

Roger P Wise

List of Publications by Year in descending order

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docs citations

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times ranked

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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. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 274-289.	1.4	4
2	An interolog-based barley interactome as an integration framework for immune signaling. <i>Genetics</i> , 2022, 221, .	1.2	3
3	FINDER: an automated software package to annotate eukaryotic genes from RNA-Seq data and associated protein sequences. <i>BMC Bioinformatics</i> , 2021, 22, 205.	1.2	17
4	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.	1.5	14
5	NGPINT: a next-generation protein-protein interaction software. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	12
6	Disruption of barley immunity to powdery mildew by an in-frame Lys-Leu deletion in the essential protein SGT1. <i>Genetics</i> , 2021, 217, .	1.2	11
7	Small RNA discovery in the interaction between barley and the powdery mildew pathogen. <i>BMC Genomics</i> , 2019, 20, 610.	1.2	37
8	Convergent Evolution of Effector Protease Recognition by <i>Arabidopsis</i> and Barley. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 550-565.	1.4	47
9	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.	1.4	1
10	A Genomic View of Biotic Stress Resistance. <i>Compendium of Plant Genomes</i> , 2018, , 233-257.	0.3	0
11	Interchromosomal Transfer of Immune Regulation During Infection of Barley with the Powdery Mildew Pathogen. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3317-3329.	0.8	6
12	DiffSLC: A graph centrality method to detect essential proteins of a protein-protein interaction network. <i>PLoS ONE</i> , 2017, 12, e0187091.	1.1	43
13	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.	3.3	162
14	Genes and Small RNA Transcripts Exhibit Dosage-Dependent Expression Pattern in Maize Copy-Number Alterations. <i>Genetics</i> , 2016, 203, 1133-1147.	1.2	12
15	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.	1.7	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). <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 968-983.	1.4	33
17	Sequencing of 15,622 gene-bearing BACs clarifies the gene-dense regions of the barley genome. <i>Plant Journal</i> , 2015, 84, 216-227.	2.8	36
18	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.	1.5	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. <i>PLoS Pathogens</i> , 2014, 10, e1003972.	2.1	137
20	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.	1.7	1
21	<i>Mla</i> and <i>Rom1</i> -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.	3.5	62
22	TENest 2.0: Computational Annotation and Visualization of Nested Transposable Elements. <i>Methods in Molecular Biology</i> , 2013, 1057, 305-319.	0.4	4
23	Anchoring and ordering NGS contig assemblies by population sequencing (POPSEQ). <i>Plant Journal</i> , 2013, 76, 718-727.	2.8	264
24	Host-Induced Gene Silencing in Barley Powdery Mildew Reveals a Class of Ribonuclease-Like Effectors. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 633-642.	1.4	190
25	Prospects for advancing defense to cereal rusts through genetical genomics. <i>Frontiers in Plant Science</i> , 2013, 4, 117.	1.7	5
26	PLEXdb: gene expression resources for plants and plant pathogens. <i>Nucleic Acids Research</i> , 2012, 40, D1194-D1201.	6.5	244
27	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012, 491, 711-716.	13.7	1,416
28	Differential accumulation of host mRNAs on polyribosomes during obligate pathogen-plant interactions. <i>Molecular BioSystems</i> , 2012, 8, 2153.	2.9	31
29	HvWRKY10, HvWRKY19, and HvWRKY28 Regulate <i>Mla</i> -Triggered Immunity and Basal Defense to Barley Powdery Mildew. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 1492-1505.	1.4	31
30	The Hordeum Toolbox: The Barley Coordinated Agricultural Project Genotype and Phenotype Resource. <i>Plant Genome</i> , 2012, 5, 81-91.	1.6	35
31	Quantitative and Temporal Definition of the <i>Mla</i> Transcriptional Regulon During Barley-Powdery Mildew Interactions. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 694-705.	1.4	24
32	<i>Rf8</i> -Mediated <i>T-urf13</i> Transcript Accumulation Coincides with a Pentatricopeptide Repeat Cluster on Maize Chromosome 2L. <i>Plant Genome</i> , 2011, 4, 283-299.	1.6	15
33	Quantitative and Qualitative Stem Rust Resistance Factors in Barley Are Associated with Transcriptional Suppression of Defense Regulons. <i>PLoS Genetics</i> , 2011, 7, e1002208.	1.5	56
34	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.	1.4	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. <i>Plant Genome</i> , 2009, 2, .	1.6	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. <i>Plant Cell</i> , 2009, 21, 3280-3295.	3.1	26

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37	<i>Blufensin1</i> Negatively Impacts Basal Defense in Response to Barley Powdery Mildew. <i>Plant Physiology</i> , 2009, 149, 271-285.	2.3	66
38	The International Barley Sequencing Consortium "At the Threshold of Efficient Access to the Barley Genome". <i>Plant Physiology</i> , 2009, 149, 142-147.	2.3	195
39	Comparative transcriptomics in the Triticeae. <i>BMC Genomics</i> , 2009, 10, 285.	1.2	62
40	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, 311-320.	1.4	58
41	Computational Finishing of Large Sequence Contigs Reveals Interspersed Nested Repeats and Gene Islands in the <i>rfl1</i> -Associated Region of Maize. <i>Plant Physiology</i> , 2009, 151, 483-495.	2.3	9
42	Genomics of Biotic Interactions in the Triticeae. , 2009, , 559-589.		5
43	A Single Molecule Scaffold for the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000711.	1.5	122
44	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, 261-272.	1.8	43
45	Diversification of <i>Lrk/Tak</i> kinase gene clusters is associated with subfunctionalization and cultivar-specific transcript accumulation in barley. <i>Functional and Integrative Genomics</i> , 2008, 8, 199-209.	1.4	7
46	Towards systems genetic analyses in barley: Integration of phenotypic, expression and genotype data into GeneNetwork. <i>BMC Genetics</i> , 2008, 9, 73.	2.7	26
47	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.	2.8	158
48	Tissue-dependent limited pleiotropy affects gene expression in barley. <i>Plant Journal</i> , 2008, 56, 287-296.	2.8	26
49	TEnest: Automated Chronological Annotation and Visualization of Nested Plant Transposable Elements. <i>Plant Physiology</i> , 2008, 146, 45-59.	2.3	61
50	SFP Genotyping From Affymetrix Arrays Is Robust But Largely Detects Cis-acting Expression Regulators. <i>Genetics</i> , 2007, 176, 789-800.	1.2	69
51	Transcript Profiling in Host-Pathogen Interactions. <i>Annual Review of Phytopathology</i> , 2007, 45, 329-369.	3.5	155
52	BarleyBase/PLEXdb. , 2007, 406, 347-363.		76
53	Stage-Specific Suppression of Basal Defense Discriminates Barley Plants Containing Fast- and Delayed-Acting <i>Mla</i> Powdery Mildew Resistance Alleles. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 939-947.	1.4	88
54	Genetic diversity contribution to errors in short oligonucleotide microarray analysis. <i>Plant Biotechnology Journal</i> , 2006, 4, 060615010054001-???	4.1	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. <i>Molecular Plant Pathology</i> , 2006, 7, 167-176.	2.0	16
56	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.	0.7	107
57	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.	1.0	27
58	An atlas of gene expression from seed to seed through barley development. <i>Functional and Integrative Genomics</i> , 2006, 6, 202-211.	1.4	138
59	Interaction-Dependent Gene Expression in Mla-Specified Response to Barley Powdery Mildew[W]. <i>Plant Cell</i> , 2004, 16, 2514-2528.	3.1	204
60	BarleyBase—an expression profiling database for plant genomics. <i>Nucleic Acids Research</i> , 2004, 33, D614-D618.	6.5	86
61	A New Resource for Cereal Genomics: 22K Barley GeneChip Comes of Age. <i>Plant Physiology</i> , 2004, 134, 960-968.	2.3	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. <i>Plant Journal</i> , 2004, 38, 215-226.	2.8	108
63	Powdery Mildew-Induced Mla mRNAs Are Alternatively Spliced and Contain Multiple Upstream Open Reading Frames. <i>Plant Physiology</i> , 2003, 131, 558-567.	2.3	129
64	Alternative Transcription Initiation Sites and Polyadenylation Sites Are Recruited During <i>mu</i> Suppression at the <i>rf2a</i> Locus of Maize. <i>Genetics</i> , 2003, 163, 685-698.	1.2	37
65	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, 10240-10242.	3.3	62
66	Genome Dynamics and Evolution of the Mla (Powdery Mildew) Resistance Locus in Barley[W]. <i>Plant Cell</i> , 2002, 14, 1903-1917.	3.1	229
67	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, 1376-1383.	1.4	17
68	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, 335-348.	2.8	192
69	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, 337-350.	3.1	203
70	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.	1.8	187
71	Disease Resistance: What's Brewing in Barley Genomics. <i>Plant Disease</i> , 2000, 84, 1160-1170.	0.7	21
72	An anchored AFLP- and retrotransposon-based map of diploid <i>Avena</i> . <i>Genome</i> , 2000, 43, 736-749.	0.9	98

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73	An anchored AFLP- and retrotransposon-based map of diploid <i>Avena</i> . <i>Genome</i> , 2000, 43, 736-749.	0.9	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. <i>Advances in Agronomy</i> , 1999, 65, 79-130.	2.4	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. <i>Genetics</i> , 1999, 153, 1929-1948.	1.2	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. <i>Trends in Plant Science</i> , 1998, 3, 175-180.	4.3	688
79	<i>Rf8</i> and <i>Rf1</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. <i>Genetics</i> , 1997, 147, 1367-1379.	1.2	75
80	The <i>rf2</i> Nuclear Restorer Gene of Male-Sterile T-Cytoplasm Maize. <i>Science</i> , 1996, 272, 1334-1336.	6.0	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> . <i>Genome</i> , 1996, 39, 155-164.	0.9	35
82	Crown Rust Resistance Loci on Linkage Groups 4 and 13 in Cultivated Oat. <i>Journal of Heredity</i> , 1996, 87, 427-432.	1.0	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>urf13</i> Mitochondrial Transcripts. <i>Genetics</i> , 1996, 143, 1383-1394.	1.2	44
84	Recombination Within a 5-centimorgan Region in Diploid <i>Avena</i> Reveals Multiple Specificities Conferring Resistance to <i>Puccinia coronata</i> . <i>Phytopathology</i> , 1996, 86, 340.	1.1	27
85	Variation in the ratio of physical to genetic distance in intervals adjacent to the. <i>Molecular Genetics and Genomics</i> , 1996, 251, 472.	2.4	3
86	Recombination of alleles conferring specific resistance to powdery mildew at the Mla locus in barley. <i>Genome</i> , 1994, 37, 460-468.	0.9	22
87	A linkage map of diploid <i>Avena</i> based on RFLP loci and a locus conferring resistance to nine isolates of <i>Puccinia coronata</i> var. <i>avenae</i> . <i>Theoretical and Applied Genetics</i> , 1994, 89-89, 831-837.	1.8	53
88	Linkage of genes conferring specific resistance to oat crown rust in diploid <i>Avena</i> . <i>Genome</i> , 1994, 37, 92-96.	0.9	11
89	Reproducibility of random amplified polymorphic DNA (RAPD) analysis among laboratories.. <i>Genome Research</i> , 1993, 2, 341-345.	2.4	335
90	Nucleotide sequence of the Bronze-1 homologous gene from <i>Hordeum vulgare</i> . <i>Plant Molecular Biology</i> , 1990, 14, 277-279.	2.0	47

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91	Expression in <i>Saccharomyces cerevisiae</i> 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.	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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1987, 84, 2858-2862.	3.3	123
93	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.	2.4	54
94	urf13-T of T cytoplasm maize mitochondria encodes a 13 kD polypeptide. <i>Plant Molecular Biology</i> , 1987, 9, 121-126.	2.0	98
95	FINE STRUCTURE AND INSTABILITY OF THE <i>MI-a</i> LOCUS IN BARLEY. <i>Genetics</i> , 1985, 111, 113-130.	1.2	36