Ruben Garrido-Oter

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8028502/publications.pdf

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26 papers 7,050 citations

20 h-index 26 g-index

35 all docs 35 does citations

35 times ranked 7269 citing authors

#	Article	IF	CITATIONS
1	Structure and Function of the Bacterial Root Microbiota in Wild and Domesticated Barley. Cell Host and Microbe, 2015, 17, 392-403.	11.0	1,102
2	Functional overlap of the Arabidopsis leaf and root microbiota. Nature, 2015, 528, 364-369.	27.8	1,062
3	Microbial Interkingdom Interactions in Roots Promote Arabidopsis Survival. Cell, 2018, 175, 973-983.e14.	28.9	707
4	NRT1.1B is associated with root microbiota composition and nitrogen use in field-grown rice. Nature Biotechnology, 2019, 37, 676-684.	17.5	641
5	Critical Assessment of Metagenome Interpretationâ€"a benchmark of metagenomics software. Nature Methods, 2017, 14, 1063-1071.	19.0	635
6	Microbiota and Host Nutrition across Plant and Animal Kingdoms. Cell Host and Microbe, 2015, 17, 603-616.	11.0	628
7	Interplay Between Innate Immunity and the Plant Microbiota. Annual Review of Phytopathology, 2017, 55, 565-589.	7.8	410
8	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
9	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
10	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
11	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
12	Root microbiota assembly and adaptive differentiation among European Arabidopsis populations. Nature Ecology and Evolution, 2020, 4, 122-131.	7.8	157
13	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
14	Critical Assessment of Metagenome Interpretation: the second round of challenges. Nature Methods, 2022, 19, 429-440.	19.0	133
15	Coordination of microbe–host homeostasis by crosstalk with plant innate immunity. Nature Plants, 2021, 7, 814-825.	9.3	95
16	High-throughput cultivation and identification of bacteria from the plant root microbiota. Nature Protocols, 2021, 16, 988-1012.	12.0	91
17	Host preference and invasiveness of commensal bacteria in the Lotus and Arabidopsis root microbiota. Nature Microbiology, 2021, 6, 1150-1162.	13.3	89
18	AMBER: Assessment of Metagenome BinnERs. GigaScience, 2018, 7, .	6.4	72

#	ARTICLE	IF	CITATION
19	<i>Lotus japonicus</i> Symbiosis Genes Impact Microbial Interactions between Symbionts and Multikingdom Commensal Communities. MBio, 2019, 10, .	4.1	41
20	Shared features and reciprocal complementation of the Chlamydomonas and Arabidopsis microbiota. Nature Communications, 2022, 13, 406.	12.8	28
21	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
22	The fungal root endophyte <i>Serendipita vermifera</i> displays inter-kingdom synergistic beneficial effects with the microbiota in <i>Arabidopsis thaliana</i> and barley. ISME Journal, 2022, 16, 876-889.	9.8	22
23	Maize Field Study Reveals Covaried Microbiota and Metabolic Changes in Roots over Plant Growth. MBio, 2022, 13, e0258421.	4.1	15
24	Tobacco Root Endophytic <i>Arthrobacter</i> Harbors Genomic Features Enabling the Catabolism of Host-Specific Plant Specialized Metabolites. MBio, 2021, 12, e0084621.	4.1	14
25	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
26	Rbec: a tool for analysis of amplicon sequencing data from synthetic microbial communities. ISME Communications, 2021, 1 , .	4.2	6