Paul Schulze-Lefert

List of Publications by Year
in descending order

70 papers	21,240 citations	31976 53 h-index	88630 70 g-index
85 all docs	85 docs citations	85 times ranked	17427 citing authors

#	Article	IF	Citations
1	Structure and Functions of the Bacterial Microbiota of Plants. Annual Review of Plant Biology, 2013, 64, 807-838.	18.7	2,589
2	Revealing structure and assembly cues for Arabidopsis root-inhabiting bacterial microbiota. Nature, 2012, 488, 91-95.	27.8	2,127
3	Functional overlap of the Arabidopsis leaf and root microbiota. Nature, 2015, 528, 364-369.	27.8	1,062
4	A Glucosinolate Metabolism Pathway in Living Plant Cells Mediates Broad-Spectrum Antifungal Defense. Science, 2009, 323, 101-106.	12.6	927
5	SNARE-protein-mediated disease resistance at the plant cell wall. Nature, 2003, 425, 973-977.	27.8	904
6	Pre- and Postinvasion Defenses Both Contribute to Nonhost Resistance in Arabidopsis. Science, 2005, 310, 1180-1183.	12.6	753
7	Genome Expansion and Gene Loss in Powdery Mildew Fungi Reveal Tradeoffs in Extreme Parasitism. Science, 2010, 330, 1543-1546.	12.6	725
8	Microbial Interkingdom Interactions in Roots Promote Arabidopsis Survival. Cell, 2018, 175, 973-983.e14.	28.9	707
9	Nuclear Activity of MLA Immune Receptors Links Isolate-Specific and Basal Disease-Resistance Responses. Science, 2007, 315, 1098-1103.	12.6	659
10	Critical Assessment of Metagenome Interpretationâ€"a benchmark of metagenomics software. Nature Methods, 2017, 14, 1063-1071.	19.0	635
11	Microbiota and Host Nutrition across Plant and Animal Kingdoms. Cell Host and Microbe, 2015, 17, 603-616.	11.0	628
12	Arabidopsis PEN3/PDR8, an ATP Binding Cassette Transporter, Contributes to Nonhost Resistance to Inappropriate Pathogens That Enter by Direct Penetration. Plant Cell, 2006, 18, 731-746.	6.6	598
13	Quantitative divergence of the bacterial root microbiota in <i>Arabidopsis thaliana</i> relatives. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 585-592.	7.1	539
14	Root Endophyte Colletotrichum tofieldiae Confers Plant Fitness Benefits that Are Phosphate Status Dependent. Cell, 2016, 165, 464-474.	28.9	510
15	Interplay Between Innate Immunity and the Plant Microbiota. Annual Review of Phytopathology, 2017, 55, 565-589.	7.8	410
16	NLR functions in plant and animal immune systems: so far and yet so close. Nature Immunology, 2011, 12, 817-826.	14.5	378
17	A molecular evolutionary concept connecting nonhost resistance, pathogen host range, and pathogen speciation. Trends in Plant Science, 2011, 16, 117-125.	8.8	374
18	Recruitment and interaction dynamics of plant penetration resistance components in a plasma membrane microdomain. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 3135-3140.	7.1	327

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19	Metabolic consequences of susceptibility and resistance (race-specific and broad-spectrum) in barley leaves challenged with powdery mildew. Plant, Cell and Environment, 2006, 29, 1061-1076.	5.7	297
20	Direct pathogen-induced assembly of an NLR immune receptor complex to form a holoenzyme. Science, 2020, 370, .	12.6	291
21	Coiled-Coil Domain-Dependent Homodimerization of Intracellular Barley Immune Receptors Defines a Minimal Functional Module for Triggering Cell Death. Cell Host and Microbe, 2011, 9, 187-199.	11.0	269
22	Root nodule symbiosis in <i>Lotus japonicus</i> drives the establishment of distinctive rhizosphere, root, and nodule bacterial communities. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E7996-E8005.	7.1	258
23	Modular Traits of the Rhizobiales Root Microbiota and Their Evolutionary Relationship with Symbiotic Rhizobia. Cell Host and Microbe, 2018, 24, 155-167.e5.	11.0	244
24	The wheat powdery mildew genome shows the unique evolution of an obligate biotroph. Nature Genetics, 2013, 45, 1092-1096.	21.4	236
25	Recognition Specificity and RAR1/SGT1 Dependence in Barley Mla Disease Resistance Genes to the Powdery Mildew Fungus. Plant Cell, 2003, 15, 732-744.	6.6	225
26	Structure-Function Analysis of Barley NLR Immune Receptor MLA10 Reveals Its Cell Compartment Specific Activity in Cell Death and Disease Resistance. PLoS Pathogens, 2012, 8, e1002752.	4.7	219
27	Survival trade-offs in plant roots during colonization by closely related beneficial and pathogenic fungi. Nature Communications, 2016, 7, 11362.	12.8	214
28	Balancing trade-offs between biotic and abiotic stress responses through leaf age-dependent variation in stress hormone cross-talk. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 2364-2373.	7.1	205
29	Cell-Autonomous Expression of Barley Mla1 Confers Race-Specific Resistance to the Powdery Mildew Fungus via a Rar1-Independent Signaling Pathway. Plant Cell, 2001, 13, 337-350.	6.6	203
30	Root-Secreted Coumarins and the Microbiota Interact to Improve Iron Nutrition in Arabidopsis. Cell Host and Microbe, 2020, 28, 825-837.e6.	11.0	199
31	Microbial genome-enabled insights into plantâ€“microorganism interactions. Nature Reviews Genetics, 2014, 15, 797-813.	16.3	187
32	Host and non-host pathogens elicit different jasmonate/ethylene responses in Arabidopsis. Plant Journal, 2004, 40, 633-646.	5.7	186
33	Rhizobacterial volatiles and photosynthesisâ€related signals coordinate <i><scp>MYB</scp>72</i> expression in Arabidopsis roots during onset of induced systemic resistance and ironâ€deficiency responses. Plant Journal, 2015, 84, 309-322.	5.7	171
34	Mosaic genome structure of the barley powdery mildew pathogen and conservation of transcriptional programs in divergent hosts. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2219-28.	7.1	165
35	Allelic barley MLA immune receptors recognize sequence-unrelated avirulence effectors of the powdery mildew pathogen. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6486-E6495.	7.1	162
36	Diversity at the<i>Mla</i>Powdery Mildew Resistance Locus from Cultivated Barley Reveals Sites of Positive Selection. Molecular Plant-Microbe Interactions, 2010, 23, 497-509.	2.6	160

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37	Root microbiota assembly and adaptive differentiation among European Arabidopsis populations. Nature Ecology and Evolution, 2020, 4, 122-131.	7.8	157
38	ESTABLISHMENT OFBIOTROPHY BYPARASITICFUNGI ANDREPROGRAMMING OFHOSTCELLS FORDISEASERESISTANCE. Annual Review of Phytopathology, 2003, 41, 641-667.	7.8	150
39	Signatures of host specialization and a recent transposable element burst in the dynamic one-speed genome of the fungal barley powdery mildew pathogen. BMC Genomics, 2018, 19, 381.	2.8	138
40	Root microbiota dynamics of perennial <i>Arabis alpina</i> are dependent on soil residence time but independent of flowering time. ISME Journal, 2017, 11, 43-55.	9.8	133
41	Critical Assessment of Metagenome Interpretation: the second round of challenges. Nature Methods, 2022, 19, 429-440.	19.0	133
42	Uncoupling of sustained MAMP receptor signaling from early outputs in an Arabidopsis endoplasmic reticulum glucosidase II allele. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 22522-22527.	7.1	119
43	Conserved ERAD-Like Quality Control of a Plant Polytopic Membrane Protein. Plant Cell, 2005, 17, 149-163.	6.6	107
44	TIR domains of plant immune receptors are 2â€²,3â€²-cAMP/cGMP synthetases mediating cell death. Cell, 2022, 185, 2370-2386.e18.	28.9	104
45	NOD-like receptor-mediated plant immunity: from structure to cell death. Nature Reviews Immunology, 2021, 21, 305-318.	22.7	103
46	Conservation and clade-specific diversification of pathogen-inducible tryptophan and indole glucosinolate metabolism in Arabidopsis thaliana relatives. New Phytologist, 2011, 192, 713-726.	7.3	100
47	Multiple pairs of allelic MLA immune receptor-powdery mildew AVRA effectors argue for a direct recognition mechanism. ELife, 2019, 8, .	6.0	96
48	Conservation of NLR-triggered immunity across plant lineages. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 20119-20123.	7.1	95
49	Coordination of microbeâ€"host homeostasis by crosstalk with plant innate immunity. Nature Plants, 2021, 7, 814-825.	9.3	95
50	High-throughput cultivation and identification of bacteria from the plant root microbiota. Nature Protocols, 2021, 16, 988-1012.	12.0	91
51	Host preference and invasiveness of commensal bacteria in the Lotus and Arabidopsis root microbiota. Nature Microbiology, 2021, 6, 1150-1162.	13.3	89
52	A dominantâ€interfering <i>camta3</i> mutation compromises primary transcriptional outputs mediated by both cell surface and intracellular immune receptors in <i>Arabidopsis thaliana</i>. New Phytologist, 2018, 217, 1667-1680.	7.3	73
53	Mutant Allele-Specific Uncoupling of PENETRATION3 Functions Reveals Engagement of the ATP-Binding Cassette Transporter in Distinct Tryptophan Metabolic Pathways. Plant Physiology, 2015, 168, 814-827.	4.8	71
54	Glutathione Transferase U13 Functions in Pathogen-Triggered Glucosinolate Metabolism. Plant Physiology, 2018, 176, 538-551.	4.8	69

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55	The CC-NB-LRR-Type Rdg2a Resistance Gene Confers Immunity to the Seed-Borne Barley Leaf Stripe Pathogen in the Absence of Hypersensitive Cell Death. PLoS ONE, 2010, 5, e12599.	2.5	56
56	A cell death assay in barley and wheat protoplasts for identification and validation of matching pathogen AVR effector and plant NLR immune receptors. Plant Methods, 2019, 15, 118.	4.3	52
57	Discovery of a Family of Mixed Lineage Kinase Domain-like Proteins in Plants and Their Role in Innate Immune Signaling. Cell Host and Microbe, 2020, 28, 813-824.e6.	11.0	50
58	The leucine-rich repeats in allelic barley MLA immune receptors define specificity towards sequence-unrelated powdery mildew avirulence effectors with a predicted common RNase-like fold. PLoS Pathogens, 2021, 17, e1009223.	4.7	50
59	Spatially Restricted Immune Responses Are Required for Maintaining Root Meristematic Activity upon Detection of Bacteria. Current Biology, 2021, 31, 1012-1028.e7.	3.9	46
60	<i>Lotus japonicus</i> Symbiosis Genes Impact Microbial Interactions between Symbionts and Multikingdom Commensal Communities. MBio, 2019, 10, .	4.1	41
61	Root-Associated Bacterial and Fungal Community Profiles of <i>Arabidopsis thaliana</i> Are Robust Across Contrasting Soil P Levels. Phytobiomes Journal, 2018, 2, 24-34.	2.7	37
62	Subfamily-Specific Specialization of RGH1/MLA Immune Receptors in Wild Barley. Molecular Plant-Microbe Interactions, 2019, 32, 107-119.	2.6	29
63	Gene expression evolution in pattern-triggered immunity within <i>Arabidopsis thaliana</i> and across Brassicaceae species. Plant Cell, 2021, 33, 1863-1887.	6.6	27
64	Peat-based gnotobiotic plant growth systems for Arabidopsis microbiome research. Nature Protocols, 2021, 16, 2450-2470.	12.0	26
65	Moonlighting Function of Phytochelatin Synthase1 in Extracellular Defense against Fungal Pathogens. Plant Physiology, 2020, 182, 1920-1932.	4.8	26
66	Maize Field Study Reveals Covaried Microbiota and Metabolic Changes in Roots over Plant Growth. MBio, 2022, 13, e0258421.	4.1	15
67	A fungal powdery mildew pathogen induces extensive local and marginal systemic changes in the <scp><i>Arabidopsis thaliana</i></scp> microbiota. Environmental Microbiology, 2021, 23, 6292-6308.	3.8	12
68	Leaf-derived bacterial communities adapt to the local environment. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 808-810.	7.1	9
69	Gnotobiotic Plant Systems for Reconstitution and Functional Studies of the Root Microbiota. Current Protocols, 2022, 2, e362.	2.9	6
70	Buy one, get two. Nature Plants, 2022, 8, 100-101.	9.3	1