Linda J Harris

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Assessment of deoxynivalenol and deoxynivalenol derivatives in <i>Fusarium graminearum</i> -inoculated Canadian maize inbreds. Canadian Journal of Plant Pathology, 2022, 44, 504-517.	1.4	2
2	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. Phytopathology, 2021, 111, 1064-1079.	2.2	107
3	CO476 corn inbred line. Canadian Journal of Plant Science, 2021, 101, 287-291.	0.9	1
4	Apicidin biosynthesis is linked to accessory chromosomes in Fusarium poae isolates. BMC Genomics, 2021, 22, 591.	2.8	7
5	Naturally Occurring Fusarium Species and Mycotoxins in Oat Grains from Manitoba, Canada. Toxins, 2021, 13, 670.	3.4	12
6	Regulation and Dynamics of Gene Expression During the Life Cycle of <i>Fusarium graminearum</i> . Phytopathology, 2020, 110, 1368-1374.	2.2	11
7	Transcriptomic and Exometabolomic Profiling Reveals Antagonistic and Defensive Modes of <i>Clonostachys rosea</i> Action Against <i>Fusarium graminearum</i> . Molecular Plant-Microbe Interactions, 2020, 33, 842-858.	2.6	23
8	Enniatin Production Influences Fusarium avenaceum Virulence on Potato Tubers, but not on Durum Wheat or Peas. Pathogens, 2020, 9, 75.	2.8	23
9	Prevalence of <i>Fusarium</i> species causing head blight of spring wheat, barley and oat in Ontario during 2001–2017. Canadian Journal of Plant Pathology, 2019, 41, 392-402.	1.4	38
10	Transcriptome profiling of two maize inbreds with distinct responses to Gibberella ear rot disease to identify candidate resistance genes. BMC Genomics, 2018, 19, 131.	2.8	43
11	Gramillin A and B: Cyclic Lipopeptides Identified as the Nonribosomal Biosynthetic Products of <i>Fusarium graminearum</i> . Journal of the American Chemical Society, 2018, 140, 16783-16791.	13.7	36
12	Multiple metabolic pathways for metabolism of <scp>l</scp> -tryptophan in <i>Fusariumgraminearum</i> . Canadian Journal of Microbiology, 2017, 63, 921-927.	1.7	9
13	A Signaling Lipid Associated with Alzheimer's Disease Promotes Mitochondrial Dysfunction. Scientific Reports, 2016, 6, 19332.	3.3	25
14	Protein engineering of Saccharomyces cerevisiae transporter Pdr5p identifies key residues that impact Fusarium mycotoxin export and resistance to inhibition. MicrobiologyOpen, 2016, 5, 979-991.	3.0	5
15	Host-preferential Fusarium graminearum gene expression during infection of wheat, barley, and maize. Fungal Biology, 2016, 120, 111-123.	2.5	93
16	Quantitative trait loci mapping for Gibberella ear rot resistance and associated agronomic traits using genotyping-by-sequencing in maize. Theoretical and Applied Genetics, 2016, 129, 17-29.	3.6	40
17	Hydroxylation of Longiborneol by a <i>Clm2</i> -Encoded CYP450 Monooxygenase to Produce Culmorin in <i>Fusarium graminearum</i> . Journal of Natural Products, 2016, 79, 81-88.	3.0	26
18	Leucine metabolism regulates <scp><i>TRI</i></scp> <i>6</i> expression and affects deoxynivalenol production and virulence in <scp><i>F</i></scp> <i>usarium graminearum</i> . Molecular Microbiology, 2015, 98, 760-769.	2.5	21

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19	Microarray transcriptional profiling of Arctic Mesorhizobium strain N33 at low temperature provides insights into cold adaption strategies. BMC Genomics, 2015, 16, 383.	2.8	35
20	The Genome of the Generalist Plant Pathogen Fusarium avenaceum Is Enriched with Genes Involved in Redox, Signaling and Secondary Metabolism. PLoS ONE, 2014, 9, e112703.	2.5	78
21	Mycotoxins that affect the North American agri-food sector: state of the art and directions for the future. World Mycotoxin Journal, 2014, 7, 63-82.	1.4	34
22	A Neurotoxic Glycerophosphocholine Impacts PtdIns-4, 5-Bisphosphate and TORC2 Signaling by Altering Ceramide Biosynthesis in Yeast. PLoS Genetics, 2014, 10, e1004010.	3.5	4
23	TED, an Autonomous and Rare Maize Transposon of the Mutator Superfamily with a High Gametophytic Excision Frequency. Plant Cell, 2013, 25, 3251-3265.	6.6	13
24	Effect of salicylic acid on Fusarium graminearum, the major causal agent of fusarium head blight in wheat. Fungal Biology, 2012, 116, 413-426.	2.5	81
25	The feruloyl esterase gene family of Fusarium graminearum is differentially regulated by aromatic compounds and hosts. Fungal Biology, 2012, 116, 478-488.	2.5	15
26	Proteomic profiling of two maize inbreds during early gibberella ear rot infection. Proteomics, 2011, 11, 3675-3684.	2.2	58
27	Next-Gen sequencing of the transcriptome of triticale. Plant Genetic Resources: Characterisation and Utilisation, 2011, 9, 181-184.	0.8	5
28	Tri6 Is a Global Transcription Regulator in the Phytopathogen Fusarium graminearum. PLoS Pathogens, 2011, 7, e1002266.	4.7	109
29	<i>CLM1</i> of <i>Fusarium graminearum</i> Encodes a Longiborneol Synthase Required for Culmorin Production. Applied and Environmental Microbiology, 2010, 76, 136-141.	3.1	70
30	Functional Genomics Analysis of the <i>Saccharomyces cerevisiae</i> Iron Responsive Transcription Factor Aft1 Reveals Iron-Independent Functions. Genetics, 2010, 185, 1111-1128.	2.9	34
31	Proteomic analyses of <i>Fusarium graminearum</i> grown under mycotoxinâ€inducing conditions. Proteomics, 2008, 8, 2256-2265.	2.2	78
32	Colonization of maize silks by <i>Fusarium graminearum</i> , the causative organism of gibberella ear rot. Canadian Journal of Botany, 2007, 85, 369-376.	1.1	36
33	A novel gene cluster in Fusarium graminearum contains a gene that contributes to butenolide synthesis. Fungal Genetics and Biology, 2007, 44, 293-306.	2.1	60
34	The <i>Fusarium graminearum</i> Genome Reveals a Link Between Localized Polymorphism and Pathogen Specialization. Science, 2007, 317, 1400-1402.	12.6	837
35	The Maize An2 Gene is Induced by Fusarium Attack and Encodes an ent-Copalyl Diphosphate Synthase. Plant Molecular Biology, 2005, 59, 881-894.	3.9	123
36	Tri1 in Fusarium graminearum Encodes a P450 Oxygenase. Applied and Environmental Microbiology, 2004, 70, 2044-2051.	3.1	116

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37	Use of a <i>Fusarium graminearum</i> strain transformed with green fluorescent protein to study infection in wheat (<i>Triticum aestivum</i>). Canadian Journal of Plant Pathology, 2004, 26, 453-463.	1.4	62
38	A modified Rpl3 gene from rice confers tolerance of the Fusarium graminearum mycotoxin deoxynivalenol to transgenic tobacco. Physiological and Molecular Plant Pathology, 2001, 58, 173-181.	2.5	63
39	Possible Role of Trichothecene Mycotoxins in Virulence of Fusarium graminearum on Maize. Plant Disease, 1999, 83, 954-960.	1.4	184
40	Large tandem duplication associated with aMu2 insertion inZea mays B-Peru gene. Plant Molecular Biology, 1994, 25, 817-828.	3.9	11
41	Evolutionarily conserved regions in Caenorhabditis transposable elements deduced by sequence comparison. Genome, 1991, 34, 6-12.	2.0	25
42	Isolation and sequence analysis ofCaenorhabditis briggsae repetitive elements related to theCaenorhabditis elegans transposon Tc1. Journal of Molecular Evolution, 1990, 30, 359-369.	1.8	24
43	Structural analysis of Tc1 elements in caenorhabditis elegans var. bristol (strain N2). Plasmid, 1989, 22, 10-21.	1.4	9
44	Sequence identity between an inverted repeat family of transposable elements in Drosophila and Caenorhabditis. Nucleic Acids Research, 1988, 16, 5991-5998.	14.5	51
45	PINE OIL, A FEEDING DETERRENT FOR THE WHITE PINE WEEVIL, PISSODES STROBI (COLEOPTERA:) TJ ETQq1 1 0.	784314 rg 0.8	$_{16}^{\rm gBT}/\rm Overloc$
46	Cortical resin monoterpenes in Sitka spruce and resistance to the white pine weevil, Pissodesstrobi (Coleoptera: Curculionidae). Canadian Journal of Forest Research, 1983, 13, 350-352.	1.7	23