution in the sixth leucine-rich repeat of barley MLA6 and MLA13 alleviates dependence on RAR1 for disease resistance signaling. Plant Journal, 2004, 38, 215-226.	5.7	108
63	Powdery Mildew-Induced Mla mRNAs Are Alternatively Spliced and Contain Multiple Upstream Open Reading Frames. Plant Physiology, 2003, 131, 558-567.	4.8	129
64	Alternative Transcription Initiation Sites and Polyadenylation Sites Are Recruited During <i>Mu</i> Suppression at the <i>rf2a</i> Locus of Maize. Genetics, 2003, 163, 685-698.	2.9	37
65	Nuclear-mediated mitochondrial gene regulation and male fertility in higher plants: Light at the end of the tunnel?. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10240-10242.	7.1	62
66	Genome Dynamics and Evolution of the <i>Mla</i> (Powdery Mildew) Resistance Locus in Barley[W]. Plant Cell, 2002, 14, 1903-1917.	6.6	229
67	Rds and Rih Mediate Hypersensitive Cell Death Independent of Gene-for-Gene Resistance to the Oat Crown Rust Pathogen Puccinia coronata f. sp. avenae. Molecular Plant-Microbe Interactions, 2001, 14, 1376-1383.	2.6	17
68	The MLA6 coiled-coil, NBS-LRR protein confers AvrMla6-dependent resistance specificity to Blumeria graminis f. sp. hordei in barley and wheat. Plant Journal, 2001, 25, 335-348.	5.7	192
69	Cell-Autonomous Expression of Barley Mla1 Confers Race-Specific Resistance to the Powdery Mildew Fungus via a Rar1-Independent Signaling Pathway. Plant Cell, 2001, 13, 337-350.	6.6	203
70	A bacterial artificial chromosome library for barley (Hordeum vulgare L.) and the identification of clones containing putative resistance genes. Theoretical and Applied Genetics, 2000, 101, 1093-1099.	3.6	187
71	Disease Resistance: What's Brewing in Barley Genomics. Plant Disease, 2000, 84, 1160-1170.	1.4	21
72	An anchored AFLP- and retrotransposon-based map of diploid <i>Avena</i> . Genome, 2000, 43, 736-749.	2.0	98

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73	An anchored AFLP- and retrotransposon-based map of diploid <i>Avena</i> . Genome, 2000, 43, 736-749.	2.0	52
74	Mitochondrial transcript processing and restoration of male fertility in T-cytoplasm maize. , 1999, 90, 380-385.		54
75	The Genetics, Pathology, and Molecular Biology of T-Cytoplasm Male Sterility in Maize. Advances in Agronomy, 1999, 65, 79-130.	5.2	55
76	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. Genetics, 1999, 153, 1929-1948.	2.9	242
77	High-resolution mapping adjacent to the Pc71 crown-rust resistance locus in hexaploid oat. , 1998, 4, 13-21.		41
78	The molecular basis of cytoplasmic male sterility and fertility restoration. Trends in Plant Science, 1998, 3, 175-180.	8.8	688
79	<i>Rf8</i> and <i>Rf</i> * Mediate Unique T- <i>urf13</i> -Transcript Accumulation, Revealing a Conserved Motif Associated With RNA Processing and Restoration of Pollen Fertility in T-Cytoplasm Maize. Genetics, 1997, 147, 1367-1379.	2.9	75
80	The rf2 Nuclear Restorer Gene of Male-Sterile T-Cytoplasm Maize. Science, 1996, 272, 1334-1336.	12.6	370
81	Comparative mapping of homoeologous group 1 regions and genes for resistance to obligate biotrophs in <i>Avena</i> , <i>Hordeum</i> , and <i>Zea mays</i> . Genome, 1996, 39, 155-164.	2.0	35
82	Crown Rust Resistance Loci on Linkage Groups 4 and 13 in Cultivated Oat. Journal of Heredity, 1996, 87, 427-432.	2.4	39
83	<i>Mutator</i> -Induced Mutations of the <i>rf1</i> Nuclear Fertility Restorer of T-Cytoplasm Maize Alter the Accumulation of T- <i>urfl3</i> Mitochondrial Transcripts. Genetics, 1996, 143, 1383-1394.	2.9	44
84	Recombination Within a 5-centimorgan Region in DiploidAvenaReveals Multiple Specificities Conferring Resistance toPuccinia coronata. Phytopathology, 1996, 86, 340.	2.2	27
85	Variation in the ratio of physical to genetic distance in intervals adjacent to the. Molecular Genetics and Genomics, 1996, 251, 472.	2.4	3
86	Recombination of alleles conferring specific resistance to powdery mildew at the Mla locus in barley. Genome, 1994, 37, 460-468.	2.0	22
87	A linkage map of diploid Avena based on RFLP loci and a locus conferring resistance to nine isolates of Puccinia coronata var. †avenae'. Theoretical and Applied Genetics, 1994, 89-89, 831-837.	3.6	53
88	Linkage of genes conferring specific resistance to oat crown rust in diploid Avena. Genome, 1994, 37, 92-96.	2.0	11
89	Reproducibility of random amplified polymorphic DNA (RAPD) analysis among laboratories Genome Research, 1993, 2, 341-345.	5.5	335
90	Nucleotide sequence of the Bronze-1 homologous gene from Hordeum vulgare. Plant Molecular Biology, 1990, 14, 277-279.	3.9	47

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91	Expression in Saccharomyces cerevisiae of a gene associated with cytoplasmic male sterility from maize: Respiratory dysfunction and uncoupling of yeast mitochondria. Molecular Genetics and Genomics, 1990, 223, 24-32.	2.4	55
92	Mutation to male fertility and toxin insensitivity in Texas (T)-cytoplasm maize is associated with a frameshift in a mitochondrial open reading frame. Proceedings of the National Academy of Sciences of the United States of America, 1987, 84, 2858-2862.	7.1	123
93	Influence of nuclear background on transcription of a maize mitochondrial region associated with Texas male sterile cytoplasm. Molecular Genetics and Genomics, 1987, 210, 399-406.	2.4	54
94	urf13-T of T cytoplasm maize mitochondria encodes a 13 kD polypeptide. Plant Molecular Biology, 1987, 9, 121-126.	3.9	98
95	FINE STRUCTURE AND INSTABILITY OF THE <i>Ml-a</i> LOCUS IN BARLEY. Genetics, 1985, 111, 113-130.	2.9	36