

# Stéphane Hacquard

## List of Publications by Year in descending order

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Version: 2024-02-01

41  
papers

7,794  
citations

159525

30  
h-index

265120

42  
g-index

49  
all docs

49  
docs citations

49  
times ranked

7950  
citing authors

#	ARTICLE	IF	CITATIONS
1	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	9.0	133
2	High-Throughput Profiling of Root-Associated Microbial Communities. <i>Methods in Molecular Biology</i> , 2022, 2494, 325-337.	0.4	4
3	Impact of global change on the plant microbiome. <i>New Phytologist</i> , 2022, 234, 1907-1909.	3.5	15
4	Climate drives rhizosphere microbiome variation and divergent selection between geographically distant <i>Arabidopsis</i> populations. <i>New Phytologist</i> , 2022, 236, 608-621.	3.5	9
5	Obtaining deeper insights into microbiome diversity using a simple method to block host and nontargets in amplicon sequencing. <i>Molecular Ecology Resources</i> , 2021, 21, 1952-1965.	2.2	9
6	Differential Impact of Plant Secondary Metabolites on the Soil Microbiota. <i>Frontiers in Microbiology</i> , 2021, 12, 666010.	1.5	31
7	A microbiota-root-shoot circuit favours <i>Arabidopsis</i> growth over defence under suboptimal light. <i>Nature Plants</i> , 2021, 7, 1078-1092.	4.7	90
8	Microbiota-root-shoot-environment axis and stress tolerance in plants. <i>Current Opinion in Plant Biology</i> , 2021, 62, 102028.	3.5	40
9	Tryptophan metabolism and bacterial commensals prevent fungal dysbiosis in <i>Arabidopsis</i> roots. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	38
10	Genetic determinants of endophytism in the <i>Arabidopsis</i> root microbiome. <i>Nature Communications</i> , 2021, 12, 7227.	5.8	58
11	Rbec: a tool for analysis of amplicon sequencing data from synthetic microbial communities. <i>ISME Communications</i> , 2021, 1, .	1.7	6
12	Host-Associated Quantitative Abundance Profiling Reveals the Microbial Load Variation of Root Microbiome. <i>Plant Communications</i> , 2020, 1, 100003.	3.6	38
13	Root microbiota assembly and adaptive differentiation among European <i>Arabidopsis</i> populations. <i>Nature Ecology and Evolution</i> , 2020, 4, 122-131.	3.4	157
14	Microbiota-mediated disease resistance in plants. <i>PLoS Pathogens</i> , 2019, 15, e1007740.	2.1	221
15	Contribution of bacterial-fungal balance to plant and animal health. <i>Current Opinion in Microbiology</i> , 2019, 49, 66-72.	2.3	45
16	Bacterial-fungal interactions: ecology, mechanisms and challenges. <i>FEMS Microbiology Reviews</i> , 2018, 42, 335-352.	3.9	468
17	Root-Associated Bacterial and Fungal Community Profiles of <i>Arabidopsis thaliana</i> Are Robust Across Contrasting Soil P Levels. <i>Phytobiomes Journal</i> , 2018, 2, 24-34.	1.4	37
18	The Rust Fungus <i>Melampsora larici-populina</i> Expresses a Conserved Genetic Program and Distinct Sets of Secreted Protein Genes During Infection of Its Two Host Plants, Larch and Poplar. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 695-706.	1.4	42

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19	Microbial interactions within the plant holobiont. <i>Microbiome</i> , 2018, 6, 58.	4.9	833
20	Microbial Interkingdom Interactions in Roots Promote Arabidopsis Survival. <i>Cell</i> , 2018, 175, 973-983.e14.	13.5	707
21	Interplay Between Innate Immunity and the Plant Microbiota. <i>Annual Review of Phytopathology</i> , 2017, 55, 565-589.	3.5	410
22	Root microbiota dynamics of perennial <i>Arabis alpina</i> are dependent on soil residence time but independent of flowering time. <i>ISME Journal</i> , 2017, 11, 43-55.	4.4	133
23	<i>Colletotrichum higginsianum</i> extracellular LysM proteins play dual roles in appressorial function and suppression of chitin-triggered plant immunity. <i>New Phytologist</i> , 2016, 211, 1323-1337.	3.5	155
24	Survival trade-offs in plant roots during colonization by closely related beneficial and pathogenic fungi. <i>Nature Communications</i> , 2016, 7, 11362.	5.8	214
25	Root Endophyte <i>Colletotrichum tofieldiae</i> Confers Plant Fitness Benefits that Are Phosphate Status Dependent. <i>Cell</i> , 2016, 165, 464-474.	13.5	510
26	Disentangling the factors shaping microbiota composition across the plant holobiont. <i>New Phytologist</i> , 2016, 209, 454-457.	3.5	97
27	Microbiota and Host Nutrition across Plant and Animal Kingdoms. <i>Cell Host and Microbe</i> , 2015, 17, 603-616.	5.1	628
28	Towards a holistic understanding of the beneficial interactions across the <i>Populus</i> microbiome. <i>New Phytologist</i> , 2015, 205, 1424-1430.	3.5	131
29	Genome analysis of poplar LRR-RLP gene clusters reveals RISP, a defense-related gene coding a candidate endogenous peptide elicitor. <i>Frontiers in Plant Science</i> , 2014, 5, 111.	1.7	30
30	The Genomics of Powdery Mildew Fungi. <i>Advances in Botanical Research</i> , 2014, 70, 109-142.	0.5	21
31	Laser microdissection and microarray analysis of <i>Tuber melanosporum</i> ectomycorrhizas reveal functional heterogeneity between mantle and Hartig net compartments. <i>Environmental Microbiology</i> , 2013, 15, 1853-1869.	1.8	62
32	Transcriptome analysis of poplar rust telia reveals overwintering adaptation and tightly coordinated karyogamy and meiosis processes. <i>Frontiers in Plant Science</i> , 2013, 4, 456.	1.7	30
33	Mosaic genome structure of the barley powdery mildew pathogen and conservation of transcriptional programs in divergent hosts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2219-28.	3.3	165
34	Sequential Delivery of Host-Induced Virulence Effectors by Appressoria and Intracellular Hyphae of the Phytopathogen <i>Colletotrichum higginsianum</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002643.	2.1	331
35	RNA-Seq of Early-Infected Poplar Leaves by the Rust Pathogen <i>Melampsora larici-populina</i> Uncovers PtSultr3;5, a Fungal-Induced Host Sulfate Transporter. <i>PLoS ONE</i> , 2012, 7, e44408.	1.1	57
36	A Comprehensive Analysis of Genes Encoding Small Secreted Proteins Identifies Candidate Effectors in <i>Melampsora larici-populina</i> (Poplar Leaf Rust). <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 279-293.	1.4	150

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37	Lifestyle transitions in plant pathogenic <i>Colletotrichum</i> fungi deciphered by genome and transcriptome analyses. <i>Nature Genetics</i> , 2012, 44, 1060-1065.	9.4	840
38	<i>Melampsora larici-populina</i> Transcript Profiling During Germination and Timecourse Infection of Poplar Leaves Reveals Dynamic Expression Patterns Associated with Virulence and Biotrophy. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 808-818.	1.4	80
39	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9166-9171.	3.3	640
40	Validation of <i>Melampsora larici-populina</i> reference genes for in planta RT-quantitative PCR expression profiling during time-course infection of poplar leaves. <i>Physiological and Molecular Plant Pathology</i> , 2011, 75, 106-112.	1.3	38
41	Laser Capture Microdissection of Uredinia Formed by <i>Melampsora larici-populina</i> Revealed a Transcriptional Switch Between Biotrophy and Sporulation. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 1275-1286.	1.4	58