

Martijn Rep

List of Publications by Year in descending order

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108
papers

14,975
citations

28274

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105
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116
all docs

116
docs citations

116
times ranked

11887
citing authors

#	ARTICLE	IF	CITATIONS
1	Profile of the in silico secretome of the palm dieback pathogen, <i>Fusarium oxysporum</i> f. sp. <i>albedinis</i> , a fungus that puts natural oases at risk. <i>PLoS ONE</i> , 2022, 17, e0260830.	2.5	4
2	Genome sequences of 38 <i>Fusarium oxysporum</i> strains. <i>BMC Research Notes</i> , 2022, 15, .	1.4	1
3	Phylogenomic Analysis of a 55.1-kb 19-Gene Dataset Resolves a Monophyletic <i>Fusarium</i> that Includes the <i>Fusarium solani</i> Species Complex. <i>Phytopathology</i> , 2021, 111, 1064-1079.	2.2	107
4	A single gene in <i>Fusarium oxysporum</i> limits host range. <i>Molecular Plant Pathology</i> , 2021, 22, 108-116.	4.2	12
5	Comparative genomics of <i>Fusarium oxysporum</i> f. sp. <i>melonis</i> strains reveals nine lineages and a new sequence type of <i>scv</i> AvrFom2. <i>Environmental Microbiology</i> , 2021, 23, 2035-2053.	3.8	5
6	Pattern-triggered immunity restricts host colonization by endophytic fusaria, but does not affect endophyte-mediated resistance. <i>Molecular Plant Pathology</i> , 2021, 22, 204-215.	4.2	14
7	Putative Effector Genes Distinguish Two Pathogenicity Groups of <i>Fusarium oxysporum</i> f. sp. <i>spinaciae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 141-156.	2.6	14
8	A pair of effectors encoded on a conditionally dispensable chromosome of <i>Fusarium oxysporum</i> suppress host-specific immunity. <i>Communications Biology</i> , 2021, 4, 707.	4.4	23
9	Quantitative resistance linked to late effectors. <i>New Phytologist</i> , 2021, 231, 1301-1303.	7.3	3
10	Number of Candidate Effector Genes in Accessory Genomes Differentiates Pathogenic From Endophytic <i>Fusarium oxysporum</i> Strains. <i>Frontiers in Plant Science</i> , 2021, 12, 761740.	3.6	17
11	Rapid evolution in plant-microbe interactions – a molecular genomics perspective. <i>New Phytologist</i> , 2020, 225, 1134-1142.	7.3	96
12	Host-specificity factors in plant pathogenic fungi. <i>Fungal Genetics and Biology</i> , 2020, 144, 103447.	2.1	38
13	From laboratory to field: applying the Fo47 biocontrol strain in potato fields. <i>European Journal of Plant Pathology</i> , 2020, 158, 645-654.	1.7	3
14	Editorial: Secretomics: More Secrets to Unravel on Plant-Fungus Interactions. <i>Frontiers in Plant Science</i> , 2020, 11, 601021.	3.6	0
15	Related mobile pathogenicity chromosomes in <i>Fusarium oxysporum</i> determine host range on cucurbits. <i>Molecular Plant Pathology</i> , 2020, 21, 761-776.	4.2	36
16	Partial pathogenicity chromosomes in <i>Fusarium oxysporum</i> are sufficient to cause disease and can be horizontally transferred. <i>Environmental Microbiology</i> , 2020, 22, 4985-5004.	3.8	29
17	The genome of opportunistic fungal pathogen <i>Fusarium oxysporum</i> carries a unique set of lineage-specific chromosomes. <i>Communications Biology</i> , 2020, 3, 50.	4.4	55
18	Diminished Pathogen and Enhanced Endophyte Colonization upon Co-inoculation of Endophytic and Pathogenic <i>Fusarium</i> Strains. <i>Microorganisms</i> , 2020, 8, 544.	3.6	15

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19	The root-invasive pathogen <i>Fusarium oxysporum</i> targets pattern-triggered immunity using both cytoplasmic and apoplasmic effectors. <i>New Phytologist</i> , 2020, 227, 1479-1492.	7.3	35
20	Endophyte-Mediated Resistance in Tomato to <i>Fusarium oxysporum</i> Is Independent of ET, JA, and SA. <i>Frontiers in Plant Science</i> , 2019, 10, 979.	3.6	70
21	Transcript accumulation in a trifold interaction gives insight into mechanisms of biocontrol. <i>New Phytologist</i> , 2019, 224, 547-549.	7.3	2
22	Pathogen-induced pH changes regulate the growth-defense balance in plants. <i>EMBO Journal</i> , 2019, 38, e101822.	7.8	65
23	<i>Fusarium oxysporum</i> colonizes the stem of resistant tomato plants, the extent varying with the R-gene present. <i>European Journal of Plant Pathology</i> , 2019, 154, 55-65.	1.7	41
24	Use of Comparative Genomics-Based Markers for Discrimination of Host Specificity in <i>Fusarium oxysporum</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	62
25	Xylem Sap Proteomics Reveals Distinct Differences Between R Gene- and Endophyte-Mediated Resistance Against <i>Fusarium</i> Wilt Disease in Tomato. <i>Frontiers in Microbiology</i> , 2018, 9, 2977.	3.5	63
26	A SIX1 homolog in <i>Fusarium oxysporum</i> f.sp. cubense tropical race 4 contributes to virulence towards Cavendish banana. <i>PLoS ONE</i> , 2018, 13, e0205896.	2.5	49
27	Multiple Evolutionary Trajectories Have Led to the Emergence of Races in <i>Fusarium oxysporum</i> f. sp. lycopersici. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	36
28	The tomato <i>Sl</i> gene for <i>Fusarium</i> wilt resistance encodes an atypical leucine-rich repeat receptor-like protein whose function is nevertheless dependent on <i>SOBIR1</i> and <i>SERK3/BAK1</i> . <i>Plant Journal</i> , 2017, 89, 1195-1209.	5.7	103
29	A mobile pathogenicity chromosome in <i>Fusarium oxysporum</i> for infection of multiple cucurbit species. <i>Scientific Reports</i> , 2017, 7, 9042.	3.3	115
30	The Distribution of Miniature Impala Elements and SIX Genes in the <i>Fusarium</i> Genus is Suggestive of Horizontal Gene Transfer. <i>Journal of Molecular Evolution</i> , 2017, 85, 14-25.	1.8	40
31	Adaptation to the Host Environment by Plant-Pathogenic Fungi. <i>Annual Review of Phytopathology</i> , 2017, 55, 427-450.	7.8	56
32	Mitochondrial genomes reveal recombination in the presumed asexual <i>Fusarium oxysporum</i> species complex. <i>BMC Genomics</i> , 2017, 18, 735.	2.8	65
33	The <i>Arabidopsis</i> leucine-rich repeat receptor kinase MIK2/LRR-KISS connects cell wall integrity sensing, root growth and response to abiotic and biotic stresses. <i>PLoS Genetics</i> , 2017, 13, e1006832.	3.5	187
34	Transcription Factors Encoded on Core and Accessory Chromosomes of <i>Fusarium oxysporum</i> Induce Expression of Effector Genes. <i>PLoS Genetics</i> , 2016, 12, e1006401.	3.5	75
35	Dispensable chromosomes in <i>Fusarium oxysporum</i> f. sp. <i>lycopersici</i> . <i>Molecular Plant Pathology</i> , 2016, 17, 1455-1466.	4.2	94
36	Exchange of core chromosomes and horizontal transfer of lineage-specific chromosomes in <i>Fusarium oxysporum</i> . <i>Environmental Microbiology</i> , 2016, 18, 3702-3713.	3.8	102

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37	Insights into Adaptations to a Near-Obligate Nematode Endoparasitic Lifestyle from the Finished Genome of <i>Drechmeria coniospora</i> . <i>Scientific Reports</i> , 2016, 6, 23122.	3.3	32
38	Nuclear dynamics and genetic rearrangement in heterokaryotic colonies of <i>Fusarium oxysporum</i> . <i>Fungal Genetics and Biology</i> , 2016, 91, 20-31.	2.1	34
39	Comparative genomics of <i>Fusarium oxysporum</i> f. sp. <i>melonis</i> reveals the secreted protein recognized by the <i>Fom2</i> resistance gene in melon. <i>New Phytologist</i> , 2016, 209, 307-318.	7.3	87
40	Suppressor of fusion, a <i>Fusarium oxysporum</i> homolog of Ndt80, is required for nutrient-dependent regulation of anastomosis. <i>Fungal Genetics and Biology</i> , 2016, 95, 49-57.	2.1	9
41	Effector profiles distinguish <i>formae speciales</i> of <i>Fusarium oxysporum</i> . <i>Environmental Microbiology</i> , 2016, 18, 4087-4102.	3.8	179
42	Non-canonical Helitrons in <i>Fusarium oxysporum</i> . <i>Mobile DNA</i> , 2016, 7, 27.	3.6	13
43	The <i>AVR2</i> gene pair is required to activate <i>MI2</i> -mediated immunity in tomato. <i>New Phytologist</i> , 2015, 208, 507-518.	7.3	113
44	The Role of Pathogen-Secreted Proteins in Fungal Vascular Wilt Diseases. <i>International Journal of Molecular Sciences</i> , 2015, 16, 23970-23993.	4.1	106
45	The effector repertoire of <i>Fusarium oxysporum</i> determines the tomato xylem proteome composition following infection. <i>Frontiers in Plant Science</i> , 2015, 6, 967.	3.6	95
46	Dynamics of the Establishment of Multinucleate Compartments in <i>Fusarium oxysporum</i> . <i>Eukaryotic Cell</i> , 2015, 14, 78-85.	3.4	11
47	Fluorescence Assisted Selection of Transformants (FAST): Using flow cytometry to select fungal transformants. <i>Fungal Genetics and Biology</i> , 2015, 76, 104-109.	2.1	14
48	<i>Fusarium oxysporum</i> . , 2014, , 99-119.		9
49	The <i>Fusarium oxysporum</i> Effector Six6 Contributes to Virulence and Suppresses I-2-Mediated Cell Death. <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 336-348.	2.6	139
50	<i>EBR1</i> genomic expansion and its role in virulence of <i>Fusarium</i> species. <i>Environmental Microbiology</i> , 2014, 16, 1982-2003.	3.8	30
51	MITEs in the promoters of effector genes allow prediction of novel virulence genes in <i>Fusarium oxysporum</i> . <i>BMC Genomics</i> , 2013, 14, 119.	2.8	233
52	Phosphatidylinositol 4-phosphate is associated to extracellular lipoproteic fractions and is detected in tomato apoplastic fluids. <i>Plant Biology</i> , 2012, 14, 41-49.	3.8	23
53	Genetic basis of carotenoid overproduction in <i>Fusarium oxysporum</i> . <i>Fungal Genetics and Biology</i> , 2012, 49, 684-696.	2.1	25
54	Horizontal Transfer of Supernumerary Chromosomes in Fungi. <i>Methods in Molecular Biology</i> , 2012, 835, 427-437.	0.9	16

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55	Degradation of aromatic compounds through the β -ketoadipate pathway is required for pathogenicity of the tomato wilt pathogen <i>Fusarium oxysporum</i> f. sp. <i>lycopersici</i> . <i>Molecular Plant Pathology</i> , 2012, 13, 1089-1100.	4.2	45
56	Variation in potential effector genes distinguishing Australian and non-Australian isolates of the cotton wilt pathogen <i>Fusarium oxysporum</i> f.sp. <i>vasinfectum</i> . <i>Plant Pathology</i> , 2011, 60, 232-243.	2.4	78
57	The <i>FRP1</i> F-box gene has different functions in sexuality, pathogenicity and metabolism in three fungal pathogens. <i>Molecular Plant Pathology</i> , 2011, 12, 548-563.	4.2	22
58	The tomato xylem sap protein XSP10 is required for full susceptibility to <i>Fusarium</i> wilt disease. <i>Journal of Experimental Botany</i> , 2011, 62, 963-973.	4.8	52
59	The genomic organization of plant pathogenicity in <i>Fusarium</i> species. <i>Current Opinion in Plant Biology</i> , 2010, 13, 420-426.	7.1	142
60	The arms race between tomato and <i>Fusarium oxysporum</i> . <i>Molecular Plant Pathology</i> , 2010, 11, 309-314.	4.2	246
61	Methyl salicylate production in tomato affects biotic interactions. <i>Plant Journal</i> , 2010, 62, 124-134.	5.7	77
62	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	27.8	1,442
63	Lessons from Fungal F-Box Proteins. <i>Eukaryotic Cell</i> , 2009, 8, 677-695.	3.4	93
64	The Nuclear Protein Sge1 of <i>Fusarium oxysporum</i> Is Required for Parasitic Growth. <i>PLoS Pathogens</i> , 2009, 5, e1000637.	4.7	135
65	The Genome of <i>Nectria haematococca</i> : Contribution of Supernumerary Chromosomes to Gene Expansion. <i>PLoS Genetics</i> , 2009, 5, e1000618.	3.5	402
66	Evolutionary relationships between <i>Fusarium oxysporum</i> f. sp. <i>lycopersici</i> and <i>F. oxysporum</i> f. sp. <i>radicis-lycopersici</i> isolates inferred from mating type, elongation factor-1 α and exopolygalacturonase sequences. <i>Mycological Research</i> , 2009, 113, 1181-1191.	2.5	38
67	The effector protein Avr2 of the xylem-colonizing fungus <i>Fusarium oxysporum</i> activates the tomato resistance protein $\text{Î}2$ intracellularly. <i>Plant Journal</i> , 2009, 58, 970-978.	5.7	267
68	Pathogen profile update: <i>Fusarium oxysporum</i> . <i>Molecular Plant Pathology</i> , 2009, 10, 311-324.	4.2	602
69	Mutation of <i>CRE1</i> in <i>Fusarium oxysporum</i> reverts the pathogenicity defects of the <i>FRP1</i> deletion mutant. <i>Molecular Microbiology</i> , 2009, 74, 1100-1113.	2.5	50
70	Effector gene screening allows unambiguous identification of <i>Fusarium oxysporum</i> f. sp. <i>lycopersici</i> races and discrimination from other <i>formae speciales</i> . <i>FEMS Microbiology Letters</i> , 2009, 300, 201-215.	1.8	221
71	Transformation of <i>Fusarium virguliforme</i> , the Causal Agent of Sudden Death Syndrome of Soybean. <i>Journal of Phytopathology</i> , 2009, 157, 319-321.	1.0	13
72	Insight into the molecular requirements for pathogenicity of <i>Fusarium oxysporum</i> f. sp. <i>lycopersici</i> through large-scale insertional mutagenesis. <i>Genome Biology</i> , 2009, 10, R4.	9.6	111

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73	Impaired Colonization and Infection of Tomato Roots by the <i>frp1</i> Mutant of <i>Fusarium oxysporum</i> Correlates with Reduced CWDE Gene Expression. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 507-518.	2.6	35
74	Recent developments in the molecular discrimination of <i>formae speciales</i> of <i>Fusarium oxysporum</i> . <i>Pest Management Science</i> , 2008, 64, 781-788.	3.4	143
75	The presence of a virulence locus discriminates <i>Fusarium oxysporum</i> isolates causing tomato wilt from other isolates. <i>Environmental Microbiology</i> , 2008, 10, 1475-1485.	3.8	130
76	Expression of effector gene SIX1 of <i>Fusarium oxysporum</i> requires living plant cells. <i>Fungal Genetics and Biology</i> , 2008, 45, 1257-1264.	2.1	99
77	Suppression of Plant Resistance Gene-Based Immunity by a Fungal Effector. <i>PLoS Pathogens</i> , 2008, 4, e1000061.	4.7	338
78	Protein Extraction from Xylem and Phloem Sap. , 2007, 355, 27-36.		14
79	Virulence Genes and the Evolution of Host Specificity in Plant-Pathogenic Fungi. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 1175-1182.	2.6	133
80	The <i>Fusarium graminearum</i> Genome Reveals a Link Between Localized Polymorphism and Pathogen Specialization. <i>Science</i> , 2007, 317, 1400-1402.	12.6	837
81	The mixed xylem sap proteome of <i>Fusarium oxysporum</i> -infected tomato plants. <i>Molecular Plant Pathology</i> , 2007, 8, 215-221.	4.2	345
82	Significance of Inducible Defense-related Proteins in Infected Plants. <i>Annual Review of Phytopathology</i> , 2006, 44, 135-162.	7.8	2,754
83	The presence of GC-AG introns in <i>Neurospora crassa</i> and other eucaryotes determined from analyses of complete genomes: implications for automated gene prediction. <i>Genomics</i> , 2006, 87, 338-347.	2.9	23
84	Small proteins of plant-pathogenic fungi secreted during host colonization. <i>FEMS Microbiology Letters</i> , 2005, 253, 19-27.	1.8	185
85	Frp1 is a <i>Fusarium oxysporum</i> F-box protein required for pathogenicity on tomato. <i>Molecular Microbiology</i> , 2005, 57, 1051-1063.	2.5	80
86	Colonization of the Arabidopsis rhizosphere by fluorescent <i>Pseudomonas</i> spp. activates a root-specific, ethylene-responsive PR-5 gene in the vascular bundle. <i>Plant Molecular Biology</i> , 2005, 57, 731-748.	3.9	62
87	<i>Fusarium oxysporum</i> Evades I-3-Mediated Resistance Without Altering the Matching Avirulence Gene. <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 15-23.	2.6	120
88	Drifter, a novel, low copy hAT-like transposon in <i>Fusarium oxysporum</i> is activated during starvation. <i>Fungal Genetics and Biology</i> , 2005, 42, 546-553.	2.1	26
89	A small, cysteine-rich protein secreted by <i>Fusarium oxysporum</i> during colonization of xylem vessels is required for I-3-mediated resistance in tomato. <i>Molecular Microbiology</i> , 2004, 53, 1373-1383.	2.5	359
90	Construction of a mitotic linkage map of <i>Fusarium oxysporum</i> based on Foxy -AFLPs. <i>Molecular Genetics and Genomics</i> , 2003, 269, 215-226.	2.1	21

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91	A tomato xylem sap protein represents a new family of small cysteine-rich proteins with structural similarity to lipid transfer proteins. <i>FEBS Letters</i> , 2003, 534, 82-86.	2.8	49
92	Mass Spectrometric Identification of Isoforms of PR Proteins in Xylem Sap of Fungus-Infected Tomato. <i>Plant Physiology</i> , 2002, 130, 904-917.	4.8	201
93	Dissection of Transient Oxidative Stress Response in <i>Saccharomyces cerevisiae</i> by Using DNA Microarrays. <i>Molecular Biology of the Cell</i> , 2002, 13, 2783-2794.	2.1	103
94	The <i>Saccharomyces cerevisiae</i> Sko1p transcription factor mediates HOG pathway-dependent osmotic regulation of a set of genes encoding enzymes implicated in protection from oxidative damage. <i>Molecular Microbiology</i> , 2001, 40, 1067-1083.	2.5	161
95	The Transcriptional Response of <i>Saccharomyces cerevisiae</i> to Osmotic Shock. <i>Journal of Biological Chemistry</i> , 2000, 275, 8290-8300.	3.4	491
96	Stimulation of the yeast high osmolarity glycerol (HOG) pathway: evidence for a signal generated by a change in turgor rather than by water stress. <i>FEBS Letters</i> , 2000, 472, 159-165.	2.8	81
97	Different signalling pathways contribute to the control of GPD1 gene expression by osmotic stress in <i>Saccharomyces cerevisiae</i> . <i>Microbiology (United Kingdom)</i> , 1999, 145, 715-727.	1.8	115
98	Osmotic Stress-Induced Gene Expression in <i>Saccharomyces cerevisiae</i> Requires Msn1p and the Novel Nuclear Factor Hot1p. <i>Molecular and Cellular Biology</i> , 1999, 19, 5474-5485.	2.3	248
99	ATP-dependent proteases that also chaperone protein biogenesis. <i>Trends in Biochemical Sciences</i> , 1997, 22, 118-123.	7.5	228
100	Afg3p, a mitochondrial ATP-dependent metalloprotease, is involved in degradation of mitochondrially-encoded Cox1, Cox3, Cob, Su6, Su8 and Su9 subunits of the inner membrane complexes III, IV and V. <i>FEBS Letters</i> , 1996, 381, 42-46.	2.8	79
101	MBA1 encodes a mitochondrial membrane-associated protein required for biogenesis of the respiratory chain. <i>FEBS Letters</i> , 1996, 388, 185-188.	2.8	21
102	Promotion of Mitochondrial Membrane Complex Assembly by a Proteolytically Inactive Yeast Lon. <i>Science</i> , 1996, 274, 103-106.	12.6	167
103	Three genes for mitochondrial proteins suppress null-mutations in both Afg3 and Rca1 when over-expressed. <i>Current Genetics</i> , 1996, 30, 206-211.	1.7	51
104	The role of protein degradation in mitochondrial function and biogenesis. <i>Current Genetics</i> , 1996, 30, 367-380.	1.7	109
105	Yeast sequencing reports. Sequence of the AFG3 gene encoding a new member of the FtsH/Yme1/Tma subfamily of the AAA-protein family. <i>Yeast</i> , 1994, 10, 1389-1394.	1.7	71
106	Single point mutations in domain II of the yeast mitochondrial release factor mRF-1 affect ribosome binding. <i>Nucleic Acids Research</i> , 1993, 21, 5308-5315.	14.5	17
107	Sequence comparison of new prokaryotic and mitochondrial members of the polypeptide chain release factor family predicts a five-domain model for release factor structure. <i>Nucleic Acids Research</i> , 1992, 20, 4423-4428.	14.5	46
108	The yeast nuclear gene MRF1 encodes a mitochondrial peptide chain release factor and cures several mitochondrial RNA splicing defects. <i>Nucleic Acids Research</i> , 1992, 20, 6339-6346.	14.5	57