Todd J Ward

List of Publications by Year in Descending Order

74 papers	6,982 citations	39 h-index	74 g-index
74 ext. papers	8,169 ext. citations	4.6 avg, IF	5.39 L-index

#	Paper	IF	Citations
74	Phylogenomic Analysis of a 55.1-kb 19-Gene Dataset Resolves a Monophyletic that Includes the Species Complex. *Phytopathology*, **2021**, 111, 1064-1079	3.8	39
73	Five-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	2.8	8
72	Intrapopulation Antagonism Can Reduce the Growth and Aggressiveness of the Wheat Head Blight Pathogen. *Phytopathology*, **2020**, 110, 916-926	3.8	3
71	Regional and field-specific differences in Fusarium species and mycotoxins associated with blighted North Carolina wheat. *International Journal of Food Microbiology*, **2020**, 323, 108594	5.8	4
70	No to : Phylogenomic and Practical Reasons for Continued Inclusion of the Fusarium solani Species Complex in the Genus. *MSphere*, **2020**, 5,	5	32
69	Synergistic Phytotoxic Effects of Culmorin and Trichothecene Mycotoxins. *Toxins*, **2019**, 11,	4.9	16
68	arabinanase (Arb93B) Enhances Wheat Head Blight Susceptibility by Suppressing Plant Immunity. *Molecular Plant-Microbe Interactions*, **2019**, 32, 888-898	3.6	10
67	Fusarium mycotoxins: a trans-disciplinary overview. *Canadian Journal of Plant Pathology*, **2018**, 40, 161-171	1.6	27
66	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	5.8	16
65	Development of a PCR-RFLP method based on the transcription elongation factor 1- gene to differentiate Fusarium graminearum from other species within the Fusarium graminearum species complex. *Food Microbiology*, **2018**, 70, 28-32	6	6
64	Species composition, toxigenic potential and aggressiveness of Fusarium isolates causing Head Blight of barley in Uruguay. *Food Microbiology*, **2018**, 76, 426-433	6	19
63	Population genomics of Fusarium graminearum reveals signatures of divergent evolution within a major cereal pathogen. *PLoS ONE*, **2018**, 13, e0194616	3.7	40
62	Listeria monocytogenes Source Distribution Analysis Indicates Regional Heterogeneity and Ecological Niche Preference among Serotype 4b Clones. *MBio*, **2018**, 9,	7.8	34
61	Characterization of a Salicylate Hydroxylase. *Frontiers in Microbiology*, **2018**, 9, 3219	5.7	9
60	Marasas et al. 1984 "Toxigenic Fusarium Species: Identity and Mycotoxicology" revisited. *Mycologia*, **2018**, 110, 1058-1080	2.4	48
59	Draft Whole-Genome Sequences of Seven Listeria monocytogenes Strains with Variations in Virulence and Stress Responses. *Microbiology Resource Announcements*, **2018**, 7,	1.3	3
58	Fusarium subtropicale, sp. nov., a novel nivalenol mycotoxin-producing species isolated from barley (Hordeum vulgare) in Brazil and sister to F. praegraminearum. *Mycologia*, **2018**, 110, 860-871	2.4	8

57	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	2.1	17
56	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	3.9	31
55	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,	4.8	28
54	Differential triazole sensitivity among members of the Fusarium graminearum species complex infecting barley grains in Brazil. *Tropical Plant Pathology*, **2017**, 42, 197-202	2.5	8
53	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, 928-38	4.8	35
52	Fusarium praegraminearum sp. nov., a novel nivalenol mycotoxin-producing pathogen from New Zealand can induce head blight on wheat. *Mycologia*, **2016**, 108, 1229-1239	2.4	10
51	Listeria monocytogenes septicemia in an immunocompromised dog. *Veterinary Clinical Pathology*, **2016**, 45, 254-259	1	9
50	Isolation and characterization of atypical Listeria monocytogenes associated with a canine urinary tract infection. *Journal of Veterinary Diagnostic Investigation*, **2016**, 28, 604-7	1.5	6
49	The geographic distribution and complex evolutionary history of the NX-2 trichothecene chemotype from Fusarium graminearum. *Fungal Genetics and Biology*, **2016**, 95, 39-48	3.9	38
48	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	3.9	72
47	New tricks of an old enemy: isolates of Fusarium graminearum produce a type A trichothecene mycotoxin. *Environmental Microbiology*, **2015**, 17, 2588-600	5.2	111
46	Population Subdivision of Fusarium graminearum from Barley and Wheat in the Upper Midwestern United States at the Turn of the Century. *Phytopathology*, **2015**, 105, 1466-74	3.8	16
45	Polyglycine hydrolases: Fungal β-lactamase-like endoproteases that cleave polyglycine regions within plant class IV chitinases. *Protein Science*, **2015**, 24, 1147-57	6.3	9
44	Fusarium dactylidis sp. nov., a novel nivalenol toxin-producing species sister to F. pseudograminearum isolated from orchard grass (Dactylis glomerata) in Oregon and New Zealand. *Mycologia*, **2015**, 107, 409-18	2.4	24
43	DNA sequence-based identification of Fusarium: Current status and future directions. *Phytoparasitica*, **2015**, 43, 583-595	1.5	165
42	Regional and field-specific factors affect the composition of fusarium head blight pathogens in subtropical no-till wheat agroecosystem of Brazil. *Phytopathology*, **2015**, 105, 246-54	3.8	80
41	Diversity of the Fusarium graminearum species complex on French cereals. *European Journal of Plant Pathology*, **2014**, 138, 133-148	2.1	50
40	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, 3632-44	4.8	21

39	Birth, death and horizontal transfer of the fumonisin biosynthetic gene cluster during the evolutionary diversification of Fusarium. *Molecular Microbiology*, **2013**, 90, 290-306	4.1	72
38	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	3.9	254
37	One fungus, one name: defining the genus Fusarium in a scientifically robust way that preserves longstanding use. *Phytopathology*, **2013**, 103, 400-8	3.8	155
36	Listeria monocytogenes **2013**, 27-38		
35	Systematics, Phylogeny and Trichothecene Mycotoxin Potential of Fusarium Head Blight Cereal Pathogens. *Mycotoxins*, **2012**, 62, 91-102	0.2	72
34	Atypical Listeria monocytogenes serotype 4b strains harboring a lineage II-specific gene cassette. *Applied and Environmental Microbiology*, **2012**, 78, 660-7	4.8	27
33	Heavy metal and disinfectant resistance of Listeria monocytogenes from foods and food processing plants. *Applied and Environmental Microbiology*, **2012**, 78, 6938-45	4.8	61
32	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, 914-20	3.9	86
31	Novel Fusarium head blight pathogens from Nepal and Louisiana revealed by multilocus genealogical concordance. *Fungal Genetics and Biology*, **2011**, 48, 1096-107	3.9	153
30	Nivalenol-type populations of Fusarium graminearum and F. asiaticum are prevalent on wheat in southern Louisiana. *Phytopathology*, **2011**, 101, 124-34	3.8	133
29	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	5.8	48
28	Cyber infrastructure for Fusarium: three integrated platforms supporting strain identification, phylogenetics, comparative genomics and knowledge sharing. *Nucleic Acids Research*, **2011**, 39, D640-6	20.1	56
27	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, 861-9	2.5	42
26	A targeted multilocus genotyping assay for lineage, serogroup, and epidemic clone typing of Listeria monocytogenes. *Applied and Environmental Microbiology*, **2010**, 76, 6680-4	4.8	40
25	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	2.1	77
24	Reconciling ecological and genomic divergence among lineages of listeria under an "extended mosaic genome concept". *Molecular Biology and Evolution*, **2009**, 26, 2605-15	8.3	22
23	A novel Asian clade within the Fusarium graminearum species complex includes a newly discovered cereal head blight pathogen from the Russian Far East. *Mycologia*, **2009**, 101, 841-52	2.4	141
22	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, 473-84	3.9	348

21	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, 1514-22	3.9	164
20	Birth-and-death evolution of the internalin multigene family in Listeria. *Gene*, **2008**, 427, 124-8	3.8	13
19	Multilocus genotyping assays for single nucleotide polymorphism-based subtyping of Listeria monocytogenes isolates. *Applied and Environmental Microbiology*, **2008**, 74, 7629-42	4.8	128
18	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, 2235-48	9.7	210
17	A single-nucleotide-polymorphism-based multilocus genotyping assay for subtyping lineage I isolates of Listeria monocytogenes. *Applied and Environmental Microbiology*, **2007**, 73, 133-47	4.8	75
16	Global molecular surveillance reveals novel Fusarium head blight species and trichothecene toxin diversity. *Fungal Genetics and Biology*, **2007**, 44, 1191-204	3.9	341
15	The Fusarium graminearum genome reveals a link between localized polymorphism and pathogen specialization. *Science*, **2007**, 317, 1400-2	33.3	668
14	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, 338-47	4.3	22
13	Conservation genomics: disequilibrium mapping of domestic cattle chromosomal segments in North American bison populations. *Molecular Ecology*, **2005**, 14, 2343-62	5.7	48
12	Suspension microarray with dendrimer signal amplification allows direct and high-throughput subtyping of Listeria monocytogenes from genomic DNA. *Journal of Clinical Microbiology*, **2005**, 43, 3255-9	9.7	41
11	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, 5084-9	11.5	149
10	Intraspecific phylogeny and lineage group identification based on the prfA virulence gene cluster of Listeria monocytogenes. *Journal of Bacteriology*, **2004**, 186, 4994-5002	3.5	164
9	FUSARIUM-ID v. 1.0: A DNA Sequence Database for Identifying Fusarium. *European Journal of Plant Pathology*, **2004**, 110, 473-479	2.1	669
8	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, 600-23	3.9	577
7	The trichothecene biosynthesis gene cluster of Fusarium graminearum F15 contains a limited number of essential pathway genes and expressed non-essential genes. *FEBS Letters*, **2003**, 539, 105-10	3.8	120
6	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, 9278-83	11.5	414
5	Evolutionary Relationships among Mucoralean Fungi (Zygomycota): Evidence for Family Polyphyly on a Large Scale. *Mycologia*, **2001**, 93, 286	2.4	96
4	Evolutionary relationships among mucoralean fungi (Zygomycota): Evidence for family polyphyly on a large scale. *Mycologia*, **2001**, 93, 286-297	2.4	124

3	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	1.9	20
2	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	3.2	66
1	Nucleotide sequence evolution at the kappa-casein locus: evidence for positive selection within the family Bovidae. *Genetics*, **1997**, 147, 1863-72	4	34