## **Martin Broberg**

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

16 18 350 10 h-index g-index citations papers 21 510 5.5 3.54 L-index avg, IF ext. citations ext. papers

#	Paper	IF	Citations
16	Ferulic acid, an abundant maize phenolic, regulates ABC and MFS transporter gene expression in the maize pathogen Cochliobolus heterostrophus. <i>Journal of Plant Diseases and Protection</i> , <b>2021</b> , 128, 1383-1391	1.5	1
15	Comparative genomics highlights the importance of drug efflux transporters during evolution of mycoparasitism in subgenus (Fungi, Ascomycota, Hypocreales). <i>Evolutionary Applications</i> , <b>2021</b> , 14, 476-	4987	5
14	Sleep apnoea is a risk factor for severe COVID-19. BMJ Open Respiratory Research, 2021, 8,	5.6	37
13	Mendelian randomization highlights insomnia as a risk factor for pain diagnoses. Sleep, 2021, 44,	1.1	4
12	LysM Proteins Regulate Fungal Development and Contribute to Hyphal Protection and Biocontrol Traits in. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 679	5.7	11
11	Host-microbiota-insect interactions drive emergent virulence in a complex tree disease. <i>Proceedings of the Royal Society B: Biological Sciences</i> , <b>2020</b> , 287, 20200956	4.4	10
10	Natural variation of root lesion nematode antagonism in the biocontrol fungus and identification of biocontrol factors through genome-wide association mapping. <i>Evolutionary Applications</i> , <b>2020</b> , 13, 2264	1- <del>22</del> 83	2
9	Extraction of Microbial and Host DNA, RNA, and Proteins from Oak Bark Tissue. <i>Methods and Protocols</i> , <b>2019</b> , 2,	2.5	2
8	Microbiome and infectivity studies reveal complex polyspecies tree disease in Acute Oak Decline. <i>ISME Journal</i> , <b>2018</b> , 12, 386-399	11.9	46
7	Integrated multi-omic analysis of host-microbiota interactions in acute oak decline. <i>Microbiome</i> , <b>2018</b> , 6, 21	16.6	36
6	Out in the Cold: Identification of Genomic Regions Associated With Cold Tolerance in the Biocontrol Fungus Through Genome-Wide Association Mapping. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 2844	5.7	11
5	Short oligogalacturonides induce pathogen resistance-associated gene expression in Arabidopsis thaliana. <i>BMC Plant Biology</i> , <b>2017</b> , 17, 19	5.3	43
4	Peroxidase-Generated Apoplastic ROS Impair Cuticle Integrity and Contribute to DAMP-Elicited Defenses. <i>Frontiers in Plant Science</i> , <b>2016</b> , 7, 1945	6.2	33
3	The global response regulator ExpA controls virulence gene expression through RsmA-mediated and RsmA-independent pathways in Pectobacterium wasabiae SCC3193. <i>Applied and Environmental Microbiology</i> , <b>2014</b> , 80, 1972-84	4.8	8
2	Lack of RsmA-mediated control results in constant hypervirulence, cell elongation, and hyperflagellation in Pectobacterium wasabiae. <i>PLoS ONE</i> , <b>2013</b> , 8, e54248	3.7	18
1	Revised phylogeny and novel horizontally acquired virulence determinants of the model soft rot phytopathogen Pectobacterium wasabiae SCC3193. <i>PLoS Pathogens</i> , <b>2012</b> , 8, e1003013	7.6	81