

# Susanna A Braus-Stromeyer

## List of Publications by Year in descending order

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Version: 2024-02-01

19  
papers

1,442  
citations

623188

14  
h-index

794141

19  
g-index

20  
all docs

20  
docs citations

20  
times ranked

1674  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . <i>Genome Biology</i> , 2017, 18, 28.	3.8	417
2	Comparative genomics of citric-acid-producing <i>Aspergillus niger</i> ATCC 1015 versus enzyme-producing CBS 513.88. <i>Genome Research</i> , 2011, 21, 885-897.	2.4	329
3	Transcriptional Activation and Production of Tryptophan-Derived Secondary Metabolites in <i>Arabidopsis</i> Roots Contributes to the Defense against the Fungal Vascular Pathogen <i>Verticillium longisporum</i> . <i>Molecular Plant</i> , 2012, 5, 1389-1402.	3.9	120
4	<i>V</i> transcription activator of adhesion <i>Vta2</i> suppresses microsclerotia formation and is required for systemic infection of plant roots. <i>New Phytologist</i> , 2014, 202, 565-581.	3.5	92
5	<i>Bacillus thuringiensis</i> and <i>Bacillus weihenstephanensis</i> Inhibit the Growth of Phytopathogenic <i>Verticillium</i> Species. <i>Frontiers in Microbiology</i> , 2016, 7, 2171.	1.5	74
6	Silencing of <i>Vlro2</i> for chorismate synthase revealed that the phytopathogen <i>Verticillium longisporum</i> induces the cross-pathway control in the xylem. <i>Applied Microbiology and Biotechnology</i> , 2010, 85, 1961-1976.	1.7	62
7	The Plant Host <i>Brassica napus</i> Induces in the Pathogen <i>Verticillium longisporum</i> the Expression of Functional Catalase Peroxidase Which Is Required for the Late Phase of Disease. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 569-581.	1.4	55
8	The <i>Cpc1</i> Regulator of the Cross-Pathway Control of Amino Acid Biosynthesis Is Required for Pathogenicity of the Vascular Pathogen <i>Verticillium longisporum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 1312-1324.	1.4	55
9	<i>Verticillium dahliae</i> transcription factors <i>Som1</i> and <i>Vta3</i> control microsclerotia formation and sequential steps of plant root penetration and colonisation to induce disease. <i>New Phytologist</i> , 2019, 221, 2138-2159.	3.5	50
10	<i>Verticillium dahliae</i> <i>VdTHI4</i> , involved in thiazole biosynthesis, stress response and DNA repair functions, is required for vascular disease induction in tomato. <i>Environmental and Experimental Botany</i> , 2014, 108, 14-22.	2.0	40
11	Infections with the vascular pathogens <i>Verticillium longisporum</i> and <i>Verticillium dahliae</i> induce distinct disease symptoms and differentially affect drought stress tolerance of <i>Arabidopsis thaliana</i> . <i>Environmental and Experimental Botany</i> , 2014, 108, 23-37.	2.0	38
12	Molecular diagnosis to discriminate pathogen and apathogen species of the hybrid <i>Verticillium longisporum</i> on the oilseed crop <i>Brassica napus</i> . <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 4467-4483.	1.7	30
13	The velvet protein <i>Vel1</i> controls initial plant root colonization and conidia formation for xylem distribution in <i>Verticillium</i> wilt. <i>PLoS Genetics</i> , 2021, 17, e1009434.	1.5	20
14	<i>Verticillium longisporum</i> Elicits Media-Dependent Secretome Responses With Capacity to Distinguish Between Plant-Related Environments. <i>Frontiers in Microbiology</i> , 2020, 11, 1876.	1.5	18
15	Fluorescent pseudomonads pursue media-dependent strategies to inhibit growth of pathogenic <i>Verticillium</i> fungi. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 817-831.	1.7	6
16	<i>Pseudomonas</i> Strains Induce Transcriptional and Morphological Changes and Reduce Root Colonization of <i>Verticillium</i> spp.. <i>Frontiers in Microbiology</i> , 2021, 12, 652468.	1.5	6
17	A 20 kb lineage-specific genomic region tames virulence in pathogenic amphidiploid <i>Verticillium longisporum</i> . <i>Molecular Plant Pathology</i> , 2021, 22, 939-953.	2.0	6
18	Draft Genome Sequence of the Phenazine-Producing <i>Pseudomonas fluorescens</i> Strain 2-79. <i>Genome Announcements</i> , 2015, 3, .	0.8	5

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19	Draft Genome Sequence of the Beneficial Rhizobacterium <i>Pseudomonas fluorescens</i> DSM 8569, a Natural Isolate of Oilseed Rape ( <i>Brassica napus</i> ). <i>Genome Announcements</i> , 2015, 3, .	0.8	2