Harold Corby Kistler

List of Publications by Year
in descending order

115 papers	16,890 citations	19636 61 h-index	21521 114 g-index
120 all docs	120 docs citations	120 times ranked	8804 citing authors

#	Article	IF	Citations
1	Multiple evolutionary origins of the fungus causing Panama disease of banana: Concordant evidence from nuclear and mitochondrial gene genealogies. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 2044-2049.	3.3	1,739
2	Comparative genomics reveals mobile pathogenicity chromosomes in Fusarium. Nature, 2010, 464, 367-373.	13.7	1,442
3	Heading for disaster: Fusarium graminearum on cereal crops. Molecular Plant Pathology, 2004, 5, 515-525.	2.0	1,105
4	The <i>Fusarium graminearum</i> Genome Reveals a Link Between Localized Polymorphism and Pathogen Specialization. Science, 2007, 317, 1400-1402.	6.0	837
5	Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of Fusarium graminearum, the fungus causing wheat scab. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 7905-7910.	3.3	759
6	Genealogical concordance between the mating type locus and seven other nuclear genes supports formal recognition of nine phylogenetically distinct species within the Fusarium graminearum clade. Fungal Genetics and Biology, 2004, 41, 600-623.	0.9	666
7	Ancestral polymorphism and adaptive evolution in the trichothecene mycotoxin gene cluster of phytopathogenic Fusarium. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 9278-9283.	3.3	489
8	A Mitogen-Activated Protein Kinase Gene (MGV1) in Fusarium graminearum Is Required for Female Fertility, Heterokaryon Formation, and Plant Infection. Molecular Plant-Microbe Interactions, 2002, 15, 1119-1127.	1.4	442
9	Global molecular surveillance reveals novel Fusarium head blight species and trichothecene toxin diversity. Fungal Genetics and Biology, 2007, 44, 1191-1204.	0.9	411
10	Functional Analysis of the Kinome of the Wheat Scab Fungus Fusarium graminearum. PLoS Pathogens, 2011, 7, e1002460.	2.1	309
11	A two-locus DNA sequence database for typing plant and human pathogens within the Fusarium oxysporum species complex. Fungal Genetics and Biology, 2009, 46, 936-948.	0.9	275
12	<i>Fusarium graminearum</i> Trichothecene Mycotoxins: Biosynthesis, Regulation, and Management. Annual Review of Phytopathology, 2019, 57, 15-39.	3.5	255
13	Role of Horizontal Gene Transfer in the Evolution of Fungi. Annual Review of Phytopathology, 2000, 38, 325-363.	3.5	249
14	Global gene regulation by <i>Fusarium</i> transcription factors <i>Tri6</i> and <i>Tri10</i> reveals adaptations for toxin biosynthesis. Molecular Microbiology, 2009, 72, 354-367.	1.2	241
15	One Fungus, One Name: Defining the Genus <i>Fusarium</i> in a Scientifically Robust Way That Preserves Longstanding Use. Phytopathology, 2013, 103, 400-408.	1.1	219
16	Pathogenicity and In Planta Mycotoxin Accumulation Among Members of the Fusarium graminearum Species Complex on Wheat and Rice. Phytopathology, 2005, 95, 1397-1404.	1.1	205
17	Genetic Diversity in the Plant-Pathogenic Fungus Fusarium oxysporum. Phytopathology, 1997, 87, 474-479.	1.1	204
18	New Modes of Genetic Change in Filamentous Fungi. Annual Review of Phytopathology, 1992, 30, 131-153.	3.5	198

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19	Multilocus genotyping and molecular phylogenetics resolve a novel head blight pathogen within the Fusarium graminearum species complex from Ethiopia. Fungal Genetics and Biology, 2008, 45, 1514-1522.	0.9	186
20	Novel Fusarium head blight pathogens from Nepal and Louisiana revealed by multilocus genealogical concordance. Fungal Genetics and Biology, 2011, 48, 1096-1107.	0.9	186
21	Population Analysis of Fusarium graminearum from Wheat Fields in Eastern China. Phytopathology, 2002, 92, 1315-1322.	1.1	183
22	Conidial germination in the filamentous fungus Fusarium graminearum. Fungal Genetics and Biology, 2008, 45, 389-399.	0.9	180
23	Effector profiles distinguish <i>formae speciales</i> of <i>Fusarium oxysporum</i>. Environmental Microbiology, 2016, 18, 4087-4102.	1.8	179
24	Genes determining pathogenicity to pea are clustered on a supernumerary chromosome in the fungal plant pathogen Nectria haematococca. Plant Journal, 2001, 25, 305-314.	2.8	178
25	Random Insertional Mutagenesis Identifies Genes Associated with Virulence in the Wheat Scab Fungus Fusarium graminearum. Phytopathology, 2005, 95, 744-750.	1.1	170
26	A novel Asian clade within the <i>Fusarium graminearum</i> species complex includes a newly discovered cereal head blight pathogen from the Russian Far East. Mycologia, 2009, 101, 841-852.	0.8	169
27	Nivalenol-Type Populations of <i>Fusarium graminearum</i> and <i>F. asiaticum</i> Are Prevalent on Wheat in Southern Louisiana. Phytopathology, 2011, 101, 124-134.	1.1	167
28	Development of a Fusarium graminearum Affymetrix GeneChip for profiling fungal gene expression in vitro and in planta. Fungal Genetics and Biology, 2006, 43, 316-325.	0.9	164
29	Population Subdivision of <i>Fusarium graminearum</i> Sensu Stricto in the Upper Midwestern United States. Phytopathology, 2007, 97, 1434-1439.	1.1	154
30	Fusarium oxysporum f. sp. cubense Consists of a Small Number of Divergent and Globally Distributed Clonal Lineages. Phytopathology, 1997, 87, 915-923.	1.1	150
31	New tricks of an old enemy: isolates of <scp><i>F</i></scp><i>usarium graminearum</i> produce a type <scp>A</scp> trichothecene mycotoxin. Environmental Microbiology, 2015, 17, 2588-2600.	1.8	145
32	The genomic organization of plant pathogenicity in Fusarium species. Current Opinion in Plant Biology, 2010, 13, 420-426.	3.5	142
33	<i>Fusarium graminearum:</i> pathogen or endophyte of North American grasses?. New Phytologist, 2018, 217, 1203-1212.	3.5	127
34	In vivo rearrangement of foreign DNA by Fusarium oxysporum produces linear self-replicating plasmids. Journal of Bacteriology, 1990, 172, 3163-3171.	1.0	124
35	The Transcriptome of <i>Fusarium graminearum</i> During the Infection of Wheat. Molecular Plant-Microbe Interactions, 2011, 24, 995-1000.	1.4	124
36	Analysis of expressed sequence tags from Gibberella zeae (anamorph Fusarium graminearum). Fungal Genetics and Biology, 2003, 38, 187-197.	0.9	120

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37	The Wor1-like Protein Fgp1 Regulates Pathogenicity, Toxin Synthesis and Reproduction in the Phytopathogenic Fungus Fusarium graminearum. PLoS Pathogens, 2012, 8, e1002724.	2.1	120
38	The fungal myosin I is essential for Fusarium toxisome formation. PLoS Pathogens, 2018, 14, e1006827.	2.1	113
39	Relatedness of Strains of<i>Fusarium oxysporum</i>from Crucifers Measured by Examination of Mitochondrial and Ribosomal DNA. Phytopathology, 1987, 77, 1289.	1.1	112
40	Comparative genomics and prediction of conditionally dispensable sequences in legumeâ€"infecting Fusarium oxysporum formae speciales facilitates identification of candidate effectors. BMC Genomics, 2016, 17, 191.	1.2	109
41	Cellular compartmentalization of secondary metabolism. Frontiers in Microbiology, 2015, 6, 68.	1.5	108
42	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.	1.1	107
43	Genetic transformation of the fungal plant wilt pathogen, Fusarium oxysporum. Current Genetics, 1988, 13, 145-149.	0.8	105
44	Chromosome Complement of the Fungal Plant Pathogen Fusarium graminearum Based on Genetic and Physical Mapping and Cytological Observations. Genetics, 2005, 171, 985-1001.	1.2	101
45	Systematics, Phylogeny and Trichothecene Mycotoxin Potential of Fusarium Head Blight Cereal Pathogens. Mycotoxins, 2012, 62, 91-102.	0.2	99
46	The <i>HDF1</i> Histone Deacetylase Gene Is Important for Conidiation, Sexual Reproduction, and Pathogenesis in <i>Fusarium graminearum</i>. Molecular Plant-Microbe Interactions, 2011, 24, 487-496.	1.4	96
47	Diversity of Fusarium head blight populations and trichothecene toxin types reveals regional differences in pathogen composition and temporal dynamics. Fungal Genetics and Biology, 2015, 82, 22-31.	0.9	96
48	Statistical Analysis of Electrophoretic Karyotype Variation Among Vegetative Compatibility Groups of<i>Fusarium oxysporum</i>f. sp.<i>cubense</i>. Molecular Plant-Microbe Interactions, 1994, 7, 196.	1.4	95
49	Cellular Development Associated with Induced Mycotoxin Synthesis in the Filamentous Fungus Fusarium graminearum. PLoS ONE, 2013, 8, e63077.	1.1	94
50	Transducin Beta-Like Gene <i>FTL1</i> Is Essential for Pathogenesis in <i>Fusarium graminearum</i>. Eukaryotic Cell, 2009, 8, 867-876.	3.4	92
51	<i>Fusarium graminearum</i> Tri12p Influences Virulence to Wheat and Trichothecene Accumulation. Molecular Plant-Microbe Interactions, 2012, 25, 1408-1418.	1.4	91
52	Origin of Race 3 of Fusarium oxysporum f. sp. lycopersici at a Single Site in California. Phytopathology, 2003, 93, 1014-1022.	1.1	87
53	The Transcription Factor FgStuAp Influences Spore Development, Pathogenicity, and Secondary Metabolism in <i>Fusarium graminearum</i>. Molecular Plant-Microbe Interactions, 2011, 24, 54-67.	1.4	85
54	Soil Fungal Communities Respond to Grassland Plant Community Richness and Soil Edaphics. Microbial Ecology, 2015, 70, 188-195.	1.4	81

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55	Linear plasmidlike DNA in the plant pathogenic fungus Fusarium oxysporum f. sp. conglutinans. Journal of Bacteriology, 1986, 167, 587-593.	1.0	79
56	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.	1.1	78
57	Systematic Numbering of Vegetative Compatibility Groups in the Plant Pathogenic Fungus Fusarium oxysporum. Phytopathology, 1998, 88, 30-32.	1.1	76
58	High Levels of Gene Flow and Heterozygote Excess Characterize Rhizoctonia solani AG-1 IA (Thanatephorus cucumeris) from Texas. Fungal Genetics and Biology, 1999, 28, 148-159.	0.9	75
59	Temporal dynamics and population genetic structure of Fusarium graminearum in the upper Midwestern United States. Fungal Genetics and Biology, 2014, 73, 83-92.	0.9	73
60	Species-specific banding patterns of restriction endonuclease-digested mitochondrial DNA from the genusPythium. Experimental Mycology, 1990, 14, 32-46.	1.8	72
61	Structural reorganization of the fungal endoplasmic reticulum upon induction of mycotoxin biosynthesis. Scientific Reports, 2017, 7, 44296.	1.6	71
62	A phosphorylated transcription factor regulates sterol biosynthesis in Fusarium graminearum. Nature Communications, 2019, 10, 1228.	5.8	66
63	Interactions between Fusarium verticillioides, Ustilago maydis, and Zea mays: An endophyte, a pathogen, and their shared plant host. Fungal Genetics and Biology, 2012, 49, 578-587.	0.9	65
64	Development of VNTR markers for two Fusarium graminearum clade species. Molecular Ecology Notes, 2004, 4, 468-470.	1.7	63
65	Plant Community Richness Mediates Inhibitory Interactions and Resource Competition between Streptomyces and Fusarium Populations in the Rhizosphere. Microbial Ecology, 2017, 74, 157-167.	1.4	63
66	Autonomously replicating plasmids and chromosome rearrangement during transformation of Nectria haematococca. Gene, 1992, 117, 81-89.	1.0	62
67	No to <i>Neocosmospora</i> : Phylogenomic and Practical Reasons for Continued Inclusion of the Fusarium solani Species Complex in the Genus <i>Fusarium</i>. MSphere, 2020, 5, .	1.3	61
68	The genome of opportunistic fungal pathogen Fusarium oxysporum carries a unique set of lineage-specific chromosomes. Communications Biology, 2020, 3, 50.	2.0	55
69	A Novel Transcriptional Factor Important for Pathogenesis and Ascosporogenesis in <i>Fusarium graminearum</i>. Molecular Plant-Microbe Interactions, 2011, 24, 118-128.	1.4	54
70	Metabolome and Transcriptome of the Interaction between Ustilago maydis and Fusarium verticillioides <i>In Vitro</i>. Applied and Environmental Microbiology, 2012, 78, 3656-3667.	1.4	54
71	Population Genetic Analysis Corroborates Dispersal of Fusarium oxysporum f. sp. radicis-lycopersici from Florida to Europe. Phytopathology, 1999, 89, 623-630.	1.1	50
72	In vitro interactions between Fusarium verticillioides and Ustilago maydis through real-time PCR and metabolic profiling. Fungal Genetics and Biology, 2011, 48, 874-885.	0.9	50

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73	A SIX1 homolog in Fusarium oxysporum f.sp. cubense tropical race 4 contributes to virulence towards Cavendish banana. PLoS ONE, 2018, 13, e0205896.	1.1	49
74	Compartmentalized gene regulatory network of the pathogenic fungus <i>Fusarium graminearum</i>. New Phytologist, 2016, 211, 527-541.	3.5	48
75	Genomic analysis of hostâ€"pathogen interaction between Fusarium graminearum and wheat during early stages of disease development. Microbiology (United Kingdom), 2006, 152, 1877-1890.	0.7	44
76	Examining the Transcriptional Response in Wheat <i>Fhb1</i> Nearâ€Isogenic Lines to <i>Fusarium graminearum</i> Infection and Deoxynivalenol Treatment. Plant Genome, 2016, 9, plantgenome2015.05.0032.	1.6	44
77	Genetic duplication in Fusarium oxysporum. Current Genetics, 1995, 28, 173-176.	0.8	38
78	The Probable Center of Origin of Fusarium oxysporum f. sp. lycopersici VCG 0033. Plant Disease, 2003, 87, 1433-1438.	0.7	37
79	Cryptic promoter activity in the coding region of the HMG-CoA reductase gene in Fusarium graminearum. Fungal Genetics and Biology, 2006, 43, 34-41.	0.9	36
80	Effort versus Reward: Preparing Samples for Fungal Community Characterization in High-Throughput Sequencing Surveys of Soils. PLoS ONE, 2015, 10, e0127234.	1.1	36
81	Fungal Innate Immunity Induced by Bacterial Microbe-Associated Molecular Patterns (MAMPs). G3: Genes, Genomes, Genetics, 2016, 6, 1585-1595.	0.8	35
82	Effector Gene Suites in Some Soil Isolates of <i>Fusarium oxysporum</i> Are Not Sufficient Predictors of Vascular Wilt in Tomato. Phytopathology, 2017, 107, 842-851.	1.1	32
83	Nutrient use preferences among soil Streptomyces suggest greater resource competition in monoculture than polyculture plant communities. Plant and Soil, 2016, 409, 329-343.	1.8	31
84	Rapid Detection of the Fusarium oxysporum Lineage Containing the Canary Island Date Palm Wilt Pathogen. Phytopathology, 1999, 89, 407-413.	1.1	30
85	<scp><i>EBR1</i></scp> genomic expansion and its role in virulence of <scp><i>F</i></scp><i>usarium</i> species. Environmental Microbiology, 2014, 16, 1982-2003.	1.8	30
86	A high proportion of NX-2 genotype strains are found among Fusarium graminearum isolates from northeastern New York State. European Journal of Plant Pathology, 2018, 150, 791-796.	0.8	29
87	Kinome Expansion in the Fusarium oxysporum Species Complex Driven by Accessory Chromosomes. MSphere, 2018, 3, .	1.3	29
88	A fungal ABC transporter FgAtm1 regulates iron homeostasis via the transcription factor cascade FgAreA-HapX. PLoS Pathogens, 2019, 15, e1007791.	2.1	29
89	Chromosome-Scale Genome Assembly of <i>Fusarium oxysporum</i> Strain Fo47, a Fungal Endophyte and Biocontrol Agent. Molecular Plant-Microbe Interactions, 2020, 33, 1108-1111.	1.4	29
90	Genome Sequence of Fusarium oxysporum f. sp. <i>melonis</i> Strain NRRL 26406, a Fungus Causing Wilt Disease on Melon. Genome Announcements, 2014, 2, .	0.8	28

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91	The mitochondrial genome of Fusarium oxysporum. Plasmid, 1989, 22, 86-89.	0.4	25
92	Expression of the Fusarium graminearum terpenome and involvement of the endoplasmic reticulum-derived toxisome. Fungal Genetics and Biology, 2019, 124, 78-87.	0.9	25
93	Metatranscriptomic Comparison of Endophytic and Pathogenic <i>Fusarium</i>â€“Arabidopsis Interactions Reveals Plant Transcriptional Plasticity. Molecular Plant-Microbe Interactions, 2021, 34, 1071-1083.	1.4	25
94	A molecular characterization of<i>Cercospora</i>species pathogenic to water hyacinth and emendation of<i>C. piaropi</i>. Mycologia, 2001, 93, 323-334.	0.8	24
95	Conservation and divergence of the cyclic adenosine monophosphateâ€“protein kinase A (cAMPâ€“<scp>PKA</scp>) pathway in two plantâ€pathogenic fungi: <i>Fusarium graminearum</i> and <i><scp>F</scp>.â€‰verticillioides</i>. Molecular Plant Pathology, 2016, 17, 196-209.	2.0	23
96	Nrs1, a Repetitive Element Linked to Pisatin Demethylase Genes on a Dispensable Chromosome of<i>Nectria haematococc</i>. Molecular Plant-Microbe Interactions, 1995, 8, 524.	1.4	23
97	A Molecular Characterization of Cercospora Species Pathogenic to Water Hyacinth and Emendation of C. piaropi. Mycologia, 2001, 93, 323.	0.8	22
98	Population Subdivision of <i>Fusarium graminearum</i> from Barley and Wheat in the Upper Midwestern United States at the Turn of the Century. Phytopathology, 2015, 105, 1466-1474.	1.1	21
99	Plant diversity and plant identity influence <i>Fusarium</i> communities in soil. Mycologia, 2017, 109, 128-139.	0.8	21
100	Fusarium BP1 is a reader of H3K27 methylation. Nucleic Acids Research, 2021, 49, 10448-10464.	6.5	20
101	Npc1 is involved in sterol trafficking in the filamentous fungus Fusarium graminearum. Fungal Genetics and Biology, 2011, 48, 725-730.	0.9	19
102	Mitochondrial plasmids do not determine host range in crucifer-infecting strains of Fusarium oxysporum. Plant Pathology, 1992, 41, 103-112.	1.2	18
103	<i>Fusarium graminearum</i> Species Complex: A Bibliographic Analysis and Web-Accessible Database for Global Mapping of Species and Trichothecene Toxin Chemotypes. Phytopathology, 2022, 112, 741-751.	1.1	18
104	Genetic diversity among isolates of Fusariumoxysporum f.sp. canariensis. Plant Pathology, 2000, 49, 155-164.	1.2	16
105	Systematic discovery of regulatory motifs in Fusarium graminearum by comparing four Fusarium genomes. BMC Genomics, 2010, 11, 208.	1.2	16
106	Phylogeny, Plant Species, and Plant Diversity Influence Carbon Use Phenotypes Among <i>Fusarium</i> Populations in the Rhizosphere Microbiome. Phytobiomes Journal, 2017, 1, 150-157.	1.4	16
107	Inhibitory and nutrient use phenotypes among coexisting <i>Fusarium</i> and <i>Streptomyces</i> populations suggest local coevolutionary interactions in soil. Environmental Microbiology, 2020, 22, 976-985.	1.8	16
108	Plant defense compound triggers mycotoxin synthesis by regulating H2B ub1 and H3K4 me2/3 deposition. New Phytologist, 2021, 232, 2106-2123.	3.5	13

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109	Genetic Manipulation of Plant Pathogenic Fungi. , 1991, , 152-170.		11
110	Nanoscale enrichment of the cytosolic enzyme trichodiene synthase near reorganized endoplasmic reticulum in Fusarium graminearum. Fungal Genetics and Biology, 2019, 124, 73-77.	0.9	11
111	The <i>Fusarium graminearum</i> t-SNARE <i>Sso2</i> Is Involved in Growth, Defense, and DON Accumulation and Virulence. Molecular Plant-Microbe Interactions, 2020, 33, 888-901.	1.4	10
112	Targeted Chromosome Breakage in Filamentous Fungi. Fungal Genetics and Biology, 1997, 22, 13-18.	0.9	2
113	Gibberella zeae Ascospore Production and Collection for Microarray Experiments.. Journal of Visualized Experiments, 2006, , 115.	0.2	2
114	Bacterial artificial chromosomeâ€"based physical map of Gibberella zeae (Fusarium graminearum). Genome, 2007, 50, 954-962.	0.9	2
115	First Report of Sphaeropsis tumefaciens on an Endangered St. John's-Wort in Florida. Plant Disease, 2002, 86, 1177-1177.	0.7	1