

Kim E Hammond-Kosack

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7036827/publications.pdf>

Version: 2024-02-01

129
papers

18,278
citations

28274

55
h-index

14759

127
g-index

134
all docs

134
docs citations

134
times ranked

16286
citing authors

#	ARTICLE	IF	CITATIONS
1	WAKsing plant immunity, waning diseases. <i>Journal of Experimental Botany</i> , 2022, 73, 22-37.	4.8	23
2	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. <i>Nucleic Acids Research</i> , 2022, 50, D996-D1003.	14.5	141
3	PHI-base in 2022: a multi-species phenotype database for Pathogen–Host Interactions. <i>Nucleic Acids Research</i> , 2022, 50, D837-D847.	14.5	53
4	Phylogenomic Analysis of a 55.1-kb 19-Gene Dataset Resolves a Monophyletic <i>Fusarium</i> that Includes the <i>Fusarium solani</i> Species Complex. <i>Phytopathology</i> , 2021, 111, 1064-1079.	2.2	107
5	The vesicular trafficking system component MIN7 is required for minimizing <i>Fusarium graminearum</i> infection. <i>Journal of Experimental Botany</i> , 2021, 72, 5010-5023.	4.8	7
6	Identifying aphid resistance in the ancestral wheat <i>Triticum monococcum</i> under field conditions. <i>Scientific Reports</i> , 2021, 11, 13495.	3.3	11
7	Take-All Disease: New Insights into an Important Wheat Root Pathogen. <i>Trends in Plant Science</i> , 2021, 26, 836-848.	8.8	20
8	Exploring the diversity of promoter and 5′UTR sequences in ancestral, historic and modern wheat. <i>Plant Biotechnology Journal</i> , 2021, 19, 2469-2487.	8.3	4
9	PHI-base: the pathogen–host interactions database. <i>Nucleic Acids Research</i> , 2020, 48, D613-D620.	14.5	145
10	Ensembl Genomes 2020—enabling non-vertebrate genomic research. <i>Nucleic Acids Research</i> , 2020, 48, D689-D695.	14.5	416
11	Proteinaceous effector discovery and characterization in filamentous plant pathogens. <i>Molecular Plant Pathology</i> , 2020, 21, 1353-1376.	4.2	41
12	Functional evaluation of a homologue of plant rapid alkalisation factor (RALF) peptides in <i>Fusarium graminearum</i> . <i>Fungal Biology</i> , 2020, 124, 753-765.	2.5	19
13	Genome Sequence of <i>Fusarium graminearum</i> Strain CML3066, Isolated from a Wheat Spike in Southern Brazil. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
14	sRNA Profiling Combined With Gene Function Analysis Reveals a Lack of Evidence for Cross-Kingdom RNAi in the Wheat – <i>Zymoseptoria tritici</i> Pathosystem. <i>Frontiers in Plant Science</i> , 2019, 10, 892.	3.6	51
15	Non-canonical fungal G-protein coupled receptors promote <i>Fusarium</i> head blight on wheat. <i>PLoS Pathogens</i> , 2019, 15, e1007666.	4.7	34
16	PHI-Nets: A Network Resource for Ascomycete Fungal Pathogens to Annotate and Identify Putative Virulence Interacting Proteins and siRNA Targets. <i>Frontiers in Microbiology</i> , 2019, 10, 2721.	3.5	8
17	Saving plants from disease. , 2019, , .		0
18	Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. <i>Nucleic Acids Research</i> , 2018, 46, D802-D808.	14.5	489

#	ARTICLE	IF	CITATIONS
19	Elite UK winter wheat cultivars differ in their ability to support the colonization of beneficial root-infecting fungi. <i>Journal of Experimental Botany</i> , 2018, 69, 3103-3115.	4.8	10
20	Sharing mutants and experimental information prepublication using FgMutantDb (https://scabusa.org/FgMutantDb). <i>Fungal Genetics and Biology</i> , 2018, 115, 90-93.	2.1	15
21	Wheat receptor-kinase-like protein Stb6 controls gene-for-gene resistance to fungal pathogen <i>Zymoseptoria tritici</i> . <i>Nature Genetics</i> , 2018, 50, 368-374.	21.4	215
22	Inter-genome comparison of the Quorn fungus <i>Fusarium venenatum</i> and the closely related plant infecting pathogen <i>Fusarium graminearum</i> . <i>BMC Genomics</i> , 2018, 19, 269.	2.8	28
23	A review of wheat diseases—a field perspective. <i>Molecular Plant Pathology</i> , 2018, 19, 1523-1536.	4.2	375
24	RNAi as an emerging approach to control <i>Fusarium</i> head blight disease and mycotoxin contamination in cereals. <i>Pest Management Science</i> , 2018, 74, 790-799.	3.4	103
25	Phosphopantetheinyl transferase (Ppt)-mediated biosynthesis of lysine, but not siderophores or DHN melanin, is required for virulence of <i>Zymoseptoria tritici</i> on wheat. <i>Scientific Reports</i> , 2018, 8, 17069.	3.3	9
26	Exploring the resilience of wheat crops grown in short rotations through minimising the build-up of an important soil-borne fungal pathogen. <i>Scientific Reports</i> , 2018, 8, 9550.	3.3	12
27	The adaptation of <i>Fusarium culmorum</i> to DMI Fungicides Is Mediated by Major Transcriptome Modifications in Response to Azole Fungicide, Including the Overexpression of a PDR Transporter (FcABC1). <i>Frontiers in Microbiology</i> , 2018, 9, 1385.	3.5	50
28	<i>Foxtail mosaic virus</i> : A Viral Vector for Protein Expression in Cereals. <i>Plant Physiology</i> , 2018, 177, 1352-1367.	4.8	85
29	PHI-base: a new interface and further additions for the multi-species pathogen–host interactions database. <i>Nucleic Acids Research</i> , 2017, 45, D604-D610.	14.5	231
30	Annotation of <i>Fusarium graminearum</i> (PH-1) Version 5.0. <i>Genome Announcements</i> , 2017, 5, .	0.8	18
31	A spatial temporal analysis of the <i>Fusarium graminearum</i> transcriptome during symptomless and symptomatic wheat infection. <i>Molecular Plant Pathology</i> , 2017, 18, 1295-1312.	4.2	64
32	CRISPR-based powdery mildew resistance in hexaploid bread wheat generated by a non-transgenic TILLING approach. <i>Plant Biotechnology Journal</i> , 2017, 15, 367-378.	8.3	163
33	The Complete Genome Sequence of the Phytopathogenic Fungus <i>Sclerotinia sclerotiorum</i> Reveals Insights into the Genome Architecture of Broad Host Range Pathogens. <i>Genome Biology and Evolution</i> , 2017, 9, 593-618.	2.5	187
34	A conserved fungal glycosyltransferase facilitates pathogenesis of plants by enabling hyphal growth on solid surfaces. <i>PLoS Pathogens</i> , 2017, 13, e1006672.	4.7	54
35	The genome of the emerging barley pathogen <i>Ramularia collo-cygni</i> . <i>BMC Genomics</i> , 2016, 17, 584.	2.8	36
36	Publishing FAIR Data: An Exemplar Methodology Utilizing PHI-Base. <i>Frontiers in Plant Science</i> , 2016, 7, 641.	3.6	25

#	ARTICLE	IF	CITATIONS
37	First Draft Genome Sequence of a UK Strain (UK99) of <i>Fusarium culmorum</i> . Genome Announcements, 2016, 4, .	0.8	27
38	GPCRs from fusarium graminearum detection, modeling and virtual screening - the search for new routes to control head blight disease. BMC Bioinformatics, 2016, 17, 463.	2.6	7
39	Pseudomonas spp. diversity is negatively associated with suppression of the wheat take-all pathogen. Scientific Reports, 2016, 6, 29905.	3.3	46
40	PhytoPath: an integrative resource for plant pathogen genomics. Nucleic Acids Research, 2016, 44, D688-D693.	14.5	42
41	The trans-kingdom identification of negative regulators of pathogen hypervirulence. FEMS Microbiology Reviews, 2016, 40, 19-40.	8.6	16
42	Searching for Novel Targets to Control Wheat Head Blight Disease—Protein Identification, 3D Modeling and Virtual Screening. Advances in Microbiology, 2016, 06, 811-830.	0.6	3
43	An analysis of <i>Pseudomonas</i> genomic diversity in take-all infected wheat fields reveals the lasting impact of wheat cultivars on the soil microbiota. Environmental Microbiology, 2015, 17, 4764-4778.	3.8	48
44	Using the pathogen-host interactions database (PHI-base) to investigate plant pathogen genomes and genes implicated in virulence. Frontiers in Plant Science, 2015, 6, 605.	3.6	31
45	Functional analysis of a wheat homeodomain protein, <i>TaR1</i> , reveals that host chromatin remodelling influences the dynamics of the switch to necrotrophic growth in the phytopathogenic fungus <i>Zymoseptoria tritici</i> . New Phytologist, 2015, 206, 598-605.	7.3	16
46	Transcriptome and Metabolite Profiling of the Infection Cycle of <i>Zymoseptoria tritici</i> on Wheat Reveals a Biphasic Interaction with Plant Immunity Involving Differential Pathogen Chromosomal Contributions and a Variation on the Hemibiotrophic Lifestyle Definition. Plant Physiology, 2015, 167, 1158-1185.	4.8	301
47	Analysis of cytochrome b5 reductase-mediated metabolism in the phytopathogenic fungus <i>Zymoseptoria tritici</i> reveals novel functionalities implicated in virulence. Fungal Genetics and Biology, 2015, 82, 69-84.	2.1	21
48	In Planta Transient Expression Systems for Monocots. , 2015, , 391-422.		8
49	Whole-genome analysis of <i>Fusarium graminearum</i> insertional mutants identifies virulence associated genes and unmasking untagged chromosomal deletions. BMC Genomics, 2015, 16, 261.	2.8	18
50	Host to a Stranger: Arabidopsis and <i>Fusarium</i> Ear Blight. Trends in Plant Science, 2015, 20, 651-663.	8.8	17
51	The completed genome sequence of the pathogenic ascomycete fungus <i>Fusarium graminearum</i> . BMC Genomics, 2015, 16, 544.	2.8	190
52	The Pathogen-Host Interactions database (PHI-base): additions and future developments. Nucleic Acids Research, 2015, 43, D645-D655.	14.5	202
53	Deregulation of Plant Cell Death Through Disruption of Chloroplast Functionality Affects Asexual Sporulation of <i>Zymoseptoria tritici</i> on Wheat. Molecular Plant-Microbe Interactions, 2015, 28, 590-604.	2.6	27
54	An Interspecies Comparative Analysis of the Predicted Secretomes of the Necrotrophic Plant Pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . PLoS ONE, 2015, 10, e0130534.	2.5	72

#	ARTICLE	IF	CITATIONS
55	Mutations in the Arabidopsis homoserine kinase gene DMR1 confer enhanced resistance to <i>Fusarium culmorum</i> and <i>F. graminearum</i> . <i>BMC Plant Biology</i> , 2014, 14, 317.	3.6	19
56	<i>Mycosphaerella graminicola</i> LysM Effector-Mediated Stealth Pathogenesis Subverts Recognition Through Both CERK1 and CEBiP Homologues in Wheat. <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 236-243.	2.6	152
57	Identifying variation in resistance to the take-all fungus, <i>Gaeumannomyces graminis</i> var. <i>tritici</i> , between different ancestral and modern wheat species. <i>BMC Plant Biology</i> , 2014, 14, 212.	3.6	26
58	Genomic clustering and co-regulation of transcriptional networks in the pathogenic fungus <i>Fusarium graminearum</i> . <i>BMC Systems Biology</i> , 2013, 7, 52.	3.0	29
59	Exploitation of genomics in fungicide research: current status and future perspectives. <i>Molecular Plant Pathology</i> , 2013, 14, 197-210.	4.2	61
60	One Fungus, One Name: Defining the Genus <i>Fusarium</i> in a Scientifically Robust Way That Preserves Longstanding Use. <i>Phytopathology</i> , 2013, 103, 400-408.	2.2	219
61	Characterization of the sterol 14 α -demethylases of <i>Fusarium graminearum</i> identifies a novel genus-specific CYP51 function. <i>New Phytologist</i> , 2013, 198, 821-835.	7.3	146
62	Network-Based Data Integration for Selecting Candidate Virulence Associated Proteins in the Cereal Infecting Fungus <i>Fusarium graminearum</i> . <i>PLoS ONE</i> , 2013, 8, e67926.	2.5	18
63	FcStuA from <i>Fusarium culmorum</i> Controls Wheat Foot and Root Rot in a Toxin Dispensable Manner. <i>PLoS ONE</i> , 2013, 8, e57429.	2.5	41
64	<i>Barley Stripe Mosaic Virus</i> Mediated Tools for Investigating Gene Function in Cereal Plants and Their Pathogens: Virus-Induced Gene Silencing, Host-Mediated Gene Silencing, and Virus-Mediated Overexpression of Heterologous Protein. <i>Plant Physiology</i> , 2012, 160, 582-590.	4.8	161
65	Shouldn't enantiomeric purity be included in the 'minimum information about a bioactive entity? Response from the MIABE group. <i>Nature Reviews Drug Discovery</i> , 2012, 11, 730-730.	46.4	0
66	The Induction of Mycotoxins by Trichothecene Producing <i>Fusarium</i> Species. <i>Methods in Molecular Biology</i> , 2012, 835, 439-455.	0.9	10
67	Defining the Predicted Protein Secretome of the Fungal Wheat Leaf Pathogen <i>Mycosphaerella graminicola</i> . <i>PLoS ONE</i> , 2012, 7, e49904.	2.5	73
68	The <i>velvet</i> gene, <i>FgVe1</i> , affects fungal development and positively regulates trichothecene biosynthesis and pathogenicity in <i>Fusarium graminearum</i> . <i>Molecular Plant Pathology</i> , 2012, 13, 363-374.	4.2	95
69	The Top 10 fungal pathogens in molecular plant pathology. <i>Molecular Plant Pathology</i> , 2012, 13, 414-430.	4.2	3,270
70	Detection of Multi-clustered Genes and Community Structure for the Plant Pathogenic Fungus <i>Fusarium graminearum</i> . <i>Lecture Notes in Computer Science</i> , 2012, , 69-86.	1.3	8
71	The Top 10 fungal pathogens in molecular plant pathology. <i>Molecular Plant Pathology</i> , 2012, , no-no.	4.2	22
72	The Predicted Secretome of the Plant Pathogenic Fungus <i>Fusarium graminearum</i> : A Refined Comparative Analysis. <i>PLoS ONE</i> , 2012, 7, e33731.	2.5	161

#	ARTICLE	IF	CITATIONS
73	Minimum information about a bioactive entity (MIABE). <i>Nature Reviews Drug Discovery</i> , 2011, 10, 661-669.	46.4	80
74	The complex interactions between host immunity and non-biotrophic fungal pathogens of wheat leaves. <i>Journal of Plant Physiology</i> , 2011, 168, 63-71.	3.5	56
75	Inactivation of plant infecting fungal and viral pathogens to achieve biological containment in drainage water using UV treatment. <i>Journal of Applied Microbiology</i> , 2011, 110, 675-687.	3.1	7
76	Evidence that wheat cultivars differ in their ability to build up inoculum of the take-all fungus, <i>Gaeumannomyces graminis</i> var. <i>tritici</i> , under a first wheat crop. <i>Plant Pathology</i> , 2011, 60, 200-206.	2.4	23
77	An exceptionally high nucleotide and haplotype diversity and a signature of positive selection for the <i>elf4E</i> resistance gene in barley are revealed by allele mining and phylogenetic analyses of natural populations. <i>Molecular Ecology</i> , 2011, 20, no-no.	3.9	48
78	Aberrant protein N-glycosylation impacts upon infection-related growth transitions of the haploid plant pathogenic fungus <i>Mycosphaerella graminicola</i> . <i>Molecular Microbiology</i> , 2011, 81, 415-433.	2.5	60
79	OmniMapFree: A unified tool to visualise and explore sequenced genomes. <i>BMC Bioinformatics</i> , 2011, 12, 447.	2.6	11
80	Characterisation of the <i>Fusarium graminearum</i> -Wheat Floral Interaction. <i>Journal of Pathogens</i> , 2011, 2011, 1-9.	1.4	40
81	Analysis of Two in Planta Expressed LysM Effector Homologs from the Fungus <i>Mycosphaerella graminicola</i> Reveals Novel Functional Properties and Varying Contributions to Virulence on Wheat. <i>Plant Physiology</i> , 2011, 156, 756-769.	4.8	333
82	Finished Genome of the Fungal Wheat Pathogen <i>Mycosphaerella graminicola</i> Reveals Dispensome Structure, Chromosome Plasticity, and Stealth Pathogenesis. <i>PLoS Genetics</i> , 2011, 7, e1002070.	3.5	532
83	A Combined ¹ H Nuclear Magnetic Resonance and Electrospray Ionization-Mass Spectrometry Analysis to Understand the Basal Metabolism of Plant-Pathogenic <i>Fusarium</i> spp.. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 1605-1618.	2.6	26
84	A Partial Chromosomal Deletion Caused by Random Plasmid Integration Resulted in a Reduced Virulence Phenotype in <i>Fusarium graminearum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 1083-1096.	2.6	13
85	A Role for Topoisomerase I in <i>Fusarium graminearum</i> and <i>F. culmorum</i> Pathogenesis and Sporulation. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 566-577.	2.6	44
86	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	27.8	1,442
87	The infection biology of <i>Fusarium graminearum</i> : Defining the pathways of spikelet to spikelet colonisation in wheat ears. <i>Fungal Biology</i> , 2010, 114, 555-571.	2.5	184
88	Identification and characterisation of <i>Mycosphaerella graminicola</i> secreted or surface-associated proteins with variable intragenic coding repeats. <i>Fungal Genetics and Biology</i> , 2010, 47, 19-32.	2.1	39
89	DArT markers: diversity analyses, genomes comparison, mapping and integration with SSR markers in <i>Triticum monococcum</i> . <i>BMC Genomics</i> , 2009, 10, 458.	2.8	55
90	High-resolution melting analysis of cDNA-derived PCR amplicons for rapid and cost-effective identification of novel alleles in barley. <i>Theoretical and Applied Genetics</i> , 2009, 119, 851-865.	3.6	63

#	ARTICLE	IF	CITATIONS
91	Lack of the plant signalling component SGT1b enhances disease resistance to <i>Fusarium culmorum</i> in Arabidopsis buds and flowers. <i>New Phytologist</i> , 2009, 181, 901-912.	7.3	27
92	Characterization of Two Unusual Features of Resistance to Soilborne cereal mosaic virus in Hexaploid Wheat: Leakiness and Gradual Elimination of Viral Coat Protein from Infected Root Tissues. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 560-574.	2.6	6
93	Molecular Characterization and Functional Analysis of MgNLP, the Sole NPP1 Domain-Containing Protein, from the Fungal Wheat Leaf Pathogen <i>Mycosphaerella graminicola</i> . <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 790-799.	2.6	151
94	<i>Fusarium graminearum</i> gene deletion mutants <i>map1</i> and <i>tri5</i> reveal similarities and differences in the pathogenicity requirements to cause disease on Arabidopsis and wheat floral tissue. <i>New Phytologist</i> , 2008, 177, 990-1000.	7.3	87
95	Phenotypic and genetic analysis of the <i>Triticum monococcum</i> <i>Mycosphaerella graminicola</i> interaction. <i>New Phytologist</i> , 2008, 179, 1121-1132.	7.3	28
96	NPR1 and EDS11 contribute to host resistance against <i>Fusarium culmorum</i> in Arabidopsis buds and flowers. <i>Molecular Plant Pathology</i> , 2008, 9, 697-704.	4.2	23
97	Plant resistance signalling hijacked by a necrotrophic fungal pathogen. <i>Plant Signaling and Behavior</i> , 2008, 3, 993-995.	2.4	67
98	The Wheat Mitogen-Activated Protein Kinases TaMPK3 and TaMPK6 Are Differentially Regulated at Multiple Levels during Compatible Disease Interactions with <i>Mycosphaerella graminicola</i> . <i>Plant Physiology</i> , 2008, 147, 802-815.	4.8	112
99	Identification and Characterization of a Novel Efficient Resistance Response to the Furoviruses SBWMV and SBCMV in Barley. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 1193-1204.	2.6	10
100	Identification of variation in adaptively important traits and genome-wide analysis of trait-marker associations in <i>Triticum monococcum</i> . <i>Journal of Experimental Botany</i> , 2007, 58, 3749-3764.	4.8	39
101	PHI-base update: additions to the pathogen host interaction database. <i>Nucleic Acids Research</i> , 2007, 36, D572-D576.	14.5	143
102	The <i>Fusarium graminearum</i> Genome Reveals a Link Between Localized Polymorphism and Pathogen Specialization. <i>Science</i> , 2007, 317, 1400-1402.	12.6	837
103	Transcriptional Adaptation of <i>Mycosphaerella graminicola</i> to Programmed Cell Death (PCD) of Its Susceptible Wheat Host. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 178-193.	2.6	202
104	The Pathogen-Host Interactions Database (PHI-base) Provides Insights into Generic and Novel Themes of Pathogenicity. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1451-1462.	2.6	68
105	Dominant-negative interference with defence signalling by truncation mutations of the tomato Cf9 disease resistance gene. <i>Plant Journal</i> , 2006, 46, 385-399.	5.7	6
106	PHI-base: a new database for pathogen host interactions. <i>Nucleic Acids Research</i> , 2006, 34, D459-D464.	14.5	256
107	<i>Agrobacterium tumefaciens</i> -mediated transformation of <i>Leptosphaeria</i> spp. and <i>Oculimacula</i> spp. with the reef coral gene <i>DsRed</i> and the jellyfish gene <i>gfp</i> . <i>FEMS Microbiology Letters</i> , 2005, 253, 67-74.	1.8	62
108	Metabolic and stress adaptation by <i>Mycosphaerella graminicola</i> during sporulation in its host revealed through microarray transcription profiling. <i>Molecular Plant Pathology</i> , 2005, 6, 527-540.	4.2	36

#	ARTICLE	IF	CITATIONS
109	Analysis of expressed sequence tags from the wheat leaf blotch pathogen <i>Mycosphaerella graminicola</i> (anamorph <i>Septoria tritici</i>). <i>Fungal Genetics and Biology</i> , 2005, 42, 376-389.	2.1	43
110	Deciphering plant-pathogen communication: fresh perspectives for molecular resistance breeding. <i>Current Opinion in Biotechnology</i> , 2003, 14, 177-193.	6.6	521
111	The <i>Fusarium graminearum</i> MAP1 gene is essential for pathogenicity and development of perithecia. <i>Molecular Plant Pathology</i> , 2003, 4, 347-359.	4.2	130
112	p-Coumaroylnoradrenaline, a Novel Plant Metabolite Implicated in Tomato Defense against Pathogens. <i>Journal of Biological Chemistry</i> , 2003, 278, 43373-43383.	3.4	88
113	<i>Arabidopsis</i> is susceptible to the cereal ear blight fungal pathogens <i>Fusarium graminearum</i> and <i>Fusarium culmorum</i> . <i>Plant Journal</i> , 2002, 32, 961-973.	5.7	111
114	Comparison of the Hypersensitive Response Induced by the Tomato Cf-4 and Cf-9 Genes in <i>Nicotiana</i> spp.. <i>Molecular Plant-Microbe Interactions</i> , 2000, 13, 465-469.	2.6	43
115	Salicylic acid is not required for Cf-2- and Cf-9-dependent resistance of tomato to <i>Cladosporium fulvum</i> . <i>Plant Journal</i> , 2000, 23, 305-318.	5.7	139
116	cDNA-AFLP Reveals a Striking Overlap in Race-Specific Resistance and Wound Response Gene Expression Profiles. <i>Plant Cell</i> , 2000, 12, 963-977.	6.6	387
117	K ⁺ channels of Cf-9 transgenic tobacco guard cells as targets for <i>Cladosporium fulvum</i> Avr9 elicitor-dependent signal transduction. <i>Plant Journal</i> , 1999, 19, 453-462.	5.7	79
118	Six <i>Arabidopsis thaliana</i> homologues of the human respiratory burst oxidase (gp91phox). <i>Plant Journal</i> , 1998, 14, 365-370.	5.7	403
119	The Tomato Cf-9 Disease Resistance Gene Functions in Tobacco and Potato to Confer Responsiveness to the Fungal Avirulence Gene Product Avr9. <i>Plant Cell</i> , 1998, 10, 1251-1266.	6.6	138
120	The Tomato Cf-9 Disease Resistance Gene Functions in Tobacco and Potato to Confer Responsiveness to the Fungal Avirulence Gene Product Avr9. <i>Plant Cell</i> , 1998, 10, 1251.	6.6	11
121	Rapid, Cf-9- and Avr9-Dependent Production of Active Oxygen Species in Tobacco Suspension Cultures. <i>Molecular Plant-Microbe Interactions</i> , 1998, 11, 1155-1166.	2.6	118
122	PLANT DISEASE RESISTANCE GENES. <i>Annual Review of Plant Biology</i> , 1997, 48, 575-607.	14.3	965
123	Novel Disease Resistance Specificities Result from Sequence Exchange between Tandemly Repeated Genes at the Cf-4/9 Locus of Tomato. <i>Cell</i> , 1997, 91, 821-832.	28.9	562
124	rbohA, a rice homologue of the mammalian gp91phox respiratory burst oxidase gene. <i>Plant Journal</i> , 1996, 10, 515-522.	5.7	294
125	Ensnaring microbes: the components of plant disease resistance. <i>New Phytologist</i> , 1996, 133, 11-34.	7.3	14
126	Plant disease resistance genes: unravelling how they work. <i>Canadian Journal of Botany</i> , 1995, 73, 495-505.	1.1	10

#	ARTICLE	IF	CITATIONS
127	Incomplete Dominance of Tomato <i>Cf</i> Genes for Resistance to <i>Cladosporium fulvum</i> . <i>Molecular Plant-Microbe Interactions</i> , 1994, 7, 58.	2.6	65
128	Changes in abundance of translatable mRNA species in potato roots and leaves following root invasion by cyst-nematode <i>G. rostochiensis</i> pathotypes. <i>Physiological and Molecular Plant Pathology</i> , 1990, 37, 339-354.	2.5	21
129	Systemic accumulation of novel proteins in the apoplast of the leaves of potato plants following root invasion by the cyst-nematode <i>Globodera rostochiensis</i> . <i>Physiological and Molecular Plant Pathology</i> , 1989, 35, 495-506.	2.5	38