

Kim E Hammond-Kosack

List of Publications by Year in descending order

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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	The Top 10 fungal pathogens in molecular plant pathology. <i>Molecular Plant Pathology</i> , 2012, 13, 414-430.	4.2	3,270
2	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	27.8	1,442
3	PLANT DISEASE RESISTANCE GENES. <i>Annual Review of Plant Biology</i> , 1997, 48, 575-607.	14.3	965
4	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
5	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
6	Finished Genome of the Fungal Wheat Pathogen <i>Mycosphaerella graminicola</i> Reveals Dispersome Structure, Chromosome Plasticity, and Stealth Pathogenesis. <i>PLoS Genetics</i> , 2011, 7, e1002070.	3.5	532
7	Deciphering plant-pathogen communication: fresh perspectives for molecular resistance breeding. <i>Current Opinion in Biotechnology</i> , 2003, 14, 177-193.	6.6	521
8	Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. <i>Nucleic Acids Research</i> , 2018, 46, D802-D808.	14.5	489
9	Ensembl Genomes 2020-enabling non-vertebrate genomic research. <i>Nucleic Acids Research</i> , 2020, 48, D689-D695.	14.5	416
10	Six <i>Arabidopsis thaliana</i> homologues of the human respiratory burst oxidase (gp91phox). <i>Plant Journal</i> , 1998, 14, 365-370.	5.7	403
11	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
12	A review of wheat diseases-a field perspective. <i>Molecular Plant Pathology</i> , 2018, 19, 1523-1536.	4.2	375
13	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
14	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. <i>Plant Physiology</i> , 2015, 167, 1158-1185.	4.8	301
15	rbohA, a rice homologue of the mammalian gp91phox respiratory burst oxidase gene. <i>Plant Journal</i> , 1996, 10, 515-522.	5.7	294
16	PHI-base: a new database for pathogen host interactions. <i>Nucleic Acids Research</i> , 2006, 34, D459-D464.	14.5	256
17	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
18	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

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19	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
20	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
21	The Pathogen-Host Interactions database (PHI-base): additions and future developments. <i>Nucleic Acids Research</i> , 2015, 43, D645-D655.	14.5	202
22	The completed genome sequence of the pathogenic ascomycete fungus <i>Fusarium graminearum</i> . <i>BMC Genomics</i> , 2015, 16, 544.	2.8	190
23	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
24	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
25	<i>mlc1</i> -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
26	Barley Stripe Mosaic Virus-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
27	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
28	<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
29	Molecular Characterization and Functional Analysis of <i>MgNLP</i> , 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
30	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
31	PHI-base: the pathogen-host interactions database. <i>Nucleic Acids Research</i> , 2020, 48, D613-D620.	14.5	145
32	PHI-base update: additions to the pathogen host interaction database. <i>Nucleic Acids Research</i> , 2007, 36, D572-D576.	14.5	143
33	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. <i>Nucleic Acids Research</i> , 2022, 50, D996-D1003.	14.5	141
34	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
35	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
36	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

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37	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
38	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
39	Arabidopsis 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
40	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
41	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
42	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
43	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
44	<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
45	<i>Foxtail mosaic virus</i> : A Viral Vector for Protein Expression in Cereals. <i>Plant Physiology</i> , 2018, 177, 1352-1367.	4.8	85
46	Minimum information about a bioactive entity (MIABE). <i>Nature Reviews Drug Discovery</i> , 2011, 10, 661-669.	46.4	80
47	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
48	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
49	An Interspecies Comparative Analysis of the Predicted Secretomes of the Necrotrophic Plant Pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS ONE</i> , 2015, 10, e0130534.	2.5	72
50	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
51	Plant resistance signalling hijacked by a necrotrophic fungal pathogen. <i>Plant Signaling and Behavior</i> , 2008, 3, 993-995.	2.4	67
52	Incomplete Dominance of Tomato Cf Genes for Resistance to <i>Cladosporium fulvum</i> . <i>Molecular Plant-Microbe Interactions</i> , 1994, 7, 58.	2.6	65
53	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
54	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

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55	Agrobacterium tumefaciens-mediated transformation of Leptosphaeria spp. and Oculimacula spp. with the reef coral gene DsRed and the jellyfish gene gfp. FEMS Microbiology Letters, 2005, 253, 67-74.	1.8	62
56	Exploitation of genomics in fungicide research: current status and future perspectives. Molecular Plant Pathology, 2013, 14, 197-210.	4.2	61
57	Aberrant protein N-glycosylation impacts upon infection-related growth transitions of the haploid plant pathogenic fungus Mycosphaerella graminicola. Molecular Microbiology, 2011, 81, 415-433.	2.5	60
58	The complex interactions between host immunity and non-biotrophic fungal pathogens of wheat leaves. Journal of Plant Physiology, 2011, 168, 63-71.	3.5	56
59	DArT markers: diversity analyses, genomes comparison, mapping and integration with SSR markers in Triticum monococcum. BMC Genomics, 2009, 10, 458.	2.8	55
60	A conserved fungal glycosyltransferase facilitates pathogenesis of plants by enabling hyphal growth on solid surfaces. PLoS Pathogens, 2017, 13, e1006672.	4.7	54
61	PHI-base in 2022: a multi-species phenotype database for Pathogen-Host Interactions. Nucleic Acids Research, 2022, 50, D837-D847.	14.5	53
62	sRNA Profiling Combined With Gene Function Analysis Reveals a Lack of Evidence for Cross-Kingdom RNAi in the Wheat-Zymoseptoria tritici Pathosystem. Frontiers in Plant Science, 2019, 10, 892.	3.6	51
63	The adaptation of Fusarium culmorum to DMI Fungicides Is Mediated by Major Transcriptome Modifications in Response to Azole Fungicide, Including the Overexpression of a PDR Transporter (FcABC1). Frontiers in Microbiology, 2018, 9, 1385.	3.5	50
64	An exceptionally high nucleotide and haplotype diversity and a signature of positive selection for the eIF4E resistance gene in barley are revealed by allele mining and phylogenetic analyses of natural populations. Molecular Ecology, 2011, 20, no-no.	3.9	48
65	An analysis of Pseudomonas 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
66	Pseudomonas spp. diversity is negatively associated with suppression of the wheat take-all pathogen. Scientific Reports, 2016, 6, 29905.	3.3	46
67	A Role for Topoisomerase I in Fusarium graminearum and F. culmorum Pathogenesis and Sporulation. Molecular Plant-Microbe Interactions, 2010, 23, 566-577.	2.6	44
68	Comparison of the Hypersensitive Response Induced by the Tomato Cf-4 and Cf-9 Genes in Nicotiana spp.. Molecular Plant-Microbe Interactions, 2000, 13, 465-469.	2.6	43
69	Analysis of expressed sequence tags from the wheat leaf blotch pathogen Mycosphaerella graminicola (anamorph Septoria tritici). Fungal Genetics and Biology, 2005, 42, 376-389.	2.1	43
70	PhytoPath: an integrative resource for plant pathogen genomics. Nucleic Acids Research, 2016, 44, D688-D693.	14.5	42
71	Proteinaceous effector discovery and characterization in filamentous plant pathogens. Molecular Plant Pathology, 2020, 21, 1353-1376.	4.2	41
72	FcStuA from Fusarium culmorum Controls Wheat Foot and Root Rot in a Toxin Dispensable Manner. PLoS ONE, 2013, 8, e57429.	2.5	41

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73	Characterisation of the <i>Fusarium graminearum</i> -Wheat Floral Interaction. <i>Journal of Pathogens</i> , 2011, 2011, 1-9.	1.4	40
74	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
75	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
76	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
77	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
78	The genome of the emerging barley pathogen <i>Ramularia collo-cygni</i> . <i>BMC Genomics</i> , 2016, 17, 584.	2.8	36
79	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
80	Using the pathogen-host interactions database (PHI-base) to investigate plant pathogen genomes and genes implicated in virulence. <i>Frontiers in Plant Science</i> , 2015, 6, 605.	3.6	31
81	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
82	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
83	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
84	Lack of the plant signalling component SGT1b enhances disease resistance to <i>Fusarium culmorum</i> in <i>Arabidopsis</i> buds and flowers. <i>New Phytologist</i> , 2009, 181, 901-912.	7.3	27
85	Deregulation of Plant Cell Death Through Disruption of Chloroplast Functionality Affects Asexual Sporulation of <i>Zymoseptoria tritici</i> on Wheat. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 590-604.	2.6	27
86	First Draft Genome Sequence of a UK Strain (UK99) of <i>Fusarium culmorum</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	27
87	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
88	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
89	Publishing FAIR Data: An Exemplar Methodology Utilizing PHI-Base. <i>Frontiers in Plant Science</i> , 2016, 7, 641.	3.6	25
90	NPR1 and EDS11 contribute to host resistance against <i>Fusarium culmorum</i> in <i>Arabidopsis</i> buds and flowers. <i>Molecular Plant Pathology</i> , 2008, 9, 697-704.	4.2	23

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91	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
92	WAKsing plant immunity, waning diseases. <i>Journal of Experimental Botany</i> , 2022, 73, 22-37.	4.8	23
93	The Top 10 fungal pathogens in molecular plant pathology. <i>Molecular Plant Pathology</i> , 2012, , no-no.	4.2	22
94	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
95	Analysis of cytochrome b5 reductase-mediated metabolism in the phytopathogenic fungus <i>Zymoseptoria tritici</i> reveals novel functionalities implicated in virulence. <i>Fungal Genetics and Biology</i> , 2015, 82, 69-84.	2.1	21
96	Take-All Disease: New Insights into an Important Wheat Root Pathogen. <i>Trends in Plant Science</i> , 2021, 26, 836-848.	8.8	20
97	Mutations in the <i>Arabidopsis</i> homoserine kinase gene <i>DMR1</i> confer enhanced resistance to <i>Fusarium culmorum</i> and <i>F. graminearum</i> . <i>BMC Plant Biology</i> , 2014, 14, 317.	3.6	19
98	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
99	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
100	Whole-genome analysis of <i>Fusarium graminearum</i> insertional mutants identifies virulence associated genes and unmasking untagged chromosomal deletions. <i>BMC Genomics</i> , 2015, 16, 261.	2.8	18
101	Annotation of <i>Fusarium graminearum</i> (PH-1) Version 5.0. <i>Genome Announcements</i> , 2017, 5, .	0.8	18
102	Host to a Stranger: <i>Arabidopsis</i> and <i>Fusarium</i> Ear Blight. <i>Trends in Plant Science</i> , 2015, 20, 651-663.	8.8	17
103	Functional analysis of a <i>Wheat</i> 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> . <i>New Phytologist</i> , 2015, 206, 598-605.	7.3	16
104	The trans-kingdom identification of negative regulators of pathogen hypervirulence. <i>FEMS Microbiology Reviews</i> , 2016, 40, 19-40.	8.6	16
105	Sharing mutants and experimental information prepublication using <i>FgMutantDb</i> (https://scabusa.org/FgMutantDb). <i>Fungal Genetics and Biology</i> , 2018, 115, 90-93.	2.1	15
106	Ensnaring microbes: the components of plant disease resistance. <i>New Phytologist</i> , 1996, 133, 11-34.	7.3	14
107	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
108	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

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109	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
110	OmniMapFree: A unified tool to visualise and explore sequenced genomes. <i>BMC Bioinformatics</i> , 2011, 12, 447.	2.6	11
111	Identifying aphid resistance in the ancestral wheat <i>Triticum monococcum</i> under field conditions. <i>Scientific Reports</i> , 2021, 11, 13495.	3.3	11
112	Plant disease resistance genes: unravelling how they work. <i>Canadian Journal of Botany</i> , 1995, 73, 495-505.	1.1	10
113	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
114	The Induction of Mycotoxins by Trichothecene Producing <i>Fusarium</i> Species. <i>Methods in Molecular Biology</i> , 2012, 835, 439-455.	0.9	10
115	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
116	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
117	In Planta Transient Expression Systems for Monocots. , 2015, , 391-422.		8
118	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
119	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
120	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
121	GPCRs from <i>Fusarium graminearum</i> detection, modeling and virtual screening - the search for new routes to control head blight disease. <i>BMC Bioinformatics</i> , 2016, 17, 463.	2.6	7
122	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
123	Dominant negative interference with defence signalling by truncation mutations of the tomato Cf-9 disease resistance gene. <i>Plant Journal</i> , 2006, 46, 385-399.	5.7	6
124	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
125	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
126	Searching for Novel Targets to Control Wheat Head Blight Disease - I-Protein Identification, 3D Modeling and Virtual Screening. <i>Advances in Microbiology</i> , 2016, 06, 811-830.	0.6	3

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127	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
128	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
129	Saving plants from disease. , 2019, , .		0