Martin - Urban

List of Publications by Year
in descending order

51 papers	5,720 citations	30 h-index (159573)
51 all docs	51 docs citations	51 times ranked

51 g-index (182417)
7907 citing authors

#	Article	IF	Citations
1	The *Fusarium graminearum* Genome Reveals a Link Between Localized Polymorphism and Pathogen Specialization. Science, 2007, 317, 1400-1402.	12.6	837
2	Ensembl Genomes 2016: more genomes, more complexity. Nucleic Acids Research, 2016, 44, D574-D580.	14.5	530
3	Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. Nucleic Acids Research, 2018, 46, D802-D808.	14.5	489
4	Ensembl Genomes 2020—enabling non-vertebrate genomic research. Nucleic Acids Research, 2020, 48, D689-D695.	14.5	416
5	The a mating type locus of U. maydis specifies cell signaling components. Cell, 1992, 68, 441-450.	28.9	398
6	PHI-base: a new database for pathogen host interactions. Nucleic Acids Research, 2006, 34, D459-D464.	14.5	256
7	PHI-base: a new interface and further additions for the multi-species pathogen—host interactions database. Nucleic Acids Research, 2017, 45, D604-D610.	14.5	231
8	The Pathogen-Host Interactions database (PHI-base): additions and future developments. Nucleic Acids Research, 2015, 43, D645-D655.	14.5	202
9	The completed genome sequence of the pathogenic ascomycete fungus Fusarium graminearum. BMC Genomics, 2015, 16, 544.	2.8	190
10	The infection biology of Fusarium graminearum: Defining the pathways of spikelet to spikelet colonisation in wheat ears. Fungal Biology, 2010, 114, 555-571.	2.5	184
11	Characterization of the sterol 14α—demethylases of *Fusarium graminearum* identifies a novel genus—specific CYP51 function. New Phytologist, 2013, 198, 821-835.	7.3	146
12	PHI-base: the pathogen—host interactions database. Nucleic Acids Research, 2020, 48, D613-D620.	14.5	145
13	PHI-base update: additions to the pathogen host interaction database. Nucleic Acids Research, 2007, 36, D572-D576.	14.5	143
14	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. Nucleic Acids Research, 2022, 50, D996-D1003.	14.5	141
15	The Fusarium graminearum MAP1 gene is essential for pathogenicity and development of perithecia. Molecular Plant Pathology, 2003, 4, 347-359.	4.2	130
16	Arabidopsis is susceptible to the cereal ear blight fungal pathogens Fusarium graminearum and Fusarium culmorum. Plant Journal, 2002, 32, 961-973.	5.7	111
17	Phylogenomic Analysis of a 55.1-kb 19-Gene Dataset Resolves a Monophyletic *Fusarium* that Includes the *Fusarium solani* Species Complex. Phytopathology, 2021, 111, 1064-1079.	2.2	107
18	RNAi as an emerging approach to control Fusarium head blight disease and mycotoxin contamination in cereals. Pest Management Science, 2018, 74, 790-799.	3.4	103

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19	The *velvet* gene, *FgVe1*, affects fungal development and positively regulates trichothecene biosynthesis and pathogenicity in *Fusarium graminearum*. Molecular Plant Pathology, 2012, 13, 363-374.	4.2	95
20	*Fusarium graminearum* gene deletion mutants *map1* and *tri5* reveal similarities and differences in the pathogenicity requirements to cause disease on Arabidopsis and wheat floral tissue. New Phytologist, 2008, 177, 990-1000.	7.3	87
21	The Pathogen-Host Interactions Database (PHI-base) Provides Insights into Generic and Novel Themes of Pathogenicity. Molecular Plant-Microbe Interactions, 2006, 19, 1451-1462.	2.6	68
22	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
23	A conserved fungal glycosyltransferase facilitates pathogenesis of plants by enabling hyphal growth on solid surfaces. PLoS Pathogens, 2017, 13, e1006672.	4.7	54
24	PHI-base in 2022: a multi-species phenotype database for Pathogen–Host Interactions. Nucleic Acids Research, 2022, 50, D837-D847.	14.5	53
25	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
26	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
27	PhytoPath: an integrative resource for plant pathogen genomics. Nucleic Acids Research, 2016, 44, D688-D693.	14.5	42
28	The biallelica mating type locus ofUstilago maydis: remnants of an additional pheromone gene indicate evolution from a multiallelic ancestor. Molecular Genetics and Genomics, 1996, 250, 414-420.	2.4	40
29	Characterisation of the *Fusarium graminearum*-Wheat Floral Interaction. Journal of Pathogens, 2011, 2011, 1-9.	1.4	40
30	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
31	Inter-genome comparison of the Quorn fungus Fusarium venenatum and the closely related plant infecting pathogen Fusarium graminearum. BMC Genomics, 2018, 19, 269.	2.8	28
32	First Draft Genome Sequence of a UK Strain (UK99) of *Fusarium culmorum*. Genome Announcements, 2016, 4, .	0.8	27
33	A Combined [1]H Nuclear Magnetic Resonance and Electrospray Ionization–Mass Spectrometry Analysis to Understand the Basal Metabolism of Plant-Pathogenic *Fusarium* spp.. Molecular Plant-Microbe Interactions, 2010, 23, 1605-1618.	2.6	26
34	Publishing FAIR Data: An Exemplar Methodology Utilizing PHI-Base. Frontiers in Plant Science, 2016, 7, 641.	3.6	25
35	Functional evaluation of a homologue of plant rapid alkalinisation factor (RALF) peptides in Fusarium graminearum. Fungal Biology, 2020, 124, 753-765.	2.5	19
36	Network-Based Data Integration for Selecting Candidate Virulence Associated Proteins in the Cereal Infecting Fungus Fusarium graminearum. PLoS ONE, 2013, 8, e67926.	2.5	18

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37	Whole-genome analysis of Fusarium graminearum insertional mutants identifies virulence associated genes and unmasks untagged chromosomal deletions. BMC Genomics, 2015, 16, 261.	2.8	18
38	Annotation of Fusarium graminearum (PH-1) Version 5.0. Genome Announcements, 2017, 5, .	0.8	18
39	The trans-kingdom identification of negative regulators of pathogen hypervirulence. FEMS Microbiology Reviews, 2016, 40, 19-40.	8.6	16
40	Sharing mutants and experimental information prepublication using FgMutantDb (https://scabusa.org/FgMutantDb). Fungal Genetics and Biology, 2018, 115, 90-93.	2.1	15
41	Control of mating and development inUstilago maydis. Antonie Van Leeuwenhoek, 1994, 65, 191-197.	1.7	14
42	A Partial Chromosomal Deletion Caused by Random Plasmid Integration Resulted in a Reduced Virulence Phenotype in <i>Fusarium graminearum</i>. Molecular Plant-Microbe Interactions, 2010, 23, 1083-1096.	2.6	13
43	OmniMapFree: A unified tool to visualise and explore sequenced genomes. BMC Bioinformatics, 2011, 12, 447.	2.6	11
44	The Induction of Mycotoxins by Trichothecene Producing Fusarium Species. Methods in Molecular Biology, 2012, 835, 439-455.	0.9	10
45	PHI-Nets: A Network Resource for Ascomycete Fungal Pathogens to Annotate and Identify Putative Virulence Interacting Proteins and siRNA Targets. Frontiers in Microbiology, 2019, 10, 2721.	3.5	8
46	Detection of Multi-clustered Genes and Community Structure for the Plant Pathogenic Fungus Fusarium graminearum. Lecture Notes in Computer Science, 2012, , 69-86.	1.3	8
47	Inactivation of plant infecting fungal and viral pathogens to achieve biological containment in drainage water using UV treatment. Journal of Applied Microbiology, 2011, 110, 675-687.	3.1	7
48	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
49	Structure-based virtual screening of hypothetical inhibitors of the enzyme longiborneol synthase—a potential target to reduce Fusarium head blight disease. Journal of Molecular Modeling, 2016, 22, 163.	1.8	3
50	Searching for Novel Targets to Control Wheat Head Blight Disease—I-Protein Identification, 3D Modeling and Virtual Screening. Advances in Microbiology, 2016, 06, 811-830.	0.6	3
51	Genome Sequence of Fusarium graminearum Strain CML3066, Isolated from a Wheat Spike in Southern Brazil. Microbiology Resource Announcements, 2020, 9, .	0.6	1