

# Roger P Wise

## List of Publications by Year in descending order

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95  
papers

9,209  
citations

50276

46  
h-index

43889

91  
g-index

103  
all docs

103  
docs citations

103  
times ranked

7972  
citing authors

#	ARTICLE	IF	CITATIONS
1	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012, 491, 711-716.	27.8	1,416
2	The molecular basis of cytoplasmic male sterility and fertility restoration. <i>Trends in Plant Science</i> , 1998, 3, 175-180.	8.8	688
3	The rf2 Nuclear Restorer Gene of Male-Sterile T-Cytoplasm Maize. <i>Science</i> , 1996, 272, 1334-1336.	12.6	370
4	Reproducibility of random amplified polymorphic DNA (RAPD) analysis among laboratories.. <i>Genome Research</i> , 1993, 2, 341-345.	5.5	335
5	A New Resource for Cereal Genomics: 22K Barley GeneChip Comes of Age. <i>Plant Physiology</i> , 2004, 134, 960-968.	4.8	287
6	Anchoring and ordering <scp>NGS</scp> contig assemblies by population sequencing (<scp>POPSEQ</scp>). <i>Plant Journal</i> , 2013, 76, 718-727.	5.7	264
7	PLEXdb: gene expression resources for plants and plant pathogens. <i>Nucleic Acids Research</i> , 2012, 40, D1194-D1201.	14.5	244
8	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.	2.9	242
9	Genome Dynamics and Evolution of the<i>Mla</i> (Powdery Mildew) Resistance Locus in Barley[W]. <i>Plant Cell</i> , 2002, 14, 1903-1917.	6.6	229
10	Interaction-Dependent Gene Expression in Mla-Specified Response to Barley Powdery Mildew[W]. <i>Plant Cell</i> , 2004, 16, 2514-2528.	6.6	204
11	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.	6.6	203
12	The International Barley Sequencing Consortiumâ€™At the Threshold of Efficient Access to the Barley Genome Â. <i>Plant Physiology</i> , 2009, 149, 142-147.	4.8	195
13	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.	5.7	192
14	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.	2.6	190
15	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.	3.6	187
16	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.	7.1	162
17	Gene expression quantitative trait locus analysis of 16â€000 barley genes reveals a complex pattern of genomeâ€™wide transcriptional regulation. <i>Plant Journal</i> , 2008, 53, 90-101.	5.7	158
18	Transcript Profiling in Hostâ€™Pathogen Interactions. <i>Annual Review of Phytopathology</i> , 2007, 45, 329-369.	7.8	155

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19	An atlas of gene expression from seed to seed through barley development. Functional and Integrative Genomics, 2006, 6, 202-211.	3.5	138
20	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
21	Powdery Mildew-Induced Mla mRNAs Are Alternatively Spliced and Contain Multiple Upstream Open Reading Frames. Plant Physiology, 2003, 131, 558-567.	4.8	129
22	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
23	A Single Molecule Scaffold for the Maize Genome. PLoS Genetics, 2009, 5, e1000711.	3.5	122
24	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
25	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
26	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
27	urf13-T of T cytoplasm maize mitochondria encodes a 13 kD polypeptide. Plant Molecular Biology, 1987, 9, 121-126.	3.9	98
28	An anchored AFLP- and retrotransposon-based map of diploid <i>Avena</i> . Genome, 2000, 43, 736-749.	2.0	98
29	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
30	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
31	BarleyBase—an expression profiling database for plant genomics. Nucleic Acids Research, 2004, 33, D614-D618.	14.5	86
32	BarleyBase/PLEXdb. , 2007, 406, 347-363.		76
33	<i>urf8</i> and <i>urf13</i> * Mediate Unique T-urf13-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
34	SFP Genotyping From Affymetrix Arrays Is Robust But Largely Detects Cis-acting Expression Regulators. Genetics, 2007, 176, 789-800.	2.9	69
35	<i>Blufensin1</i> Negatively Impacts Basal Defense in Response to Barley Powdery Mildew. Plant Physiology, 2009, 149, 271-285.	4.8	66
36	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

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37	Comparative transcriptomics in the Triticeae. BMC Genomics, 2009, 10, 285.	2.8	62
38	<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. New Phytologist, 2014, 201, 1396-1412.	7.3	62
39	TEnest: Automated Chronological Annotation and Visualization of Nested Plant Transposable Elements. Plant Physiology, 2008, 146, 45-59.	4.8	61
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	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
42	Expression in <i>Saccharomyces cerevisiae</i> 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
43	The Genetics, Pathology, and Molecular Biology of T-Cytoplasm Male Sterility in Maize. Advances in Agronomy, 1999, 65, 79-130.	5.2	55
44	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
45	Mitochondrial transcript processing and restoration of male fertility in T-cytoplasm maize. , 1999, 90, 380-385.		54
46	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> <sup>TM</sup> . Theoretical and Applied Genetics, 1994, 89-89, 831-837.	3.6	53
47	An anchored AFLP- and retrotransposon-based map of diploid <i>Avena</i> . Genome, 2000, 43, 736-749.	2.0	52
48	Nucleotide sequence of the Bronze-1 homologous gene from <i>Hordeum vulgare</i> . Plant Molecular Biology, 1990, 14, 277-279.	3.9	47
49	Convergent Evolution of Effector Protease Recognition by <i>Arabidopsis</i> and Barley. Molecular Plant-Microbe Interactions, 2019, 32, 550-565.	2.6	47
50	<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
51	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. Theoretical and Applied Genetics, 2008, 117, 261-272.	3.6	43
52	DiffSLC: A graph centrality method to detect essential proteins of a protein-protein interaction network. PLoS ONE, 2017, 12, e0187091.	2.5	43
53	High-resolution mapping adjacent to the Pc71 crown-rust resistance locus in hexaploid oat. , 1998, 4, 13-21.		41
54	Crown Rust Resistance Loci on Linkage Groups 4 and 13 in Cultivated Oat. Journal of Heredity, 1996, 87, 427-432.	2.4	39

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55	Small RNA discovery in the interaction between barley and the powdery mildew pathogen. BMC Genomics, 2019, 20, 610.	2.8	37
56	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
57	Sequencing of 15,622 genes bearing BACs clarifies the gene-dense regions of the barley genome. Plant Journal, 2015, 84, 216-227.	5.7	36
58	FINE STRUCTURE AND INSTABILITY OF THE <i>Mla</i> LOCUS IN BARLEY. Genetics, 1985, 111, 113-130.	2.9	36
59	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
60	The Hordeum Toolbox: The Barley Coordinated Agricultural Project Genotype and Phenotype Resource. Plant Genome, 2012, 5, 81-91.	2.8	35
61	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
62	Differential accumulation of host mRNAs on polyribosomes during obligate pathogen-plant interactions. Molecular BioSystems, 2012, 8, 2153.	2.9	31
63	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
64	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
65	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
66	Recombination Within a 5-centimorgan Region in Diploid <i>Avena</i> Reveals Multiple Specificities Conferring Resistance to <i>Puccinia coronata</i> . Phytopathology, 1996, 86, 340.	2.2	27
67	Genetic diversity contribution to errors in short oligonucleotide microarray analysis. Plant Biotechnology Journal, 2006, 4, 060615010054001-???	8.3	26
68	Towards systems genetic analyses in barley: Integration of phenotypic, expression and genotype data into GeneNetwork. BMC Genetics, 2008, 9, 73.	2.7	26
69	Tissue-dependent limited pleiotropy affects gene expression in barley. Plant Journal, 2008, 56, 287-296.	5.7	26
70	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. Plant Cell, 2009, 21, 3280-3295.	6.6	26
71	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
72	Recombination of alleles conferring specific resistance to powdery mildew at the <i>Mla</i> locus in barley. Genome, 1994, 37, 460-468.	2.0	22

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73	Disease Resistance: What's Brewing in Barley Genomics. <i>Plant Disease</i> , 2000, 84, 1160-1170.	1.4	21
74	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.	2.6	17
75	FINDER: an automated software package to annotate eukaryotic genes from RNA-Seq data and associated protein sequences. <i>BMC Bioinformatics</i> , 2021, 22, 205.	2.6	17
76	Upstream open reading frames of the barley <i>Mla13</i> powdery mildew resistance gene function co-operatively to down-regulate translation. <i>Molecular Plant Pathology</i> , 2006, 7, 167-176.	4.2	16
77	<i>Rf8</i> -Mediated T- <i>urf13</i> Transcript Accumulation Coincides with a Pentatricopeptide Repeat Cluster on Maize Chromosome 2L. <i>Plant Genome</i> , 2011, 4, 283-299.	2.8	15
78	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.	3.6	14
79	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.	3.2	14
80	Genes and Small RNA Transcripts Exhibit Dosage-Dependent Expression Pattern in Maize Copy-Number Alterations. <i>Genetics</i> , 2016, 203, 1133-1147.	2.9	12
81	NGPINT: a next-generation protein-protein interaction software. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	12
82	Linkage of genes conferring specific resistance to oat crown rust in diploid <i>Avena</i> . <i>Genome</i> , 1994, 37, 92-96.	2.0	11
83	Disruption of barley immunity to powdery mildew by an in-frame Lys-Leu deletion in the essential protein SGT1. <i>Genetics</i> , 2021, 217, .	2.9	11
84	Computational Finishing of Large Sequence Contigs Reveals Interspersed Nested Repeats and Gene Islands in the <i>rf1</i> -Associated Region of Maize. <i>Plant Physiology</i> , 2009, 151, 483-495.	4.8	9
85	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.	3.5	7
86	Interchromosomal Transfer of Immune Regulation During Infection of Barley with the Powdery Mildew Pathogen. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3317-3329.	1.8	6
87	Prospects for advancing defense to cereal rusts through genetical genomics. <i>Frontiers in Plant Science</i> , 2013, 4, 117.	3.6	5
88	Genomics of Biotic Interactions in the Triticeae. , 2009, , 559-589.		5
89	TEnest 2.0: Computational Annotation and Visualization of Nested Transposable Elements. <i>Methods in Molecular Biology</i> , 2013, 1057, 305-319.	0.9	4
90	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.	2.6	4

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91	Variation in the ratio of physical to genetic distance in intervals adjacent to the. Molecular Genetics and Genomics, 1996, 251, 472.	2.4	3
92	An interolog-based barley interactome as an integration framework for immune signaling. Genetics, 2022, 221, .	2.9	3
93	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
94	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
95	A Genomic View of Biotic Stress Resistance. Compendium of Plant Genomes, 2018, , 233-257.	0.5	0