

Elizabeth E Rogers

List of Publications by Year in descending order

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42
papers

4,437
citations

331670

21
h-index

289244

40
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docs citations

42
times ranked

4503
citing authors

#	ARTICLE	IF	CITATIONS
1	Viral Reservoir Capacity of Wild <i>Prunus</i> Alternative Hosts of Plum Pox Virus Through Multiple Cycles of Transmission and Dormancy. <i>Plant Disease</i> , 2022, 106, 101-106.	1.4	1
2	Insights regarding resistance of Nemaguard™ rootstock to the bacterium <i>Xylella fastidiosa</i> . <i>Plant Disease</i> , 2022, .	1.4	1
3	Translatome Profiling of Plum Pox Virus-Infected Leaves in European Plum Reveals Temporal and Spatial Coordination of Defense Responses in Phloem Tissues. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 66-77.	2.6	17
4	Dynamic changes impact the plum pox virus population structure during leaf and bud development. <i>Virology</i> , 2020, 548, 192-199.	2.4	7
5	Immunoreagents for development of a diagnostic assay specific for <i>Rathayibacter toxicus</i> . <i>Food and Agricultural Immunology</i> , 2020, 31, 231-242.	1.4	3
6	Grapevine phenolic compounds influence cell surface adhesion of <i>Xylella fastidiosa</i> and bind to lipopolysaccharide. <i>PLoS ONE</i> , 2020, 15, e0240101.	2.5	6
7	The Identification and Conservation of Tunicaminyuracil-Related Biosynthetic Gene Clusters in Several <i>Rathayibacter</i> Species Collected From Australia, Africa, Eurasia, and North America. <i>Frontiers in Microbiology</i> , 2019, 10, 2914.	3.5	3
8	Partial Proteome of the Corynetoxin-Producing Gram-Positive Bacterium, <i>Rathayibacter toxicus</i> . <i>Proteomics</i> , 2018, 18, 1700350.	2.2	2
9	Evolution of the U.S. Biological Select Agent <i>Rathayibacter toxicus</i> . <i>MBio</i> , 2018, 9, .	4.1	10
10	<i>Rathayibacter toxicus</i> , Other <i>Rathayibacter</i> Species Inducing Bacterial Head Blight of Grasses, and the Potential for Livestock Poisonings. <i>Phytopathology</i> , 2017, 107, 804-815.	2.2	39
11	Complete Genome Sequence of <i>Rathayibacter toxicus</i> Phage NCPPB3778. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
12	Whole genome sequence of two <i>Rathayibacter toxicus</i> strains reveals a tunicamycin biosynthetic cluster similar to <i>Streptomyces chartreusis</i> . <i>PLoS ONE</i> , 2017, 12, e0183005.	2.5	13
13	Deep 16S rRNA gene sequencing of anterior foregut microbiota from the blue-green sharpshooter (<i>Graphocephala atropunctata</i>). <i>Journal of Applied Entomology</i> , 2016, 140, 801-805.	1.8	7
14	Direct Evidence of Egestion and Salivation of <i>Xylella fastidiosa</i> Suggests Sharpshooters Can Be "Flying Syringes". <i>Phytopathology</i> , 2015, 105, 608-620.	2.2	25
15	Susceptibility to <i>Xylella fastidiosa</i> in a First-generation Hybrid from a non-traditional Peach-Almond Cross. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2015, 50, 337-340.	1.0	6
16	Anterior Foregut Microbiota of the Glassy-Winged Sharpshooter Explored Using Deep 16S rRNA Gene Sequencing from Individual Insects. <i>PLoS ONE</i> , 2014, 9, e106215.	2.5	23
17	Toxin-antitoxin systems <i>mqsR/ygiT</i> and <i>dinJ/reI</i> of <i>Xylella fastidiosa</i> . <i>Physiological and Molecular Plant Pathology</i> , 2014, 87, 59-68.	2.5	29
18	<i>Xylella fastidiosa</i> Plasmid-Encoded PemK Toxin Is an Endoribonuclease. <i>Phytopathology</i> , 2012, 102, 32-40.	2.2	25

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19	Evaluation of <i>Arabidopsis thaliana</i> as a Model Host for <i>Xylella fastidiosa</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 747-754.	2.6	8
20	A Conjugative 38 kB Plasmid Is Present in Multiple Subspecies of <i>Xylella fastidiosa</i> . <i>PLoS ONE</i> , 2012, 7, e52131.	2.5	23
21	Regulation of growth response to water stress in the soybean primary root. I. Proteomic analysis reveals region-specific regulation of phenylpropanoid metabolism and control of free iron in the elongation zone. <i>Plant, Cell and Environment</i> , 2010, 33, 223-243.	5.7	158
22	Functional Characterization of Replication and Stability Factors of an Incompatibility Group P-1 Plasmid from <i>Xylella fastidiosa</i> . <i>Applied and Environmental Microbiology</i> , 2010, 76, 7734-7740.	3.1	14
23	Plasmids of <i>Xylella fastidiosa</i> mulberry-infecting strains share extensive sequence identity and gene complement with pVEIS01 from the earthworm symbiont <i>Verminephrobacter eiseniae</i> . <i>Physiological and Molecular Plant Pathology</i> , 2010, 74, 238-245.	2.5	19
24	Two MATE proteins play a role in iron efficiency in soybean. <i>Journal of Plant Physiology</i> , 2009, 166, 1453-1459.	3.5	56
25	Differential Susceptibility of <i>Prunus</i> Germplasm (Subgenus <i>Amygdalus</i>) to a California Isolate of <i>Xylella fastidiosa</i> . <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2009, 44, 1928-1931.	1.0	28
26	The <i>Arabidopsis</i> AtOPT3 Protein Functions in Metal Homeostasis and Movement of Iron to Developing Seeds. <i>Plant Physiology</i> , 2008, 146, 323-324.	4.8	225
27	The FRD3-Mediated Efflux of Citrate into the Root Vasculature Is Necessary for Efficient Iron Translocation. <i>Plant Physiology</i> , 2007, 144, 197-205.	4.8	525
28	<i>Arabidopsis</i> <i>scpFtsY</i> mutants exhibit pleiotropic defects including an inability to increase iron deficiency-inducible root Fe(III) chelate reductase activity. <i>Plant Journal</i> , 2006, 47, 467-479.	5.7	23
29	Role of FRD3 in Iron Translocation and Homeostasis. , 2006, , 327-339.		1
30	FRD3 Controls Iron Localization in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2004, 136, 2523-2531.	4.8	254
31	Genomic scale profiling of nutrient and trace elements in <i>Arabidopsis thaliana</i> . <i>Nature Biotechnology</i> , 2003, 21, 1215-1221.	17.5	407
32	FRD3, a Member of the Multidrug and Toxin Efflux Family, Controls Iron Deficiency Responses in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2002, 14, 1787-1799.	6.6	311
33	Iron Acquisition in Plants. , 2002, , .		3
34	Altered selectivity in an <i>Arabidopsis</i> metal transporter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 12356-12360.	7.1	436
35	Correlation of defense gene induction defects with powdery mildew susceptibility in <i>Arabidopsis</i> enhanced disease susceptibility mutants. <i>Plant Journal</i> , 1998, 16, 473-485.	5.7	232
36	<i>Arabidopsis</i> enhanced disease susceptibility mutants exhibit enhanced susceptibility to several bacterial pathogens and alterations in PR-1 gene expression.. <i>Plant Cell</i> , 1997, 9, 305-316.	6.6	227

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37	USE OF ARABIDOPSIS FOR GENETIC DISSECTION OF PLANT DEFENSE RESPONSES. Annual Review of Genetics, 1997, 31, 547-569.	7.6	136
38	Phytoalexin-Deficient Mutants of Arabidopsis Reveal That <i>PAD4</i> Encodes a Regulatory Factor and That Four <i>PAD</i> Genes Contribute to Downy Mildew Resistance. Genetics, 1997, 146, 381-392.	2.9	332
39	Isolation of Arabidopsis Mutants With Enhanced Disease Susceptibility by Direct Screening. Genetics, 1996, 143, 973-982.	2.9	520
40	Mode of Action of the <i>Arabidopsis thaliana</i> Phytoalexin Camalexin and Its Role in <i>Arabidopsis</i> -Pathogen Interactions. Molecular Plant-Microbe Interactions, 1996, 9, 748.	2.6	139
41	Purification and characterization of multiple forms of the pineapple-stem-derived cysteine proteinases ananain and comosain. Biochemical Journal, 1994, 301, 727-735.	3.7	105
42	Concerning the formation and the kinetics of phenylium ions. International Journal of Mass Spectrometry and Ion Processes, 1989, 92, 65-77.	1.8	34