

# Francisco Dini-Andreote

## List of Publications by Year in descending order

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Version: 2024-02-01

72  
papers

4,858  
citations

147801

31  
h-index

106344

65  
g-index

74  
all docs

74  
docs citations

74  
times ranked

5620  
citing authors

#	ARTICLE	IF	CITATIONS
1	Exploring rhizo-microbiome transplants as a tool for protective plant-microbiome manipulation. ISME Communications, 2022, 2, .	4.2	48
2	Microbial phylogenetic relatedness links to distinct successional patterns of bacterial and fungal communities. Environmental Microbiology, 2022, 24, 3985-4000.	3.8	11
3	Ecological and Evolutionary Implications of Microbial Dispersal. Frontiers in Microbiology, 2022, 13, 855859.	3.5	36
4	Embracing Complexity in Ecosystem Response to Global Change. Environmental Science & Technology, 2022, 56, 9832-9834.	10.0	6
5	Soil Microbial Diversity Affects the Plant-Root Colonization by Arbuscular Mycorrhizal Fungi. Microbial Ecology, 2021, 82, 100-103.	2.8	25
6	Towards meaningful scales in ecosystem microbiome research. Environmental Microbiology, 2021, 23, 1-4.	3.8	10
7	Interactive Effects of Scion and Rootstock Genotypes on the Root Microbiome of Grapevines (Vitis spp.) Tj ETQq1 1 0.784314 rgBT / Qve 2.5 20	2.5	20
8	Soil microbial interconnections along ecological restoration gradients of lowland forests after slash-and-burn agriculture. FEMS Microbiology Ecology, 2021, 97, .	2.7	8
9	Successive plant growth amplifies genotype-specific assembly of the tomato rhizosphere microbiome. Science of the Total Environment, 2021, 772, 144825.	8.0	38
10	Microbial community assembly in soil aggregates: A dynamic interplay of stochastic and deterministic processes. Applied Soil Ecology, 2021, 163, 103911.	4.3	15
11	Development of fungal-mediated soil suppressiveness against Fusarium wilt disease via plant residue manipulation. Microbiome, 2021, 9, 200.	11.1	38
12	Promoting soil microbial-mediated suppressiveness against Fusarium wilt disease by the enrichment of specific fungal taxa via crop rotation. Biology and Fertility of Soils, 2021, 57, 1137-1153.	4.3	11
13	Modulation of the Tomato Rhizosphere Microbiome via Changes in Root Exudation Mediated by the Ethylene Receptor NR. Microorganisms, 2021, 9, 2456.	3.6	12
14	Editorial: Advancements in the Understanding of Anthropogenic Impacts on the Microbial Ecology and Function of Aquatic Environments. Frontiers in Microbiology, 2021, 12, 820697.	3.5	0
15	Effects of plastic mulch film residues on wheat rhizosphere and soil properties. Journal of Hazardous Materials, 2020, 387, 121711.	12.4	347
16	Dispersal mitigates bacterial dominance over microalgal competitor in metacommunities. Oecologia, 2020, 193, 677-687.	2.0	1
17	Organism body size structures the soil microbial and nematode community assembly at a continental and global scale. Nature Communications, 2020, 11, 6406.	12.8	113
18	Divergent Co-occurrence Patterns and Assembly Processes Structure the Abundant and Rare Bacterial Communities in a Salt Marsh Ecosystem. Applied and Environmental Microbiology, 2020, 86, .	3.1	66

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19	DiSCount: computer vision for automated quantification of <i>Striga</i> seed germination. <i>Plant Methods</i> , 2020, 16, 60.	4.3	11
20	Comparing the Influence of Assembly Processes Governing Bacterial Community Succession Based on DNA and RNA Data. <i>Microorganisms</i> , 2020, 8, 798.	3.6	13
21	Phenotypic traits of <i>Burkholderia</i> spp. associated with ecological adaptation and plant-host interaction. <i>Microbiological Research</i> , 2020, 236, 126451.	5.3	7
22	Endophytes: The Second Layer of Plant Defense. <i>Trends in Plant Science</i> , 2020, 25, 319-322.	8.8	82
23	Changes in bulk soil affect the disease-suppressive rhizosphere microbiome against <i>Fusarium</i> wilt disease. <i>Frontiers of Agricultural Science and Engineering</i> , 2020, 7, 307.	1.4	11
24	Harnessing the microbiome to control plant parasitic weeds. <i>Current Opinion in Microbiology</i> , 2019, 49, 26-33.	5.1	37
25	Genomic signatures and co-occurrence patterns of the ultra-small <i>Saccharimonadia</i> (phylum) Tj ETQq1 1 0.784314 rgBT / Overlock 101	3.9	101
26	Ecology and Evolution of Plant Microbiomes. <i>Annual Review of Microbiology</i> , 2019, 73, 69-88.	7.3	379
27	Bacterial Community Assembly in a Typical Estuarine Marsh with Multiple Environmental Gradients. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	46
28	Marine probiotics: increasing coral resistance to bleaching through microbiome manipulation. <i>ISME Journal</i> , 2019, 13, 921-936.	9.8	269
29	The Soil Microbiome—An Overview. , 2019, , 37-48.		4
30	Embracing Community Ecology in Plant Microbiome Research. <i>Trends in Plant Science</i> , 2018, 23, 467-469.	8.8	63
31	The impact of failure: unsuccessful bacterial invasions steer the soil microbial community away from the invader's niche. <i>ISME Journal</i> , 2018, 12, 728-741.	9.8	165
32	Community Assembly Processes of the Microbial Rare Biosphere. <i>Trends in Microbiology</i> , 2018, 26, 738-747.	7.7	232
33	Organic Amendment Under Increasing Agricultural Intensification: Effects on Soil Bacterial Communities and Plant Productivity. <i>Frontiers in Microbiology</i> , 2018, 9, 2612.	3.5	11
34	Compositional and abundance changes of nitrogen-cycling genes in plant-root microbiomes along a salt marsh chronosequence. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 2061-2078.	1.7	5
35	Contrasting the Genetic Patterns of Microbial Communities in Soda Lakes with and without Cyanobacterial Bloom. <i>Frontiers in Microbiology</i> , 2018, 9, 244.	3.5	25
36	Dispersal-competition tradeoff in microbiomes in the quest for land colonization. <i>Scientific Reports</i> , 2018, 8, 9451.	3.3	15

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37	Successional patterns of key genes and processes involved in the microbial nitrogen cycle in a salt marsh chronosequence. <i>Biogeochemistry</i> , 2017, 132, 185-201.	3.5	17
38	Ecological Insights into the Dynamics of Plant Biomass-Degrading Microbial Consortia. <i>Trends in Microbiology</i> , 2017, 25, 788-796.	7.7	59
39	Transcriptional Responses of the Bacterium <i>Burkholderia terrae</i> BS001 to the Fungal Host <i>Lyophyllum</i> sp. Strain Karsten under Soil-Mimicking Conditions. <i>Microbial Ecology</i> , 2017, 73, 236-252.	2.8	17
40	Serotonin Transporter Genotype Modulates the Gut Microbiota Composition in Young Rats, an Effect Augmented by Early Life Stress. <i>Frontiers in Cellular Neuroscience</i> , 2017, 11, 222.	3.7	65
41	Light induced intraspecific variability in response to thermal stress in the hard coral <i>Stylophora pistillata</i> . <i>PeerJ</i> , 2017, 5, e3802.	2.0	12
42	Reconstructing the Genetic Potential of the Microbially-Mediated Nitrogen Cycle in a Salt Marsh Ecosystem. <i>Frontiers in Microbiology</i> , 2016, 7, 902.	3.5	39
43	Aligning the Measurement of Microbial Diversity with Macroecological Theory. <i>Frontiers in Microbiology</i> , 2016, 7, 1487.	3.5	13
44	Ecological succession reveals potential signatures of marine-terrestrial transition in salt marsh fungal communities. <i>ISME Journal</i> , 2016, 10, 1984-1997.	9.8	76
45	Linking the Composition of Bacterial and Archaeal Communities to Characteristics of Soil and Flora Composition in the Atlantic Rainforest. <i>PLoS ONE</i> , 2016, 11, e0146566.	2.5	18
46	Bacterial Communities Differ among <i>Drosophila melanogaster</i> Populations and Affect Host Resistance against Parasitoids. <i>PLoS ONE</i> , 2016, 11, e0167726.	2.5	24
47	Effects of vegetation and seasonality on bacterial communities in Amazonian dark earth and adjacent soils. <i>African Journal of Microbiology Research</i> , 2015, 9, 2119-2134.	0.4	6
48	Disentangling mechanisms that mediate the balance between stochastic and deterministic processes in microbial succession. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1326-32.	7.1	972
49	Genes related to antioxidant metabolism are involved in <i>Methylobacterium mesophilicum</i> -soybean interaction. <i>Antonie Van Leeuwenhoek</i> , 2015, 108, 951-963.	1.7	11
50	Compositional profile of epoxide hydrolase fold proteins in mangrove soil metagenomes: prevalence of epoxide hydrolases and haloalkane dehalogenases in oil-contaminated sites. <i>Microbial Biotechnology</i> , 2015, 8, 604-613.	4.2	17
51	Draft Genome Sequence of <i>Bacillus thuringiensis</i> Strain BrMgv02-JM63, a Chitinolytic Bacterium Isolated from Oil-Contaminated Mangrove Soil in Brazil. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
52	Dynamics of bacterial and fungal communities associated with eggshells during incubation. <i>Ecology and Evolution</i> , 2014, 4, 1140-1157.	1.9	43
53	Metataxonomic profiling and prediction of functional behaviour of wheat straw degrading microbial consortia. <i>Biotechnology for Biofuels</i> , 2014, 7, 92.	6.2	88
54	Dynamics of bacterial community succession in a salt marsh chronosequence: evidences for temporal niche partitioning. <i>ISME Journal</i> , 2014, 8, 1989-2001.	9.8	221

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55	Climate change affects key nitrogen-fixing bacterial populations on coral reefs. <i>ISME Journal</i> , 2014, 8, 2272-2279.	9.8	130
56	Biotechnological potential of <i>Candida</i> spp. for the bioconversion of D-xylose to xylitol. <i>African Journal of Microbiology Research</i> , 2014, 8, 2030-2036.	0.4	6
57	Back to the basics: The need for ecophysiological insights to enhance our understanding of microbial behaviour in the rhizosphere. <i>Plant and Soil</i> , 2013, 373, 1-15.	3.7	34
58	Draft Genome Sequence of <i>Bacillus stratosphericus</i> LAMA 585, Isolated from the Atlantic Deep Sea. <i>Genome Announcements</i> , 2013, 1, .	0.8	9
59	Draft Genome Sequence of <i>Methylobacterium mesophilicum</i> Strain SR1.6/6, Isolated from Citrus sinensis. <i>Genome Announcements</i> , 2013, 1, .	0.8	7
60	Different Selective Effects on Rhizosphere Bacteria Exerted by Genetically Modified versus Conventional Potato Lines. <i>PLoS ONE</i> , 2013, 8, e67948.	2.5	49
61	Abundance and Genetic Diversity of <i>nifH</i> Gene Sequences in Anthropogenically Affected Brazilian Mangrove Sediments. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7960-7967.	3.1	44
62	The Microbiome of Brazilian Mangrove Sediments as Revealed by Metagenomics. <i>PLoS ONE</i> , 2012, 7, e38600.	2.5	222
63	Analysis of 16S rRNA and <i>mxoF</i> genes revealing insights into <i>Methylobacterium</i> niche-specific plant association. <i>Genetics and Molecular Biology</i> , 2012, 35, 142-148.	1.3	26
64	Bacterial Genomes: Habitat Specificity and Uncharted Organisms. <i>Microbial Ecology</i> , 2012, 64, 1-7.	2.8	37
65	Archaeal communities in the sediments of three contrasting mangroves. <i>Journal of Soils and Sediments</i> , 2011, 11, 1466-1476.	3.0	50
66	Endophytic Bacteria Associated to Sharpshooters (Hemiptera: Cicadellidae), Insect Vectors of <i>Xylella fastidiosa</i> Subsp. <i>pauca</i> . <i>Journal of Plant Pathology &amp; Microbiology</i> , 2011, 02, .	0.3	7
67	Genetic diversity and plant-growth related features of <i>Burkholderia</i> spp. from sugarcane roots. <i>World Journal of Microbiology and Biotechnology</i> , 2010, 26, 1829-1836.	3.6	66
68	Bacterial soil community in a Brazilian sugarcane field. <i>Plant and Soil</i> , 2010, 336, 337-349.	3.7	16
69	Genetic variability of Brazilian isolates of <i>Alternaria alternata</i> detected by AFLP and RAPD techniques. <i>Brazilian Journal of Microbiology</i> , 2009, 40, 670-677.	2.0	13
70	Diversity and biotechnological potential of culturable bacteria from Brazilian mangrove sediment. <i>World Journal of Microbiology and Biotechnology</i> , 2009, 25, 1305-1311.	3.6	79
71	Transgenic tobacco revealing altered bacterial diversity in the rhizosphere during early plant development. <i>Antonie Van Leeuwenhoek</i> , 2008, 93, 415-424.	1.7	53
72	Analysis of the bacterial community in glassy-winged sharpshooter heads. <i>Entomological Research</i> , 2007, 37, 261-266.	1.1	27