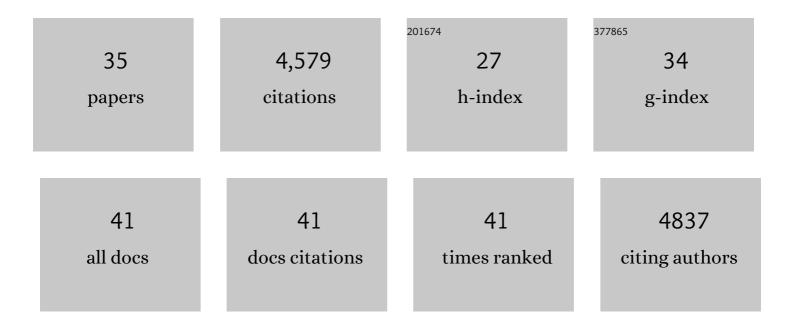
Elisabeth Fournier

List of Publications by Year in descending order

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FUSARETH FOURNIER

#	Article	IF	CITATIONS
1	A Genomic Approach to Develop a New qPCR Test Enabling Detection of the <i>Pyricularia oryzae</i> Lineage Causing Wheat Blast. Plant Disease, 2020, 104, 60-70.	1.4	20
2	A PCR, qPCR, and LAMP Toolkit for the Detection of the Wheat Blast Pathogen in Seeds. Plants, 2020, 9, 277.	3.5	15
3	Emergence of Southern Rice Black-Streaked Dwarf Virus in the Centuries-Old Chinese Yuanyang Agrosystem of Rice Landraces. Viruses, 2019, 11, 985.	3.3	7
4	<i>Pyricularia graminisâ€ŧritici </i> is not the correct species name for the wheat blast fungus: response to Ceresini <i>etÂal</i> . (MPP 20:2). Molecular Plant Pathology, 2019, 20, 173-179.	4.2	42
5	Gene Flow between Divergent Cereal- and Grass-Specific Lineages of the Rice Blast Fungus <i>Magnaporthe oryzae</i> . MBio, 2018, 9, .	4.1	163
6	Coexistence of Multiple Endemic and Pandemic Lineages of the Rice Blast Pathogen. MBio, 2018, 9, .	4.1	59
7	Pathogen effectors and plant immunity determine specialization of the blast fungus to rice subspecies. ELife, 2016, 5, .	6.0	67
8	Evolution of Compatibility Range in the Riceâ^' <i>Magnaporthe oryzae</i> System: An Uneven Distribution of R Genes Between Rice Subspecies. Phytopathology, 2016, 106, 348-354.	2.2	21
9	Emergence of wheat blast in Bangladesh was caused by a South American lineage of Magnaporthe oryzae. BMC Biology, 2016, 14, 84.	3.8	355
10	Structure Analysis Uncovers a Highly Diverse but Structurally Conserved Effector Family in Phytopathogenic Fungi. PLoS Pathogens, 2015, 11, e1005228.	4.7	188
11	Deciphering Genome Content and Evolutionary Relationships of Isolates from the Fungus <i>Magnaporthe oryzae</i> Attacking Different Host Plants. Genome Biology and Evolution, 2015, 7, 2896-2912.	2.5	96
12	Population structure and temporal maintenance of the multihost fungal pathogen <scp><i>B</i></scp> <i>otrytis cinerea</i> : causes and implications for disease management. Environmental Microbiology, 2015, 17, 1261-1274.	3.8	44
13	Southâ€East Asia is the center of origin, diversity and dispersion of the rice blast fungus, <i>Magnaporthe oryzae</i> . New Phytologist, 2014, 201, 1440-1456.	7.3	95
14	The Rice Resistance Protein Pair RGA4/RGA5 Recognizes the <i>Magnaporthe oryzae</i> Effectors AVR-Pia and AVR1-CO39 by Direct Binding Â. Plant Cell, 2013, 25, 1463-1481.	6.6	466
15	The â€~ <scp>D</scp> r <scp>J</scp> ekyll and <scp>M</scp> r <scp>H</scp> yde fungus': noble rot versus gray mold symptoms of <i><scp>B</scp>otrytis cinerea</i> on grapes. Evolutionary Applications, 2013, 6, 960-969.	3.1	40
16	The variety mixture strategy assessed in a G × G experiment with rice and the blast fungus Magnaporthe oryzae. Frontiers in Genetics, 2013, 4, 312.	2.3	10
17	Asexual reproduction induces a rapid and permanent loss of sexual reproduction capacity in the rice fungal pathogen Magnaporthe oryzae: results of in vitroexperimental evolution assays. BMC Evolutionary Biology, 2012, 12, 42.	3.2	36
18	Arms race coâ€evolution of <i>Magnaporthe oryzae AVRâ€Pik</i> and rice <i>Pik</i> genes driven by their physical interactions. Plant Journal, 2012, 72, 894-907.	5.7	249

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19	Genes under positive selection in a model plant pathogenic fungus, Botrytis. Infection, Genetics and Evolution, 2012, 12, 987-996.	2.3	40
20	Sex at the origin: an Asian population of the rice blast fungus <i>Magnaporthe oryzae</i> reproduces sexually. Molecular Ecology, 2012, 21, 1330-1344.	3.9	91
21	Genomic Analysis of the Necrotrophic Fungal Pathogens Sclerotinia sclerotiorum and Botrytis cinerea. PLoS Genetics, 2011, 7, e1002230.	3.5	902
22	<i>Botrytis pseudocinerea</i> , a New Cryptic Species Causing Gray Mold in French Vineyards in Sympatry with <i>Botrytis cinerea</i> . Phytopathology, 2011, 101, 1433-1445.	2.2	146
23	Microsatellite loci to recognize species for the cheese starter and contaminating strains associated with cheese manufacturing. International Journal of Food Microbiology, 2010, 137, 204-213.	4.7	56
24	Rapidly evolving genes in pathogens: Methods for detecting positive selection and examples among fungi, bacteria, viruses and protists. Infection, Genetics and Evolution, 2009, 9, 656-670.	2.3	100
25	World Population Structure and Migration of the Rice Blast Fungus, Magnaporthe oryzae. , 2009, , 209-215.		36
26	Funybase: a Fungal phylogenomic database. BMC Bioinformatics, 2008, 9, 456.	2.6	60
27	Challenges of microsatellite isolation in fungi. Fungal Genetics and Biology, 2007, 44, 933-949.	2.1	166
28	PHYLOGENETIC EVIDENCE OF HOST-SPECIFIC CRYPTIC SPECIES IN THE ANTHER SMUT FUNGUS. Evolution; International Journal of Organic Evolution, 2007, 61, 15-26.	2.3	209
29	<i>Botrytis cinerea</i> virulence factors: new insights into a necrotrophic and polyphageous pathogen. FEMS Microbiology Letters, 2007, 277, 1-10.	1.8	392
30	Partition of the Botrytis cinerea complex in France using multiple gene genealogies. Mycologia, 2005, 97, 1251-1267.	1.9	112
31	Characterization of Bc- <i>hch,</i> the <i>Botrytis cinerea</i> homolog of the <i>Neurospora crassahet-c</i> vegetative incompatibility locus, and its use as a population marker. Mycologia, 2003, 95, 251-261.	1.9	82
32	Foraging activity of the carabid beetle Pterostichus melanarius III. in field margin habitats. Agriculture, Ecosystems and Environment, 2002, 89, 253-259.	5.3	24
33	Activity and satiation state in Pterostichus melanarius : an experiment in different agricultural habitats. Ecological Entomology, 2001, 26, 235-244.	2.2	22
34	Title is missing!. Landscape Ecology, 2001, 16, 17-32.	4.2	77
35	Effects of newly planted hedges on ground-beetle diversity (Coleoptera, Carabidae) in an agricultural landscape. Ecography, 1999, 22, 87-97.	4.5	78