

# Ronnie de Jonge

## List of Publications by Year in descending order

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Version: 2024-02-01

50  
papers

5,947  
citations

201674

27  
h-index

254184

43  
g-index

58  
all docs

58  
docs citations

58  
times ranked

5742  
citing authors

#	ARTICLE	IF	CITATIONS
1	Seedborne <i>Cercospora beticola</i> Can Initiate Cercospora Leaf Spot from Sugar Beet ( <i>Beta</i> ) Tj ETQq1 1 0.784314 rgBT <sub>4</sub> /Overlo	2.2	4
2	Sexual reproduction contributes to the evolution of resistance-breaking isolates of the spinach pathogen <i>Peronospora effusa</i> . Environmental Microbiology, 2022, 24, 1622-1637.	3.8	8
3	<i>Pseudomonas simiae</i> WCS417: star track of a model beneficial rhizobacterium. Plant and Soil, 2021, 461, 245-263.	3.7	53
4	Transcriptome Signatures in <i>Pseudomonas simiae</i> WCS417 Shed Light on Role of Root-Secreted Coumarins in Arabidopsis-Mutualist Communication. Microorganisms, 2021, 9, 575.	3.6	12
5	Understanding plant-microorganism interactions to envision a future of sustainable agriculture. Environmental Microbiology, 2021, 23, 1809-1811.	3.8	2
6	A 20 kb lineage-specific genomic region tames virulence in pathogenic amphidiploid <i>Verticillium longisporum</i> . Molecular Plant Pathology, 2021, 22, 939-953.	4.2	6
7	Rapid evolution of bacterial mutualism in the plant rhizosphere. Nature Communications, 2021, 12, 3829.	12.8	51
8	Experimental-Evolution-Driven Identification of <i>Arabidopsis</i> Rhizosphere Competence Genes in <i>Pseudomonas protegens</i> . MBio, 2021, 12, e0092721.	4.1	19
9	Fungal social influencers: secondary metabolites as a platform for shaping the plant-associated community. Plant Journal, 2021, 108, 632-645.	5.7	14
10	Identification and characterization of <i>Cercospora beticola</i> necrosis-inducing effector CbNip1. Molecular Plant Pathology, 2021, 22, 301-316.	4.2	14
11	<i>Cercospora beticola</i> : The intoxicating lifestyle of the leaf spot pathogen of sugar beet. Molecular Plant Pathology, 2020, 21, 1020-1041.	4.2	39
12	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization. PLoS Pathogens, 2020, 16, e1008652.	4.7	44
13	Genome comparisons suggest an association between <i>Ceratocystis</i> host adaptations and effector clusters in unique transposable element families. Fungal Genetics and Biology, 2020, 143, 103433.	2.1	9
14	The Soil-Borne Identity and Microbiome-Assisted Agriculture: Looking Back to the Future. Molecular Plant, 2020, 13, 1394-1401.	8.3	80
15	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization. , 2020, 16, e1008652.		0
16	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization. , 2020, 16, e1008652.		0
17	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization. , 2020, 16, e1008652.		0
18	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization. , 2020, 16, e1008652.		0

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19	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization. , 2020, 16, e1008652.		0
20	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization. , 2020, 16, e1008652.		0
21	The Age of Coumarins in Plant-Microbe Interactions. Plant and Cell Physiology, 2019, 60, 1405-1419.	3.1	241
22	Molecular dialogue between arbuscular mycorrhizal fungi and the nonhost plant <i>Arabidopsis thaliana</i> switches from initial detection to antagonism. New Phytologist, 2019, 223, 867-881.	7.3	49
23	Gene cluster conservation identifies melanin and perylenequinone biosynthesis pathways in multiple plant pathogenic fungi. Environmental Microbiology, 2019, 21, 913-927.	3.8	16
24	The Soil-Borne Legacy. Cell, 2018, 172, 1178-1180.	28.9	366
25	MYB72-dependent coumarin exudation shapes root microbiome assembly to promote plant health. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5213-E5222.	7.1	608
26	Genome Sequence of a Lethal Strain of Xylem-Invading <i>Verticillium nonalfalfae</i> . Genome Announcements, 2018, 6, .	0.8	13
27	Disease-induced assemblage of a plant-beneficial bacterial consortium. ISME Journal, 2018, 12, 1496-1507.	9.8	603
28	Gene cluster conservation provides insight into cercosporin biosynthesis and extends production to the genus <i>Colletotrichum</i> . Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5459-E5466.	7.1	61
29	Microbial small molecules – weapons of plant subversion. Natural Product Reports, 2018, 35, 410-433.	10.3	105
30	Genetic characterization of T-DNA insertions in the genome of the <i>Arabidopsis thaliana</i> sumo1/2 knock-down line. Plant Signaling and Behavior, 2017, 12, e1293216.	2.4	4
31	<i>Verticillium dahliae</i> LysM effectors differentially contribute to virulence on plant hosts. Molecular Plant Pathology, 2017, 18, 596-608.	4.2	122
32	Fermentation assays reveal differences in sugar and (off-) flavor metabolism across different <i>Brettanomyces bruxellensis</i> strains. FEMS Yeast Research, 2017, 17, .	2.3	34
33	RNA-sequencing of <i>Cercospora beticola</i> DMI-sensitive and -resistant isolates after treatment with tetraconazole identifies common and contrasting pathway induction. Fungal Genetics and Biology, 2016, 92, 1-13.	2.1	30
34	The Soil-Borne Supremacy. Trends in Plant Science, 2016, 21, 171-173.	8.8	159
35	Complete mitochondrial genome of the <i>Verticillium</i> -wilt causing plant pathogen <i>Verticillium nonalfalfae</i> . PLoS ONE, 2016, 11, e0148525.	2.5	19
36	Comparative phenomics and targeted use of genomics reveals variation in carbon and nitrogen assimilation among different <i>Brettanomyces bruxellensis</i> strains. Applied Microbiology and Biotechnology, 2015, 99, 9123-9134.	3.6	47

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37	The heterothallic sugarbeet pathogen <i>Cercospora beticola</i> contains exon fragments of both MAT genes that are homogenized by concerted evolution. <i>Fungal Genetics and Biology</i> , 2014, 62, 43-54.	2.1	15
38	Optimized Agroinfiltration and Virus-Induced Gene Silencing to Study Ve1-Mediated <i>Verticillium</i> Resistance in Tobacco. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 182-190.	2.6	50
39	Extensive chromosomal reshuffling drives evolution of virulence in an asexual pathogen. <i>Genome Research</i> , 2013, 23, 1271-1282.	5.5	338
40	The transcriptome of <i>Verticillium dahliae</i> -infected <i>Nicotiana benthamiana</i> determined by deep RNA sequencing. <i>Plant Signaling and Behavior</i> , 2012, 7, 1065-1069.	2.4	42
41	Endoplasmic Reticulum-Quality Control Chaperones Facilitate the Biogenesis of Cf Receptor-Like Proteins Involved in Pathogen Resistance of Tomato. <i>Plant Physiology</i> , 2012, 159, 1819-1833.	4.8	63
42	Tomato immune receptor Ve1 recognizes effector of multiple fungal pathogens uncovered by genome and RNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5110-5115.	7.1	491
43	In Silico Identification and Characterization of Effector Catalogs. <i>Methods in Molecular Biology</i> , 2012, 835, 415-425.	0.9	11
44	How filamentous pathogens co-opt plants: the ins and outs of fungal effectors. <i>Current Opinion in Plant Biology</i> , 2011, 14, 400-406.	7.1	211
45	Comparative Genomics Yields Insights into Niche Adaptation of Plant Vascular Wilt Pathogens. <i>PLoS Pathogens</i> , 2011, 7, e1002137.	4.7	477
46	Conserved Fungal LysM Effector Ecp6 Prevents Chitin-Triggered Immunity in Plants. <i>Science</i> , 2010, 329, 953-955.	12.6	696
47	RNA silencing is required for <i>Arabidopsis</i> defence against <i>Verticillium</i> wilt disease. <i>Journal of Experimental Botany</i> , 2009, 60, 591-602.	4.8	189
48	Fungal LysM effectors: extinguishers of host immunity?. <i>Trends in Microbiology</i> , 2009, 17, 151-157.	7.7	243
49	The novel <i>Cladosporium fulvum</i> lysin motif effector Ecp6 is a virulence factor with orthologues in other fungal species. <i>Molecular Microbiology</i> , 2008, 69, 119-136.	2.5	275
50	Rapid Evolution of Plant-Bacterium Mutualism in the Rhizosphere. <i>SSRN Electronic Journal</i> , 0, , .	0.4	3