

Richard Michelmore

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5990425/publications.pdf>

Version: 2024-02-01

174
papers

23,828
citations

11908

72
h-index

9118

149
g-index

190
all docs

190
docs citations

190
times ranked

17614
citing authors

#	ARTICLE	IF	CITATIONS
1	Ancestral Chromosomes for Family Peronosporaceae Inferred from a Telomere-to-Telomere Genome Assembly of <i>Peronospora effusa</i> . <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 450-463.	1.4	9
2	Viral Load Among Vaccinated and Unvaccinated, Asymptomatic and Symptomatic Persons Infected With the SARS-CoV-2 Delta Variant. <i>Open Forum Infectious Diseases</i> , 2022, 9, ofac135.	0.4	40
3	Variance of allele balance calculated from low coverage sequencing data infers departure from a diploid state. <i>BMC Bioinformatics</i> , 2022, 23, 150.	1.2	1
4	Identification of genetic loci in lettuce mediating quantitative resistance to fungal pathogens. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2481-2500.	1.8	6
5	Identification of Major Quantitative Trait Loci Controlling Field Resistance to Downy Mildew in Cultivated Lettuce (<i>Lactuca sativa</i>). <i>Phytopathology</i> , 2021, 111, 541-547.	1.1	8
6	Genetics of robustness under nitrogen- and water-deficient conditions in field-grown lettuce. <i>Crop Science</i> , 2021, 61, 1582-1619.	0.8	3
7	Identification and mapping of new genes for resistance to downy mildew in lettuce. <i>Theoretical and Applied Genetics</i> , 2021, 134, 519-528.	1.8	11
8	High-resolution genetic dissection of the major QTL for tipburn resistance in lettuce, <i>Lactuca sativa</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	4
9	A Composite Analysis of Flowering Time Regulation in Lettuce. <i>Frontiers in Plant Science</i> , 2021, 12, 632708.	1.7	24
10	Isolating an active and inactive CACTA transposon from lettuce color mutants and characterizing their family. <i>Plant Physiology</i> , 2021, 186, 929-944.	2.3	5
11	Drone phenotyping and machine learning enable discovery of loci regulating daily floral opening in lettuce. <i>Journal of Experimental Botany</i> , 2021, 72, 2979-2994.	2.4	8
12	AFLAP: assembly-free linkage analysis pipeline using k-mers from genome sequencing data. <i>Genome Biology</i> , 2021, 22, 115.	3.8	8
13	Genetics of Partial Resistance Against <i>Verticillium dahliae</i> Race 2 in Wild and Cultivated Lettuce. <i>Phytopathology</i> , 2021, 111, 842-849.	1.1	12
14	The genetic basis of water-use efficiency and yield in lettuce. <i>BMC Plant Biology</i> , 2021, 21, 237.	1.6	8
15	Quantitative Trait Loci and Candidate Genes Associated with Photoperiod Sensitivity in Lettuce (<i>Lactuca</i> spp.). <i>Theoretical and Applied Genetics</i> , 2021, 134, 3473-3487.	1.8	2
16	Hypersensitivity to triforine in lettuce is triggered by a TNL gene through the disease-resistance pathway. <i>Plant Biotechnology Journal</i> , 2021, 19, 2144-2146.	4.1	1
17	<i>Pseudomonas syringae</i> effector HopZ3 suppresses the bacterial AvrPto1-tomato PTO immune complex via acetylation. <i>PLoS Pathogens</i> , 2021, 17, e1010017.	2.1	10
18	Characterization of four polymorphic genes controlling red leaf colour in lettuce that have undergone disruptive selection since domestication. <i>Plant Biotechnology Journal</i> , 2020, 18, 479-490.	4.1	56

#	ARTICLE	IF	CITATIONS
19	Phytopathogen Effectors Use Multiple Mechanisms to Manipulate Plant Autophagy. <i>Cell Host and Microbe</i> , 2020, 28, 558-571.e6.	5.1	28
20	Identification of Factors Affecting the Deterioration Rate of Fresh-Cut Lettuce in Modified Atmosphere Packaging. <i>Food and Bioprocess Technology</i> , 2020, 13, 1997-2011.	2.6	14
21	Upregulation of a <i>KN1</i> homolog by transposon insertion promotes leafy head development in lettuce. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 33668-33678.	3.3	35
22	Genome-Wide Analysis of Cyclophilin Proteins in 21 Oomycetes. <i>Pathogens</i> , 2020, 9, 24.	1.2	3
23	Effector prediction and characterization in the oomycete pathogen <i>Bremia lactucae</i> reveal host-recognized WY domain proteins that lack the canonical RXLR motif. <i>PLoS Pathogens</i> , 2020, 16, e1009012.	2.1	30
24	Title is missing!. , 2020, 16, e1009012.		0
25	Title is missing!. , 2020, 16, e1009012.		0
26	Title is missing!. , 2020, 16, e1009012.		0
27	Title is missing!. , 2020, 16, e1009012.		0
28	The <i>LsVe1L</i> allele provides a molecular marker for resistance to <i>Verticillium dahliae</i> race 1 in lettuce. <i>BMC Plant Biology</i> , 2019, 19, 305.	1.6	13
29	The alternative reality of plant mitochondrial DNA: One ring does not rule them all. <i>PLoS Genetics</i> , 2019, 15, e1008373.	1.5	184
30	Linked-read sequencing of gametes allows efficient genome-wide analysis of meiotic recombination. <i>Nature Communications</i> , 2019, 10, 4310.	5.8	41
31	Genomic signatures of heterokaryosis in the oomycete pathogen <i>Bremia lactucae</i> . <i>Nature Communications</i> , 2019, 10, 2645.	5.8	67
32	The genetics of resistance to lettuce drop (<i>Sclerotinia</i> spp.) in lettuce in a recombinant inbred line population from <i>Reine des Glaces</i> – <i>Eruption</i> . <i>Theoretical and Applied Genetics</i> , 2019, 132, 2439-2460.	1.8	25
33	Genetic architecture of tipburn resistance in lettuce. <i>Theoretical and Applied Genetics</i> , 2019, 132, 2209-2222.	1.8	34
34	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , 2019, 51, 877-884.	9.4	439
35	Genetic analysis of resistance to bacterial leaf spot in the heirloom lettuce cultivar <i>Reine des Glaces</i> . <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	11
36	High-Resolution Analysis of the Efficiency, Heritability, and Editing Outcomes of CRISPR/Cas9-Induced Modifications of <i>NCED4</i> in Lettuce (<i>Lactuca sativa</i>). <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1513-1521.	0.8	83

#	ARTICLE	IF	CITATIONS
37	Molecular markers reliably predict post-harvest deterioration of fresh-cut lettuce in modified atmosphere packaging. <i>Horticulture Research</i> , 2018, 5, 21.	2.9	15
38	Comparative genomics of downy mildews reveals potential adaptations to biotrophy. <i>BMC Genomics</i> , 2018, 19, 851.	1.2	59
39	Genome-wide functional analyses of plant coiled-coil NLR-type pathogen receptors reveal essential roles of their N-terminal domain in oligomerization, networking, and immunity. <i>PLoS Biology</i> , 2018, 16, e2005821.	2.6	52
40	From Short Reads to Chromosome-Scale Genome Assemblies. <i>Methods in Molecular Biology</i> , 2018, 1848, 151-197.	0.4	7
41	Metabolic Reprogramming in Leaf Lettuce Grown Under Different Light Quality and Intensity Conditions Using Narrow-Band LEDs. <i>Scientific Reports</i> , 2018, 8, 7914.	1.6	77
42	Genome assembly with in vitro proximity ligation data and whole-genome triplication in lettuce. <i>Nature Communications</i> , 2017, 8, 14953.	5.8	330
43	Genetics of resistance in lettuce to races 1 and 2 of <i>Verticillium dahliae</i> from different host species. <i>Euphytica</i> , 2017, 213, 1.	0.6	16
44	RNA sequencing provides insights into the evolution of lettuce and the regulation of flavonoid biosynthesis. <i>Nature Communications</i> , 2017, 8, 2264.	5.8	133
45	Genetic Variation for Thermotolerance in Lettuce Seed Germination Is Associated with Temperature-Sensitive Regulation of <i>ETHYLENE RESPONSE FACTOR1</i> (<i>ERF1</i>). <i>Plant Physiology</i> , 2016, 170, 472-488.	2.3	39
46	Detection and Quantification of <i>Bremia lactucae</i> by Spore Trapping and Quantitative PCR. <i>Phytopathology</i> , 2016, 106, 1426-1437.	1.1	39
47	Rationalization of genes for resistance to <i>Bremia lactucae</i> in lettuce. <i>Euphytica</i> , 2016, 210, 309-326.	0.6	80
48	The genome sequences of <i>Arachis duranensis</i> and <i>Arachis ipaensis</i> , the diploid ancestors of cultivated peanut. <i>Nature Genetics</i> , 2016, 48, 438-446.	9.4	761
49	Elucidating the genetic basis of antioxidant status in lettuce (<i>Lactuca sativa</i>). <i>Horticulture Research</i> , 2015, 2, 15055.	2.9	27
50	Genome Sequence and Architecture of the Tobacco Downy Mildew Pathogen <i>Peronospora tabacina</i> . <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 1198-1215.	1.4	70
51	Ultra-High Density, Transcript-Based Genetic Maps of Pepper Define Recombination in the Genome and Synteny Among Related Species. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2341-2355.	0.8	23
52	Host-induced gene silencing inhibits the biotrophic pathogen causing downy mildew of lettuce. <i>Plant Biotechnology Journal</i> , 2015, 13, 875-883.	4.1	116
53	Genome-Wide Architecture of Disease Resistance Genes in Lettuce. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2655-2669.	0.8	54
54	Acetylation of an NB-LRR Plant Immune-Effector Complex Suppresses Immunity. <i>Cell Reports</i> , 2015, 13, 1670-1682.	2.9	78

#	ARTICLE	IF	CITATIONS
55	Dissection of Two Complex Clusters of Resistance Genes in Lettuce (<i>Lactuca sativa</i>). <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 751-765.	1.4	20
56	Wheat rusts never sleep but neither do sequencers: will pathogenomics transform the way plant diseases are managed?. <i>Genome Biology</i> , 2015, 16, 44.	3.8	15
57	Resistance to Downy Mildew in Lettuce "La Brillante"™ is Conferred by <i>Dm50</i> Gene and Multiple QTL. <i>Phytopathology</i> , 2015, 105, 1220-1228.	1.1	20
58	Distinctive profiles of small RNA couple inverted repeat-induced post-transcriptional gene silencing with endogenous RNA silencing pathways in <i>Arabidopsis</i> . <i>Rna</i> , 2014, 20, 1987-1999.	1.6	16
59	A target enrichment method for gathering phylogenetic information from hundreds of loci: An example from the Compositae. <i>Applications in Plant Sciences</i> , 2014, 2, 1300085.	0.8	178
60	Abiotic stress QTL in lettuce crop-wild hybrids: comparing greenhouse and field experiments. <i>Ecology and Evolution</i> , 2014, 4, 2395-2409.	0.8	28
61	Genetic analysis of safflower domestication. <i>BMC Plant Biology</i> , 2014, 14, 43.	1.6	40
62	Differential interactions between strains of <i>Rhizorhapis</i> , <i>Sphingobium</i> , <i>Sphingopyxis</i> or <i>Rhizorhabdus</i> and accessions of <i>Lactuca</i> spp. with respect to severity of corky root disease. <i>Plant Pathology</i> , 2014, 63, 1053-1061.	1.2	10
63	A mixed-model QTL analysis for salt tolerance in seedlings of crop-wild hybrids of lettuce. <i>Molecular Breeding</i> , 2014, 34, 1389-1400.	1.0	10
64	The inheritance of resistance to bacterial leaf spot of lettuce caused by <i>Xanthomonas campestris</i> pv. <i>vitians</i> in three lettuce cultivars. <i>Horticulture Research</i> , 2014, 1, 14066.	2.9	20
65	Strain- and plasmid-level deconvolution of a synthetic metagenome by sequencing proximity ligation products. <i>PeerJ</i> , 2014, 2, e415.	0.9	111
66	An intra-specific linkage map of lettuce (<i>Lactuca sativa</i>) and genetic analysis of postharvest discolouration traits. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2737-2752.	1.8	18
67	Quantitative trait loci associated with tipburn, heat stress-induced physiological disorders, and maturity traits in crisphead lettuce. <i>Theoretical and Applied Genetics</i> , 2013, 126, 3065-3079.	1.8	47
68	RNA-seq based transcriptome analysis of <i>Lactuca sativa</i> infected by the fungal necrotroph <i>Botrytis cinerea</i> . <i>Plant, Cell and Environment</i> , 2013, 36, 1992-2007.	2.8	129
69	Impacts of Resistance Gene Genetics, Function, and Evolution on a Durable Future. <i>Annual Review of Phytopathology</i> , 2013, 51, 291-319.	3.5	131
70	An Ultra-High-Density, Transcript-Based, Genetic Map of Lettuce. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 617-631.	0.8	91
71	Identification of QTLs conferring resistance to downy mildew in legacy cultivars of lettuce. <i>Scientific Reports</i> , 2013, 3, 2875.	1.6	40
72	The Role of TIR-NBS and TIR-X Proteins in Plant Basal Defense Responses. <i>Plant Physiology</i> , 2013, 162, 1459-1472.	2.3	150

#	ARTICLE	IF	CITATIONS
73	Characterization of <i>Capsicum annuum</i> Genetic Diversity and Population Structure Based on Parallel Polymorphism Discovery with a 30K Unigene Pepper GeneChip. <i>PLoS ONE</i> , 2013, 8, e56200.	1.1	99
74	Consequences of Normalizing Transcriptomic and Genomic Libraries of Plant Genomes Using a Duplex-Specific Nuclease and Tetramethylammonium Chloride. <i>PLoS ONE</i> , 2013, 8, e55913.	1.1	37
75	Type III Secretion and Effectors Shape the Survival and Growth Pattern of <i>Pseudomonas syringae</i> on Leaf Surfaces. <i>Plant Physiology</i> , 2012, 158, 1803-1818.	2.3	70
76	Hybridization between crops and wild relatives: the contribution of cultivated lettuce to the vigour of crop-wild hybrids under drought, salinity and nutrient deficiency conditions. <i>Theoretical and Applied Genetics</i> , 2012, 125, 1097-1111.	1.8	23
77	Genomics of Compositae weeds: EST libraries, microarrays, and evidence of introgression. <i>American Journal of Botany</i> , 2012, 99, 209-218.	0.8	80
78	Development and application of a 6.5 million feature Affymetrix Genechip® for massively parallel discovery of single position polymorphisms in lettuce (<i>Lactuca</i> spp.). <i>BMC Genomics</i> , 2012, 13, 185.	1.2	36
79	Advances in <i>Arachis</i> genomics for peanut improvement. <i>Biotechnology Advances</i> , 2012, 30, 639-651.	6.0	258
80	Agroecology: A Review from a Global-Change Perspective. <i>Annual Review of Environment and Resources</i> , 2011, 36, 193-222.	5.6	191
81	Mapping a dominant negative mutation for triforine sensitivity in lettuce and its use as a selectable marker for detecting hybrids. <i>Euphytica</i> , 2011, 182, 157-166.	0.6	14
82	A gene encoding an abscisic acid biosynthetic enzyme (LsNCED4) collocalizes with the high temperature germination locus Htg6.1 in lettuce (<i>Lactuca</i> sp.). <i>Theoretical and Applied Genetics</i> , 2011, 122, 95-108.	1.8	59
83	The inheritance of resistance to <i>Verticillium</i> wilt caused by race 1 isolates of <i>Verticillium dahliae</i> in the lettuce cultivar La Brillante. <i>Theoretical and Applied Genetics</i> , 2011, 123, 509-517.	1.8	93
84	Effective Population Size Is Positively Correlated with Levels of Adaptive Divergence among Annual Sunflowers. <i>Molecular Biology and Evolution</i> , 2011, 28, 1569-1580.	3.5	88
85	Next Generation Sequencing Provides Rapid Access to the Genome of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> , the Causal Agent of Wheat Stripe Rust. <i>PLoS ONE</i> , 2011, 6, e24230.	1.1	169
86	<i>Arabidopsis thaliana</i> Genes Encoding Defense Signaling and Recognition Proteins Exhibit Contrasting Evolutionary Dynamics. <i>Genetics</i> , 2009, 181, 671-684.	1.2	41
87	Proteolysis of a Negative Regulator of Innate Immunity Is Dependent on Resistance Genes in Tomato and <i>Nicotiana benthamiana</i> and Induced by Multiple Bacterial Effectors. <i>Plant Cell</i> , 2009, 21, 2458-2472.	3.1	74
88	<i>Rin4</i> Causes Hybrid Necrosis and Race-Specific Resistance in an Interspecific Lettuce Hybrid. <i>Plant Cell</i> , 2009, 21, 3368-3378.	3.1	146
89	Association mapping and marker-assisted selection of the lettuce dieback resistance gene <i>Tvr1</i> . <i>BMC Plant Biology</i> , 2009, 9, 135.	1.6	47
90	The genomic architecture of disease resistance in lettuce. <i>Theoretical and Applied Genetics</i> , 2009, 118, 565-580.	1.8	66

#	ARTICLE	IF	CITATIONS
91	Development, polymorphism, and cross-taxon utility of ESTâ€‘SSR markers from safflower (<i>Carthamus</i>) Tj ETQq1	1.0, 1.8	784314, 85
92	Comparative Large-Scale Analysis of Interactions between Several Crop Species and the Effector Repertoires from Multiple Pathovars of <i>Pseudomonas</i> and <i>Ralstonia</i> . Plant Physiology, 2009, 150, 1733-1749.	2.3	100
93	Classical and molecular genetics of <i>Bremia lactucae</i> , cause of lettuce downy mildew. European Journal of Plant Pathology, 2008, 122, 19-30.	0.8	50
94	Genetic diversity and genomic distribution of homologs encoding NBS-LRR disease resistance proteins in sunflower. Molecular Genetics and Genomics, 2008, 280, 111-125.	1.0	94
95	Frequent sequence exchanges between homologs of <i>RPP8</i> in <i>Arabidopsis</i> are not necessarily associated with genomic proximity. Plant Journal, 2008, 54, 69-80.	2.8	47
96	Trans-specific gene silencing between host and parasitic plants. Plant Journal, 2008, 56, 389-397.	2.8	143
97	Multiple Paleopolyploidizations during the Evolution of the Compositae Reveal Parallel Patterns of Duplicate Gene Retention after Millions of Years. Molecular Biology and Evolution, 2008, 25, 2445-2455.	3.5	322
98	Evolution and Genetic Population Structure of Prickly Lettuce (<i>Lactuca serriola</i>) and Its RGC2 Resistance Gene Cluster. Genetics, 2008, 178, 1547-1558.	1.2	34
99	Discovery of ADP-Ribosylation and Other Plant Defense Pathway Elements Through Expression Profiling of Four Different <i>Arabidopsis</i> â€‘ <i>Pseudomonas R-avr</i> Interactions. Molecular Plant-Microbe Interactions, 2008, 21, 646-657.	1.4	57
100	Classical and molecular genetics of <i>Bremia lactucae</i> , cause of lettuce downy mildew. , 2008, , 19-30.		1
101	Global eQTL Mapping Reveals the Complex Genetic Architecture of Transcript-Level Variation in <i>Arabidopsis</i> . Genetics, 2007, 175, 1441-1450.	1.2	352
102	QTLs for shelf life in lettuce co-locate with those for leaf biophysical properties but not with those for leaf developmental traits. Journal of Experimental Botany, 2007, 58, 1433-1449.	2.4	44
103	Natural Variation among <i>Arabidopsis thaliana</i> Accessions for Transcriptome Response to Exogenous Salicylic Acid. Plant Cell, 2007, 19, 2099-2110.	3.1	101
104	Natural Variation in the Pto Disease Resistance Gene Within Species of Wild Tomato (<i>Lycopersicon</i>). II. Population Genetics of Pto. Genetics, 2007, 175, 1307-1319.	1.2	77
105	Silencing of the major family of NBS-LRR-encoding genes in lettuce results in the loss of multiple resistance specificities. Plant Journal, 2007, 51, 803-818.	2.8	109
106	Global expression analysis of nucleotide binding site-leucine rich repeat-encoding and related genes in <i>Arabidopsis</i> . BMC Plant Biology, 2007, 7, 56.	1.6	166
107	A high-density, integrated genetic linkage map of lettuce (<i>Lactuca</i> spp.). Theoretical and Applied Genetics, 2007, 115, 735-46.	1.8	97
108	Plant NBS-LRR proteins: adaptable guards. Genome Biology, 2006, 7, 212.	13.9	804

#	ARTICLE	IF	CITATIONS
109	Analyses of Synteny Between <i>Arabidopsis thaliana</i> and Species in the Asteraceae Reveal a Complex Network of Small Syntenic Segments and Major Chromosomal Rearrangements. <i>Genetics</i> , 2006, 173, 2227-2235.	1.2	29
110	The disease resistance gene <i>Dm3</i> is infrequent in natural populations of <i>Lactuca serriola</i> due to deletions and frequent gene conversions at the <i>RGC2</i> locus. <i>Plant Journal</i> , 2006, 47, 38-48.	2.8	34
111	Identification and comparison of natural rubber from two <i>Lactuca</i> species. <i>Phytochemistry</i> , 2006, 67, 2590-2596.	1.4	59
112	High-density haplotyping with microarray-based expression and single feature polymorphism markers in <i>Arabidopsis</i> . <i>Genome Research</i> , 2006, 16, 787-795.	2.4	179
113	Genomic Survey of Gene Expression Diversity in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2006, 172, 1179-1189.	1.2	104
114	Optimization of <i>Agrobacterium</i> -mediated transient assays of gene expression in lettuce, tomato and <i>Arabidopsis</i> . <i>Plant Biotechnology Journal</i> , 2005, 3, 259-273.	4.1	487
115	Quantitative trait loci associated with seed and seedling traits in <i>Lactuca</i> . <i>Theoretical and Applied Genetics</i> , 2005, 111, 1365-1376.	1.8	81
116	Functional Analysis of the Plant Disease Resistance Gene <i>Pto</i> Using DNA Shuffling. <i>Journal of Biological Chemistry</i> , 2005, 280, 23073-23083.	1.6	20
117	Multiple Genetic Processes Result in Heterogeneous Rates of Evolution within the Major Cluster Disease Resistance Genes in Lettuce [W]. <i>Plant Cell</i> , 2004, 16, 2870-2894.	3.1	276
118	The Maintenance of Extreme Amino Acid Diversity at the Disease Resistance Gene, <i>RPP13</i> , in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2004, 166, 1517-1527.	1.2	240
119	Insensitivity to the Fungicide Fosetyl-Aluminum in California Isolates of the Lettuce Downy Mildew Pathogen, <i>Bremia lactucae</i> . <i>Plant Disease</i> , 2004, 88, 502-508.	0.7	76
120	The impact zone: genomics and breeding for durable disease resistance. <i>Current Opinion in Plant Biology</i> , 2003, 6, 397-404.	3.5	78
121	A genetic map of the lettuce downy mildew pathogen, <i>Bremia lactucae</i> , constructed from molecular markers and avirulence genes. <i>Fungal Genetics and Biology</i> , 2003, 39, 16-30.	0.9	30
122	SNP-based codominant markers for a recessive gene conferring resistance to corky root rot (<i>Rhizomonas suberifaciens</i>) in lettuce (<i>Lactuca sativa</i>). <i>Genome</i> , 2003, 46, 1059-1069.	0.9	23
123	Genome-Wide Analysis of NBS-LRR-Encoding Genes in <i>Arabidopsis</i> [W]. <i>Plant Cell</i> , 2003, 15, 809-834.	3.1	1,457
124	Patterns of Positive Selection in the Complete NBS-LRR Gene Family of <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2002, 12, 1305-1315.	2.4	278
125	<i>Dm3</i> Is One Member of a Large Constitutively Expressed Family of Nucleotide Binding Site-Leucine-Rich Repeat Encoding Genes. <i>Molecular Plant-Microbe Interactions</i> , 2002, 15, 251-261.	1.4	83
126	Functional Analyses of the <i>Pto</i> Resistance Gene Family in Tomato and the Identification of a Minor Resistance Determinant in a Susceptible Haplotype. <i>Molecular Plant-Microbe Interactions</i> , 2002, 15, 281-291.	1.4	64

#	ARTICLE	IF	CITATIONS
127	TIR-X and TIR-NBS proteins: two new families related to disease resistance TIR-NBS-LRR proteins encoded in Arabidopsis and other plant genomes. <i>Plant Journal</i> , 2002, 32, 77-92.	2.8	241
128	Functional Studies of the Bacterial Avirulence Protein AvrPto by Mutational Analysis. <i>Molecular Plant-Microbe Interactions</i> , 2001, 14, 451-459.	1.4	29
129	Recombination and Spontaneous Mutation at the Major Cluster of Resistance Genes in Lettuce (<i>Lactuca sativa</i>). <i>Genetics</i> , 2001, 157, 831-849.	1.2	88
130	avrPto Enhances Growth and Necrosis Caused by <i>Pseudomonas syringae</i> pv. tomato in Tomato Lines Lacking Either Pto or Prf. <i>Molecular Plant-Microbe Interactions</i> , 2000, 13, 568-571.	1.4	81
131	Genomic approaches to plant disease resistance. <i>Current Opinion in Plant Biology</i> , 2000, 3, 125-131.	3.5	83
132	Lettuce, a shallow-rooted crop, and <i>Lactuca serriola</i> , its wild progenitor, differ at QTL determining root architecture and deep soil water exploitation. <i>Theoretical and Applied Genetics</i> , 2000, 101, 1066-1073.	1.8	124
133	Mapping morphological genes relative to molecular markers in lettuce (<i>Lactuca sativa</i> L.). <i>Heredity</i> , 1999, 82, 245-251.	1.2	30
134	Constitutively active Pto induces a Prf-dependent hypersensitive response in the absence of AvrPto. <i>EMBO Journal</i> , 1999, 18, 3232-3240.	3.5	140
135	Molecular diversity at the major cluster of disease resistance genes in cultivated and wild <i>Lactuca</i> spp.. <i>Theoretical and Applied Genetics</i> , 1999, 99, 405-418.	1.8	56
136	Identification of PCR-based markers flanking the recessive LMV resistance gene mo1 in an intraspecific cross in lettuce. <i>Genome</i> , 1999, 42, 982-986.	0.9	11
137	Plant disease resistance genes encode members of an ancient and diverse protein family within the nucleotide-binding superfamily. <i>Plant Journal</i> , 1999, 20, 317-332.	2.8	729
138	The Major Resistance Gene Cluster in Lettuce Is Highly Duplicated and Spans Several Megabases. <i>Plant Cell</i> , 1998, 10, 1817-1832.	3.1	290
139	Clusters of Resistance Genes in Plants Evolve by Divergent Selection and a Birth-and-Death Process. <i>Genome Research</i> , 1998, 8, 1113-1130.	2.4	942
140	Resistance Gene Candidates Identified by PCR with Degenerate Oligonucleotide Primers Map to Clusters of Resistance Genes in Lettuce. <i>Molecular Plant-Microbe Interactions</i> , 1998, 11, 815-823.	1.4	213
141	Receptor-like Genes in the Major Resistance Locus of Lettuce Are Subject to Divergent Selection. <i>Plant Cell</i> , 1998, 10, 1833-1846.	3.1	288
142	The Major Resistance Gene Cluster in Lettuce Is Highly Duplicated and Spans Several Megabases. <i>Plant Cell</i> , 1998, 10, 1817.	3.1	29
143	Receptor-Like Genes in the Major Resistance Locus of Lettuce Are Subject to Divergent Selection. <i>Plant Cell</i> , 1998, 10, 1833.	3.1	15
144	A Transgenic Mutant of <i>Lactuca sativa</i> (Lettuce) with a T-DNA Tightly Linked to Loss of Downy Mildew Resistance. <i>Molecular Plant-Microbe Interactions</i> , 1997, 10, 970-977.	1.4	24

#	ARTICLE	IF	CITATIONS
145	Construction of a bacterial artificial chromosome library containing large Eco RI and Hin dIII genomic fragments of lettuce. <i>Theoretical and Applied Genetics</i> , 1997, 94, 390-399.	1.8	118
146	Molecular Basis of Gene-for-Gene Specificity in Bacterial Speck Disease of Tomato. <i>Science</i> , 1996, 274, 2063-2065.	6.0	532
147	Molecular analysis of irradiation-induced and spontaneous deletion mutants at a disease resistance locus in <i>Lactuca sativa</i> . <i>Molecular Genetics and Genomics</i> , 1996, 251, 316-325.	2.4	22
148	Flood warning "resistance genes unleashed. <i>Nature Genetics</i> , 1996, 14, 376-378.	9.4	21
149	Sources and genetic structure of a cluster of genes for resistance to three pathogens in lettuce. <i>Theoretical and Applied Genetics</i> , 1995, 91, 178-188.	1.8	82
150	Rapid mapping of two genes for resistance to downy mildew from <i>Lactuca serriola</i> to existing clusters of resistance genes. <i>Theoretical and Applied Genetics</i> , 1994, 89, 96-104.	1.8	71
151	Analysis of a detailed genetic linkage map of <i>Lactuca sativa</i> (lettuce) constructed from RFLP and RAPD markers. <i>Genetics</i> , 1994, 136, 1435-1446.	1.2	175
152	Mutants of downy mildew resistance in <i>Lactuca sativa</i> (lettuce). <i>Genetics</i> , 1994, 137, 867-874.	1.2	23
153	Development of reliable PCR-based markers linked to downy mildew resistance genes in lettuce. <i>Theoretical and Applied Genetics</i> , 1993, 85, 985-993.	1.8	1,169
154	Two Classes of Chromosome-Sized Molecules Are Present in <i>Bremia lactucae</i> . <i>Experimental Mycology</i> , 1993, 17, 284-300.	1.8	31
155	Expression and antisense inhibition of transgenes in <i>Phytophthora infestans</i> is modulated by choice of promoter and position effects. <i>Gene</i> , 1993, 133, 63-69.	1.0	58
156	Temperature and genotype interactions in the expression of host resistance in lettuce downy mildew. <i>Physiological and Molecular Plant Pathology</i> , 1992, 40, 233-245.	1.3	29
157	Regulatory sequences for expressing genes in oomycete fungi. <i>Molecular Genetics and Genomics</i> , 1992, 234, 138-146.	2.4	60
158	Identification of restriction fragment length polymorphism and random amplified polymorphic DNA markers linked to downy mildew resistance genes in lettuce, using near-isogenic lines. <i>Genome</i> , 1991, 34, 1021-1027.	0.9	203
159	Transient expression of genes in the oomycete <i>Phytophthora infestans</i> using <i>Bremia lactucae</i> regulatory sequences. <i>Current Genetics</i> , 1991, 19, 453-459.	0.8	45
160	Variation at RFLP loci in <i>Lactuca</i> spp. and origin of cultivated lettuce (<i>L. sativa</i>). <i>Genome</i> , 1991, 34, 430-436.	0.9	123
161	Identification of markers linked to disease-resistance genes by bulked segregant analysis: a rapid method to detect markers in specific genomic regions by using segregating populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991, 88, 9828-9832.	3.3	4,074
162	Transformation of the Oomycete Pathogen, <i>Phytophthora infestans</i> . <i>Molecular Plant-Microbe Interactions</i> , 1991, 4, 602.	1.4	167

#	ARTICLE	IF	CITATIONS
163	Genome size and complexity of the obligate fungal pathogen, <i>Bremia lactucae</i> . <i>Experimental Mycology</i> , 1990, 14, 299-309.	1.8	37
164	Highly Abundant and Stage-Specific mRNAs in the Obligate Pathogen <i>Bremia lactucae</i> . <i>Molecular Plant-Microbe Interactions</i> , 1990, 3, 225.	1.4	25
165	Structure and expression of a gene encoding heat-shock protein Hsp70 from the Oomycete fungus <i>Bremia lactucae</i> . <i>Gene</i> , 1989, 79, 207-217.	1.0	41
166	Genetic analysis of the fungus, <i>Bremia lactucae</i> , using restriction fragment length polymorphisms.. <i>Genetics</i> , 1988, 120, 947-958.	1.2	246
167	Molecular Markers for Genetic Analysis of Phytopathogenic Fungi. <i>Annual Review of Phytopathology</i> , 1987, 25, 383-404.	3.5	139
168	Comparison of restriction endonucleases and sources of probes for their efficiency in detecting restriction fragment length polymorphisms in lettuce (<i>Lactuca sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 1987, 74, 646-653.	1.8	96
169	Resistance in <i>Lactuca</i> spp. to <i>Microdochium panattoniana</i> (lettuce anthracnose). <i>Euphytica</i> , 1987, 36, 609-614.	0.6	12
170	Genetic analysis of factors for resistance to downy mildew (<i>Bremia lactucae</i>) in species of lettuce (<i>Lactuca sativa</i> and <i>L. serriola</i>). <i>Plant Pathology</i> , 1987, 36, 499-514.	1.2	102
171	A Genetic Map of Lettuce (<i>Lactuca sativa</i> L.) With Restriction Fragment Length Polymorphism, Isozyme, Disease Resistance and Morphological Markers. <i>Genetics</i> , 1987, 116, 331-337.	1.2	244
172	Linkage analysis of genes for resistance to downy mildew (<i>Bremia lactucae</i>) in lettuce (<i>Lactuca sativa</i>). <i>Theoretical and Applied Genetics</i> , 1985, 70, 520-528.	1.8	78
173	The inheritance of virulence in <i>Bremia lactucae</i> to match resistance factors 3, 4, 5, 6, 8, 9, 10 and 11 in lettuce (<i>Lactuca sativa</i>). <i>Plant Pathology</i> , 1984, 33, 301-315.	1.2	47
174	Nucleation rates of ice in undercooled water and aqueous solutions of polyethylene glycol. <i>Cryobiology</i> , 1982, 19, 163-171.	0.3	75