Todd J Ward

List of Publications by Year
in descending order

74 papers	8,959 citations	57631 44 h-index	79541 73 g-index
74 all docs	74 docs citations	74 times ranked	6326 citing authors

#	Article	IF	Citations
1	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
2	Fiveâ€year survey uncovers extensive diversity and temporal fluctuations among fusarium head blight pathogens of wheat and barley in Brazil. Plant Pathology, 2021, 70, 426-435.	1.2	16
3	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
4	Intrapopulation Antagonism Can Reduce the Growth and Aggressiveness of the Wheat Head Blight Pathogen <i>Fusarium graminearum</i>. Phytopathology, 2020, 110, 916-926.	1.1	7
5	Regional and field-specific differences in Fusarium species and mycotoxins associated with blighted North Carolina wheat. International Journal of Food Microbiology, 2020, 323, 108594.	2.1	17
6	Synergistic Phytotoxic Effects of Culmorin and Trichothecene Mycotoxins. Toxins, 2019, 11, 555.	1.5	32
7	<i>Fusarium graminearum</i> arabinanase (Arb93B) Enhances Wheat Head Blight Susceptibility by Suppressing Plant Immunity. Molecular Plant-Microbe Interactions, 2019, 32, 888-898.	1.4	27
8	<i>Fusarium</i> mycotoxins: a trans-disciplinary overview. Canadian Journal of Plant Pathology, 2018, 40, 161-171.	0.8	37
9	Regional differences in the composition of Fusarium Head Blight pathogens and mycotoxins associated with wheat in Mexico. International Journal of Food Microbiology, 2018, 273, 11-19.	2.1	34
10	Development of a PCR-RFLP method based on the transcription elongation factor 1-Î± gene to differentiate Fusarium graminearum from other species within the Fusarium graminearum species complex. Food Microbiology, 2018, 70, 28-32.	2.1	11
11	Marasas et al. 1984 â€œToxigenic <i>Fusarium</i> Species: Identity and Mycotoxicologyâ€•revisited. Mycologia, 2018, 110, 1058-1080.	0.8	79
12	Draft Whole-Genome Sequences of Seven Listeria monocytogenes Strains with Variations in Virulence and Stress Responses. Microbiology Resource Announcements, 2018, 7, .	0.3	3
13	Fusarium subtropicale, sp. nov., a novel nivalenol mycotoxinâ€“producing species isolated from barley (Hordeum vulgare) in Brazil and sister to F. praegraminearum. Mycologia, 2018, 110, 860-871.	0.8	10
14	Four new species of Metschnikowia and the transfer of seven Candida species to Metschnikowia and Clavispora as new combinations. Antonie Van Leeuwenhoek, 2018, 111, 2017-2035.	0.7	31
15	Species composition, toxigenic potential and aggressiveness of Fusarium isolates causing Head Blight of barley in Uruguay. Food Microbiology, 2018, 76, 426-433.	2.1	38
16	Population genomics of Fusarium graminearum reveals signatures of divergent evolution within a major cereal pathogen. PLoS ONE, 2018, 13, e0194616.	1.1	75
17	Listeria monocytogenes Source Distribution Analysis Indicates Regional Heterogeneity and Ecological Niche Preference among Serotype 4b Clones. MBio, 2018, 9, .	1.8	57
18	Characterization of a Fusarium graminearum Salicylate Hydroxylase. Frontiers in Microbiology, 2018, 9, 3219.	1.5	14

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19	Population genetic structure and mycotoxin potential of the wheat crown rot and head blight pathogen Fusarium culmorum in Algeria. Fungal Genetics and Biology, 2017, 103, 34-41.	0.9	44
20	The Arsenic Resistance-Associated Listeria Genomic Island LGI2 Exhibits Sequence and Integration Site Diversity and a Propensity for Three Listeria monocytogenes Clones with Enhanced Virulence. Applied and Environmental Microbiology, 2017, 83, .	1.4	50
21	Differential triazole sensitivity among members of the Fusarium graminearum species complex infecting barley grains in Brazil. Tropical Plant Pathology, 2017, 42, 197-202.	0.8	11
22	<i>Listeria monocytogenes</i> septicemia in an immunocompromised dog. Veterinary Clinical Pathology, 2016, 45, 254-259.	0.3	11
23	Isolation and characterization of atypical Listeria monocytogenes associated with a canine urinary tract infection. Journal of Veterinary Diagnostic Investigation, 2016, 28, 604-607.	0.5	8
24	The geographic distribution and complex evolutionary history of the NX-2 trichothecene chemotype from Fusarium graminearum. Fungal Genetics and Biology, 2016, 95, 39-48.	0.9	55
25	Determination of Evolutionary Relationships of Outbreak-Associated Listeria monocytogenes Strains of Serotypes 1/2a and 1/2b by Whole-Genome Sequencing. Applied and Environmental Microbiology, 2016, 82, 928-938.	1.4	58
26	Fusarium praegraminearum sp. nov., a novel nivalenol mycotoxin-producing pathogen from New Zealand can induce head blight on wheat. Mycologia, 2016, 108, 1229-1239.	0.8	12
27	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
28	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
29	Polyglycine hydrolases: Fungal Î²â€lactamaseâ€like endoproteases that cleave polyglycine regions within plant class IV chitinases. Protein Science, 2015, 24, 1147-1157.	3.1	12
30	<i>Fusarium dactylidis</i> sp. nov., a novel nivalenol toxin-producing species sister to <i>F. pseudograminearum</i> isolated from orchard grass (<i>Dactylis glomerata</i>) in Oregon and New Zealand. Mycologia, 2015, 107, 409-418.	0.8	34
31	DNA sequence-based identification of Fusarium: Current status and future directions. Phytoparasitica, 2015, 43, 583-595.	0.6	275
32	Regional and Field-Specific Factors Affect the Composition of Fusarium Head Blight Pathogens in Subtropical No-Till Wheat Agroecosystem of Brazil. Phytopathology, 2015, 105, 246-254.	1.1	106
33	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
34	Diversity of the Fusarium graminearum species complex on French cereals. European Journal of Plant Pathology, 2014, 138, 133-148.	0.8	60
35	Population Structure of Listeria monocytogenes Serotype 4b Isolates from Sporadic Human Listeriosis Cases in the United States from 2003 to 2008. Applied and Environmental Microbiology, 2014, 80, 3632-3644.	1.4	25
36	Birth, death and horizontal transfer of the fumonisin biosynthetic gene cluster during the evolutionary diversification of <i><scp>F</scp>usarium</i>. Molecular Microbiology, 2013, 90, 290-306.	1.2	118

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37	Phylogenetic analyses of RPB1 and RPB2 support a middle Cretaceous origin for a clade comprising all agriculturally and medically important fusaria. Fungal Genetics and Biology, 2013, 52, 20-31.	0.9	366
38	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
39	Listeria monocytogenes. , 2013, , 27-38.		1
40	Atypical Listeria monocytogenes Serotype 4b Strains Harboring a Lineage II-Specific Gene Cassette. Applied and Environmental Microbiology, 2012, 78, 660-667.	1.4	45
41	Heavy Metal and Disinfectant Resistance of Listeria monocytogenes from Foods and Food Processing Plants. Applied and Environmental Microbiology, 2012, 78, 6938-6945.	1.4	72
42	Systematics, Phylogeny and Trichothecene Mycotoxin Potential of Fusarium Head Blight Cereal Pathogens. Mycotoxins, 2012, 62, 91-102.	0.2	99
43	Analysis of the Fusarium graminearum species complex from wheat, barley and maize in South Africa provides evidence of species-specific differences in host preference. Fungal Genetics and Biology, 2011, 48, 914-920.	0.9	116
44	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
45	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
46	Fusarium sibiricum sp. nov, a novel type A trichothecene-producing Fusarium from northern Asia closely related to F. sporotrichioides and F. langsethiae. International Journal of Food Microbiology, 2011, 147, 58-68.	2.1	61
47	Cyber infrastructure for Fusarium: three integrated platforms supporting strain identification, phylogenetics, comparative genomics and knowledge sharing. Nucleic Acids Research, 2011, 39, D640-D646.	6.5	63
48	A comparison of aggressiveness and deoxynivalenol production between Canadian Fusarium graminearum isolates with 3-acetyl and 15-acetyldeoxynivalenol chemotypes in field-grown spring wheat. European Journal of Plant Pathology, 2010, 127, 407-417.	0.8	84
49	Molecular and Phenotypic Characterization of Listeria monocytogenes from U.S. Department of Agriculture Food Safety and Inspection Service Surveillance of Ready-to-Eat Foods and Processing Facilities. Journal of Food Protection, 2010, 73, 861-869.	0.8	46
50	A Targeted Multilocus Genotyping Assay for Lineage, Serogroup, and Epidemic Clone Typing of <i>Listeria monocytogenes</i>. Applied and Environmental Microbiology, 2010, 76, 6680-6684.	1.4	48
51	Reconciling Ecological and Genomic Divergence among Lineages of Listeria under an "Extended Mosaic Genome Concept". Molecular Biology and Evolution, 2009, 26, 2605-2615.	3.5	23
52	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
53	An adaptive evolutionary shift in Fusarium head blight pathogen populations is driving the rapid spread of more toxigenic Fusarium graminearum in North America. Fungal Genetics and Biology, 2008, 45, 473-484.	0.9	427
54	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

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55	Birth-and-death evolution of the internalin multigene family in Listeria. Gene, 2008, 427, 124-128.	1.0	13
56	Multilocus Genotyping Assays for Single Nucleotide Polymorphism-Based Subtyping of <i>Listeria monocytogenes</i> Isolates. Applied and Environmental Microbiology, 2008, 74, 7629-7642.	1.4	173
57	A Single-Nucleotide-Polymorphism-Based Multilocus Genotyping Assay for Subtyping Lineage I Isolates of Listeria monocytogenes. Applied and Environmental Microbiology, 2007, 73, 133-147.	1.4	80
58	Global molecular surveillance reveals novel Fusarium head blight species and trichothecene toxin diversity. Fungal Genetics and Biology, 2007, 44, 1191-1204.	0.9	411
59	The <i>Fusarium graminearum</i> Genome Reveals a Link Between Localized Polymorphism and Pathogen Specialization. Science, 2007, 317, 1400-1402.	6.0	837
60	Phylogenetic Diversity and Microsphere Array-Based Genotyping of Human Pathogenic Fusaria, Including Isolates from the Multistate Contact Lens-Associated U.S. Keratitis Outbreaks of 2005 and 2006. Journal of Clinical Microbiology, 2007, 45, 2235-2248.	1.8	257
61	The presence of GC-AG introns in Neurospora crassa and other euascomycetes determined from analyses of complete genomes: implications for automated gene prediction. Genomics, 2006, 87, 338-347.	1.3	23
62	Conservation genomics: disequilibrium mapping of domestic cattle chromosomal segments in North American bison populations. Molecular Ecology, 2005, 14, 2343-2362.	2.0	50
63	Suspension Microarray with Dendrimer Signal Amplification Allows Direct and High-Throughput Subtyping of Listeria monocytogenes from Genomic DNA. Journal of Clinical Microbiology, 2005, 43, 3255-3259.	1.8	51
64	Evolution of a large ribosomal RNA multigene family in filamentous fungi: Birth and death of a concerted evolution paradigm. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 5084-5089.	3.3	169
65	Intraspecific Phylogeny and Lineage Group Identification Based on the prfA Virulence Gene Cluster of Listeria monocytogenesâ€. Journal of Bacteriology, 2004, 186, 4994-5002.	1.0	181
66	FUSARIUM-ID v. 1.0: A DNA Sequence Database for Identifying Fusarium. European Journal of Plant Pathology, 2004, 110, 473-479.	0.8	860
67	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
68	The trichothecene biosynthesis gene cluster ofFusarium graminearumF15 contains a limited number of essential pathway genes and expressed non-essential genes. FEBS Letters, 2003, 539, 105-110.	1.3	138
69	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
70	Evolutionary Relationships among Mucoralean Fungi (Zygomycota): Evidence for Family Polyphyly on a Large Scale. Mycologia, 2001, 93, 286.	0.8	103
71	Evolutionary relationships among mucoralean fungi (Zygomycota): Evidence for family polyphyly on a large scale. Mycologia, 2001, 93, 286-297.	0.8	145
72	Phylogenetic analysis with newly characterized Babesia bovis hsp70 and hsp90 provides strong support for paraphyly within the piroplasms. Molecular and Biochemical Parasitology, 2000, 109, 67-72.	0.5	24

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73	Identification of domestic cattle hybrids in wild cattle and bison species: a general approach using mtDNA markers and the parametric bootstrap. Animal Conservation, 1999, 2, 51-57.	1.5	70
74	Nucleotide Sequence Evolution at the <i>Îº</i>-Casein Locus: Evidence for Positive Selection Within the Family Bovidae. Genetics, 1997, 147, 1863-1872.	1.2	44