Steven J Klosterman

List of Publications by Year
in descending order

92 papers	4,844 citations	147801 31 h-index	102487 66 g-index
95 all docs	95 docs citations	95 times ranked	4208 citing authors

#	Article	IF	Citations
1	Insights from the genome of the biotrophic fungal plant pathogen Ustilago maydis. Nature, 2006, 444, 97-101.	27.8	1,113
2	Diversity, Pathogenicity, and Management of Verticillium Species. Annual Review of Phytopathology, 2009, 47, 39-62.	7.8	624
3	Comparative Genomics Yields Insights into Niche Adaptation of Plant Vascular Wilt Pathogens. PLoS Pathogens, 2011, 7, e1002137.	4.7	477
4	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 May 2009â€“31 July 2009. Molecular Ecology Resources, 2009, 9, 1460-1466.	4.8	128
5	Genomics Spurs Rapid Advances in Our Understanding of the Biology of Vascular Wilt Pathogens in the Genus <i>Verticillium</i>. Annual Review of Phytopathology, 2015, 53, 181-198.	7.8	96
6	One Step Construction of Agrobacterium-Recombination-ready-plasmids (OSCAR), an efficient and robust tool for ATMT based gene deletion construction in fungi. Fungal Genetics and Biology, 2011, 48, 677-684.	2.1	88
7	Population analyses of the vascular plant pathogen Verticillium dahliae detect recombination and transcontinental gene flow. Fungal Genetics and Biology, 2010, 47, 416-422.	2.1	86
8	RNA-seq analyses of gene expression in the microsclerotia of Verticillium dahliae. BMC Genomics, 2013, 14, 607.	2.8	75
9	Identification of Pathogenicity-Related Genes in the Vascular Wilt Fungus Verticillium dahliae by Agrobacterium tumefaciens-Mediated T-DNA Insertional Mutagenesis. Molecular Biotechnology, 2011, 49, 209-221.	2.4	71
10	The mitogen-activated protein kinase gene, VdHog1, regulates osmotic stress response, microsclerotia formation and virulence in Verticillium dahliae. Fungal Genetics and Biology, 2016, 88, 13-23.	2.1	71
11	Genetics of Morphogenesis and Pathogenic Development of Ustilago maydis. Advances in Genetics, 2007, 57, 1-47.	1.8	69
12	Deep mRNA sequencing reveals stage-specific transcriptome alterations during microsclerotia development in the smoke tree vascular wilt pathogen, Verticillium dahliae. BMC Genomics, 2014, 15, 324.	2.8	68
13	Transposable elements in phytopathogenic Verticillium spp.: insights into genome evolution and inter- and intra-specific diversification. BMC Genomics, 2012, 13, 314.	2.8	62
14	Comparative genomics of downy mildews reveals potential adaptations to biotrophy. BMC Genomics, 2018, 19, 851.	2.8	59
15	Multi-locus tree and species tree approaches toward resolving a complex clade of downy mildews (Straminipila, Oomycota), including pathogens of beet and spinach. Molecular Phylogenetics and Evolution, 2015, 86, 24-34.	2.7	58
16	Transcription factor VdCmr1 is required for pigment production, protection from UV irradiation, and regulates expression of melanin biosynthetic genes in Verticillium dahliae. Microbiology (United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 1	1.8	57
17	Molecular Variation Among Isolates of <i>Verticillium dahliae</i> and Polymerase Chain Reaction-Based Differentiation of Races. Phytopathology, 2010, 100, 1222-1230.	2.2	55
18	Coupling Spore Traps and Quantitative PCR Assays for Detection of the Downy Mildew Pathogens of Spinach (<i>Peronospora effusa</i>) and Beet (<i>P. schachtii</i>). Phytopathology, 2014, 104, 1349-1359.	2.2	55

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19	Proteome and metabolome analyses reveal differential responses in tomato -Verticillium dahliae-interactions. Journal of Proteomics, 2019, 207, 103449.	2.4	51
20	A Comparison of the Effects of DNA-Damaging Agents and Biotic Elicitors on the Induction of Plant Defense Genes, Nuclear Distortion, and Cell Death. Plant Physiology, 2001, 125, 752-762.	4.8	47
21	A Real-Time PCR Assay for Detection and Quantification of <i>Verticillium dahliae</i> in Spinach Seed. Phytopathology, 2012, 102, 443-451.	2.2	46
22	Vayg1 is required for microsclerotium formation and melanin production in Verticillium dahliae. Fungal Genetics and Biology, 2017, 98, 1-11.	2.1	46
23	The <i>Gossypium hirsutum</i> TIRâ€NBSâ€LRR gene <i>GhDSC1 </i>mediates resistance against Verticillium wilt. Molecular Plant Pathology, 2019, 20, 857-876.	4.2	46
24	Functional analyses of small secreted cysteineâ€rich proteins identified candidate effectors in <i>Verticillium dahliae</i>. Molecular Plant Pathology, 2020, 21, 667-685.	4.2	46
25	Population genomics demystifies the defoliation phenotype in the plant pathogen <i>Verticillium dahliae</i>. New Phytologist, 2019, 222, 1012-1029.	7.3	41
26	The bZIP transcription factor VdAtf1 regulates virulence by mediating nitrogen metabolism in <i>Verticillium dahliae</i>. New Phytologist, 2020, 226, 1461-1479.	7.3	41
27	Detection and Quantification of <i>Bremia lactucae</i> by Spore Trapping and Quantitative PCR. Phytopathology, 2016, 106, 1426-1437.	2.2	39
28	SNARE-Encoding Genes VdSec22 and VdSso1 Mediate Protein Secretion Required for Full Virulence in Verticillium dahliae. Molecular Plant-Microbe Interactions, 2018, 31, 651-664.	2.6	39
29	Characterization of two homeodomain transcription factors with critical but distinct roles in virulence in the vascular pathogen <i>Verticillium dahliae</i>. Molecular Plant Pathology, 2018, 19, 986-1004.	4.2	39
30	Spinach Downy Mildew: Advances in Our Understanding of the Disease Cycle and Prospects for Disease Management. Plant Disease, 2019, 103, 791-803.	1.4	38
31	A Singleâ€Nucleotide Mutation in a GLUTAMATE RECEPTORâ€LIKE Gene Confers Resistance to Fusarium Wilt in <i>Gossypium hirsutum</i>. Advanced Science, 2021, 8, 2002723.	11.2	37
32	Heterologous Expression of the Cotton NBS-LRR Gene GbaNA1 Enhances Verticillium Wilt Resistance in Arabidopsis. Frontiers in Plant Science, 2018, 9, 119.	3.6	36
33	The <i>Verticillium dahliae</i> Sho1â€MAPK pathway regulates melanin biosynthesis and is required for cotton infection. Environmental Microbiology, 2019, 21, 4852-4874.	3.8	36
34	Characterization of a 20ÂkDa DNase elicitor from <i>Fusarium solani</i> f. sp. <i>phaseoli</i> and its expression at the onset of induced resistance in <i>Pisum sativum</i>. Molecular Plant Pathology, 2001, 2, 147-158.	4.2	33
35	Plant HMG proteins bearing the AT-hook motif. Plant Science, 2002, 162, 855-866.	3.6	32
36	Season-Long Dynamics of Spinach Downy Mildew Determined by Spore Trapping and Disease Incidence. Phytopathology, 2016, 106, 1311-1318.	2.2	32

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37	Colonization of Spinach by <i>Verticillium dahliae</i> and Effects of Pathogen Localization on the Efficacy of Seed Treatments. Phytopathology, 2013, 103, 268-280.	2.2	31
38	The endochitinase VDECH from Verticillium dahliae inhibits spore germination and activates plant defense responses. Plant Science, 2017, 259, 12-23.	3.6	31
39	Two Verticillium dahliae MAPKKKs, VdSsk2 and VdSte11, Have Distinct Roles in Pathogenicity, Microsclerotial Formation, and Stress Adaptation. MSphere, 2019, 4, .	2.9	31
40	GhMYB4 downregulates lignin biosynthesis and enhances cotton resistance to Verticillium dahliae. Plant Cell Reports, 2021, 40, 735-751.	5.6	31
41	Genome-Wide Identification and Functional Analyses of the CRK Gene Family in Cotton Reveals GbCRK18 Confers Verticillium Wilt Resistance in Gossypium barbadense. Frontiers in Plant Science, 2018, 9, 1266.	3.6	30
42	The Transcription Factor VdHapX Controls Iron Homeostasis and Is Crucial for Virulence in the Vascular Pathogen Verticillium dahliae. MSphere, 2018, 3, .	2.9	28
43	Hormone Signaling and Its Interplay With Development and Defense Responses in Verticillium-Plant Interactions. Frontiers in Plant Science, 2020, 11, 584997.	3.6	27
44	Cytotoxic function of xylanase VdXyn4 in the plant vascular wilt pathogen <i>Verticillium dahliae</i>. Plant Physiology, 2021, 187, 409-429.	4.8	27
45	Analysis of pea HMG-I/Y expression suggests a role in defence gene regulation. Molecular Plant Pathology, 2003, 4, 249-258.	4.2	26
46	The Arabidopsis SENESCENCE-ASSOCIATED GENE 13 Regulates Dark-Induced Senescence and Plays Contrasting Roles in Defense Against Bacterial and Fungal Pathogens. Molecular Plant-Microbe Interactions, 2020, 33, 754-766.	2.6	26
47	Ubc2, an Ortholog of the Yeast Ste50p Adaptor, Possesses a Basidiomycete-Specific Carboxy Terminal Extension Essential for Pathogenicity Independent of Pheromone Response. Molecular Plant-Microbe Interactions, 2008, 21, 110-121.	2.6	25
48	Frequency of <i>Verticillium</i> Species in Commercial Spinach Fields and Transmission of <i>V. dahliae</i> from Spinach to Subsequent Lettuce Crops. Phytopathology, 2015, 105, 80-90.	2.2	25
49	Measurements of Aerial Spore Load by qPCR Facilitates Lettuce Downy Mildew Risk Advisement. Plant Disease, 2020, 104, 82-93.	1.4	23
50	Transcriptional analyses of differential cultivars during resistant and susceptible interactions with Peronospora effusa, the causal agent of spinach downy mildew. Scientific Reports, 2020, 10, 6719.	3.3	22
51	SSH reveals a linkage between a senescence-associated protease and Verticillium wilt symptom development in lettuce (Lactuca sativa). Physiological and Molecular Plant Pathology, 2011, 76, 48-58.	2.5	21
52	Plasmolysis and Vital Staining Reveal Viable Oospores of <i>Peronospora effusa</i> in Spinach Seed Lots. Plant Disease, 2016, 100, 59-65.	1.4	19
53	Genomewide Transcriptome Profiles Reveal How Bacillus subtilis Lipopeptides Inhibit Microsclerotia Formation in Verticillium dahliae. Molecular Plant-Microbe Interactions, 2019, 32, 622-634.	2.6	19
54	Selection for Resistance to Verticillium Wilt Caused by Race 2 Isolates of Verticillium dahliae in Accessions of Lettuce (Lactuca sativa L.). Hortscience: A Publication of the American Society for Hortcultural Science, 2011, 46, 201-206.	1.0	19

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55	Verticillium dahliae CFEM proteins manipulate host immunity and differentially contribute to virulence. BMC Biology, 2022, 20, 55.	3.8	19
56	Analysis of <i>Verticillium dahliae</i> Suggests a Lack of Correlation Between Genotypic Diversity and Virulence Phenotypes. Plant Disease, 2011, 95, 1224-1232.	1.4	18
57	A Framework for Optimizing Phytosanitary Thresholds in Seed Systems. Phytopathology, 2017, 107, 1219-1228.	2.2	18
58	Sporangiospore Viability and Oospore Production in the Spinach Downy Mildew Pathogen, <i>Peronospora effusa</i>. Plant Disease, 2020, 104, 2634-2641.	1.4	16
59	Key Insights and Research Prospects at the Dawn of the Population Genomics Era for Verticillium dahliae. Annual Review of Phytopathology, 2021, 59, 31-51.	7.8	16
60	Convergent and distinctive functions of transcription factors VdYap1, VdAtf1, and VdSkn7 in the regulation of nitrosative stress resistance, microsclerotia formation, and virulence in Verticillium dahliae. Molecular Plant Pathology, 2020, 21, 1451-1466.	4.2	15
61	A secreted ribonuclease effector from <i>Verticillium dahliae</i> localizes in the plant nucleus to modulate host immunity. Molecular Plant Pathology, 2022, 23, 1122-1140.	4.2	15
62	The secretome of <i>Verticillium dahliae</i> in collusion with plant defence responses modulates <scp>Verticillium</scp> wilt symptoms. Biological Reviews, 2022, 97, 1810-1822.	10.4	15
63	Focus Issue Articles on Emerging and Re-Emerging Plant Diseases. Phytopathology, 2015, 105, 852-854.	2.2	14
64	Disease Management in the Genomics Eraâ€"Summaries of Focus Issue Papers. Phytopathology, 2016, 106, 1068-1070.	2.2	14
65	Detached leaf inoculation assay for evaluating resistance to the spinach downy mildew pathogen. European Journal of Plant Pathology, 2020, 158, 511-520.	1.7	13
66	Iceberg Lettuce Breeding Lines with Resistance to Verticillium Wilt Caused by Race 1 Isolates of Verticillium dahliae. Hortscience: A Publication of the American Society for Hortcultural Science, 2011, 46, 501-504.	1.0	13
67	Detection of Latent <i>Peronospora effusa</i> Infections in Spinach. Plant Disease, 2018, 102, 1766-1771.	1.4	12
68	Insights into VdCmr1â€mediated protection against high temperature stress and UV irradiation in <i>Verticillium dahliae</i>. Environmental Microbiology, 2019, 21, 2977-2996.	3.8	12
69	Real-Time PCR for the Quantification of Fungi In Planta. Methods in Molecular Biology, 2012, 835, 121-132.	0.9	11
70	VdCYC8, Encoding CYC8 Glucose Repression Mediator Protein, Is Required for Microsclerotia Formation and Full Virulence in Verticillium dahliae. PLoS ONE, 2015, 10, e0144020.	2.5	11
71	A polyketide synthase from Verticillium dahliae modulates melanin biosynthesis and hyphal growth to promote virulence. BMC Biology, 2022, 20, .	3.8	11
72	A Soilless Verticillium Wilt Assay Using an Early Flowering Lettuce Line. Plant Disease, 2009, 93, 691-698.	1.4	10

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73	Spatiotemporal Patterns in the Airborne Dispersal of Spinach Downy Mildew. Phytopathology, 2017, 107, 50-58.	2.2	10
74	Arabidopsis defense mutant ndr1-1 displays accelerated development and early flowering mediated by the hormone gibberellic acid. Plant Science, 2019, 285, 200-213.	3.6	9
75	<i>Verticillium klebahnii</i> and <i>V. isaacii</i> Isolates Exhibit Host-Dependent Biological Control of Verticillium Wilt Caused by <i>V. dahliae</i>. PhytoFrontiers, 2021, 1, 276-290.	1.6	9
76	The bZip Transcription Factor VdMRTF1 is a Negative Regulator of Melanin Biosynthesis and Virulence in Verticillium dahliae. Microbiology Spectrum, 2022, 10, e0258121.	3.0	8
77	Functional Genomics and Comparative Lineage-Specific Region Analyses Reveal Novel Insights into Race Divergence in Verticillium dahliae. Microbiology Spectrum, 2021, 9, e0111821.	3.0	7
78	miR398b negatively regulates cotton immune responses to Verticillium dahliae via multiple targets. Crop Journal, 2022, 10, 1026-1036.	5.2	6
79	Genetics of Morphogenesis in Basidiomycetes. Applied Mycology and Biotechnology, 2005, , 353-422.	0.3	5
80	Genome Sequences of <i>Verticillium dahliae</i> Defoliating Strain XJ592 and Nondefoliating Strain XJ511. Molecular Plant-Microbe Interactions, 2020, 33, 565-568.	2.6	5
81	The Verticillium dahliae Spt-Ada-Gcn5 Acetyltransferase Complex Subunit Ada1 Is Essential for Conidia and Microsclerotia Production and Contributes to Virulence. Frontiers in Microbiology, 2022, 13, 852571.	3.5	5
82	Attenuation of ethylene signaling increases cotton resistance to a defoliating strain of Verticillium dahliae. Crop Journal, 2023, 11, 89-98.	5.2	5
83	Genome Sequence of <i>Verticillium dahliae</i> Race 1 Isolate VdLs.16 From Lettuce. Molecular Plant-Microbe Interactions, 2020, 33, 1265-1269.	2.6	4
84	Identification of long non-coding RNAs in Verticillium dahliae following inoculation of cotton. Microbiological Research, 2022, 257, 126962.	5.3	4
85	Characterization of Spinach Germplasm for Resistance Against Two Races of Verticillium dahliae. Hortscience: A Publication of the American Society for Hortcultural Science, 2015, 50, 1631-1635.	1.0	3
86	Crustacean Meal Elicits Expression of Growth and Defense-Related Genes in Roots of Lettuce and Tomato. PhytoFrontiers, 2022, 2, 10-20.	1.6	2
87	Biological Characteristics of Verticillium dahliae MAT1-1 and MAT1-2 Strains. International Journal of Molecular Sciences, 2021, 22, 7148.	4.1	2
88	Genome Sequence Data of MAT1-1 and MAT1-2 Idiomorphs from Verticillium dahliae. Phytopathology, 2021, , PHYTO01210012A.	2.2	1
89	Dynamics of Verticillium dahliae race 1 population under managed agricultural ecosystems. BMC Biology, 2021, 19, 131.	3.8	1
90	Transcriptome Variations in Verticillium dahliae in Response to Two Different Inorganic Nitrogen Sources. Frontiers in Microbiology, 2021, 12, 712701.	3.5	1

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91	Welcoming PhytoFrontiersâ„¢ into Our APS Family of Journals. PhytoFrontiers, 2021, 1, 2-3.	1.6	0
92	Composition of the Microbiomes from Spinach Seeds Infested or Noninfested with <i>Peronospora effusa</i> or <i>Verticillium dahliae</i>. Phytobiomes Journal, 2022, 6, 169-180.	2.7	0