Davide Bulgarelli

List of Publications by Year in descending order

24 papers	7,170 citations	471509 17 h-index	642732 23 g-index
33 all docs	33 docs citations	33 times ranked	7217 citing authors

#	Article	IF	Citations
1	The fungal root endophyte Serendipita vermifera displays inter-kingdom synergistic beneficial effects with the microbiota in Arabidopsis thaliana and barley. ISME Journal, 2022, 16, 876-889.	9.8	22
2	Genome-Annotated Bacterial Collection of the Barley Rhizosphere Microbiota. Microbiology Resource Announcements, 2022, 11, e0106421.	0.6	3
3	Identifying plant genes shaping microbiota composition in the barley rhizosphere. Nature Communications, 2022, 13, .	12.8	44
4	Bacterial Communities in the Embryo of Maize Landraces: Relation with Susceptibility to Fusarium Ear Rot. Microorganisms, 2021, 9, 2388.	3.6	7
5	Applications of the indole-alkaloid gramine modulate the assembly of individual members of the barley rhizosphere microbiota. PeerJ, 2021, 9, e12498.	2.0	12
6	A footprint of plant eco-geographic adaptation on the composition of the barley rhizosphere bacterial microbiota. Scientific Reports, 2020, 10, 12916.	3.3	48
7	Nitrogen Fertilizers Shape the Composition and Predicted Functions of the Microbiota of Field-Grown Tomato Plants. Phytobiomes Journal, 2019, 3, 315-325.	2.7	26
8	Tracing the evolutionary routes of plantâ€“microbiota interactions. Current Opinion in Microbiology, 2019, 49, 34-40.	5.1	60
9	The bacterial community associated with adult vine weevil (Otiorhynchus sulcatus) in <scp>UK</scp> populations growing on strawberry is dominated by Candidatus Nardonella. Entomologia Experimentalis Et Applicata, 2019, 167, 186-196.	1.4	8
10	Beneficial Soil Microbiome for Sustainable Agriculture Production. Sustainable Agriculture Reviews, 2018, , 443-481.	1.1	27
11	Unraveling the Composition of the Root-Associated Bacterial Microbiota of Phragmites australis and Typha latifolia. Frontiers in Microbiology, 2018, 9, 1650.	3.5	46
12	Root Hair Mutations Displace the Barley Rhizosphere Microbiota. Frontiers in Plant Science, 2017, 8, 1094.	3.6	85
13	Crop Establishment Practices Are a Driver of the Plant Microbiota in Winter Oilseed Rape (Brassica) Tj ETQq1 1 0.784314 rgBT /Overlock	3.5	34
14	Plantâ€“Microbiota Interactions as a Driver of the Mineral Turnover in the Rhizosphere. Advances in Applied Microbiology, 2016, 95, 1-67.	2.4	105
15	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
16	The Plant Microbiome at Work. Molecular Plant-Microbe Interactions, 2015, 28, 212-217.	2.6	493
17	Structure and Functions of the Bacterial Microbiota of Plants. Annual Review of Plant Biology, 2013, 64, 807-838.	18.7	2,589
18	The CC-NB-LRR-type Rdg2a Resistance Gene Evolved Through Recombination and Confers Immunity to the Seed-Borne Barley Leaf Stripe Pathogen in the Absence of Hypersensitive Cell Death. , 2013, , 217-228.		4

#	Article	IF	Citations
19	Revealing structure and assembly cues for Arabidopsis root-inhabiting bacterial microbiota. Nature, 2012, 488, 91-95.	27.8	2,127
20	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
21	Histological and molecular analysis of Rdg2a barley resistance to leaf stripe. Molecular Plant Pathology, 2008, 9, 463-478.	4.2	21
22	Haplotype characterization and markers at the barley Mlo powdery mildew resistance locus as tools for marker-assisted selection. Genome, 2006, 49, 864-872.	2.0	10
23	Marker assisted selection in crop plants. Plant Cell, Tissue and Organ Culture, 2005, 82, 317-342.	2.3	176
24	High-resolution genetic mapping of the leaf stripe resistance gene Rdg2a in barley. Theoretical and Applied Genetics, 2004, 108, 1401-1408.	3.6	34