

# Vitor J Carrião

## List of Publications by Year in descending order

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Version: 2024-02-01

32  
papers

3,133  
citations

279487

23  
h-index

395343

33  
g-index

41  
all docs

41  
docs citations

41  
times ranked

3405  
citing authors

#	ARTICLE	IF	CITATIONS
1	The ubiquitous catechol moiety elicits siderophore and angucycline production in <i>Streptomyces</i> . <i>Communications Chemistry</i> , 2022, 5, .	2.0	9
2	Acidic amelioration of soil amendments improves soil health by impacting rhizosphere microbial assemblies. <i>Soil Biology and Biochemistry</i> , 2022, 167, 108599.	4.2	26
3	<i>Bacillus subtilis</i> EA-CB0575 inoculation of micropropagated banana plants suppresses black Sigatoka and induces changes in the root microbiome. <i>Plant and Soil</i> , 2022, 479, 513-527.	1.8	2
4	Disentangling the genetic basis of rhizosphere microbiome assembly in tomato. <i>Nature Communications</i> , 2022, 13, .	5.8	53
5	A community resource for paired genomic and metabolomic data mining. <i>Nature Chemical Biology</i> , 2021, 17, 363-368.	3.9	81
6	Successive plant growth amplifies genotype-specific assembly of the tomato rhizosphere microbiome. <i>Science of the Total Environment</i> , 2021, 772, 144825.	3.9	38
7	Mitigation of <i>Pseudomonas syringae</i> virulence by signal inactivation. <i>Science Advances</i> , 2021, 7, eabg2293.	4.7	8
8	Consecutive lactate formation and chain elongation to reduce exogenous chemicals input in repeated-batch food waste fermentation. <i>Water Research</i> , 2020, 169, 115215.	5.3	132
9	Atypical Spirotetronate Polyketides Identified in the Underexplored Genus <i>Streptacidiphilus</i> . <i>Journal of Organic Chemistry</i> , 2020, 85, 10648-10657.	1.7	10
10	Beyond Plant Microbiome Composition: Exploiting Microbial Functions and Plant Traits via Integrated Approaches. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 896.	2.0	44
11	Deciphering rhizosphere microbiome assembly of wild and modern common bean ( <i>Phaseolus vulgaris</i> ) in native and agricultural soils from Colombia. <i>Microbiome</i> , 2019, 7, 114.	4.9	140
12	Pathogen-induced activation of disease-suppressive functions in the endophytic root microbiome. <i>Science</i> , 2019, 366, 606-612.	6.0	621
13	Ecology and Evolution of Plant Microbiomes. <i>Annual Review of Microbiology</i> , 2019, 73, 69-88.	2.9	379
14	Legacy of land use history determines reprogramming of plant physiology by soil microbiome. <i>ISME Journal</i> , 2019, 13, 738-751.	4.4	166
15	Microbial Community Composition in Take-All Suppressive Soils. <i>Frontiers in Microbiology</i> , 2018, 9, 2198.	1.5	46
16	Priming of Plant Growth Promotion by Volatiles of Root-Associated <i>Microbacterium</i> spp. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	71
17	The wild side of plant microbiomes. <i>Microbiome</i> , 2018, 6, 143.	4.9	199
18	Involvement of Burkholderiaceae and sulfurous volatiles in disease-suppressive soils. <i>ISME Journal</i> , 2018, 12, 2307-2321.	4.4	131

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19	Linking rhizosphere microbiome composition of wild and domesticated <i>Phaseolus vulgaris</i> to genotypic and root phenotypic traits. <i>ISME Journal</i> , 2017, 11, 2244-2257.	4.4	298
20	Indexing the <i>Pseudomonas</i> specialized metabolome enabled the discovery of poaeamide B and the bananamides. <i>Nature Microbiology</i> , 2017, 2, 16197.	5.9	121
21	Plant Phenotypic and Transcriptional Changes Induced by Volatiles from the Fungal Root Pathogen <i>Rhizoctonia solani</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1262.	1.7	78
22	Screening and Characterization of Potentially Suppressive Soils against <i>Gaeumannomyces graminis</i> under Extensive Wheat Cropping by Chilean Indigenous Communities. <i>Frontiers in Microbiology</i> , 2017, 8, 1552.	1.5	41
23	Diversity and functions of volatile organic compounds produced by <i>Streptomyces</i> from a disease-suppressive soil. <i>Frontiers in Microbiology</i> , 2015, 6, 1081.	1.5	174
24	Cellulose production in <i>Pseudomonas syringae</i> pv. <i>syringae</i> : a compromise between epiphytic and pathogenic lifestyles. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv071.	1.3	25
25	Bioinformatics Analysis of the Complete Genome Sequence of the Mango Tree Pathogen <i>Pseudomonas syringae</i> pv. <i>syringae</i> UMAF0158 Reveals Traits Relevant to Virulence and Epiphytic Lifestyle. <i>PLoS ONE</i> , 2015, 10, e0136101.	1.1	25
26	darR and darS are regulatory genes that modulate 2-hexyl, 5-propyl resorcinol transcription in <i>Pseudomonas chlororaphis</i> PCL1606. <i>Microbiology (United Kingdom)</i> , 2014, 160, 2670-2680.	0.7	7
27	Mangotoxin production of <i>Pseudomonas syringae</i> pv. <i>syringae</i> is regulated by MgoA. <i>BMC Microbiology</i> , 2014, 14, 46.	1.3	24
28	The Mangotoxin Biosynthetic Operon ( <i>mbo</i> ) Is Specifically Distributed within <i>Pseudomonas syringae</i> Genomespecies 1 and Was Acquired Only Once during Evolution. <i>Applied and Environmental Microbiology</i> , 2013, 79, 756-767.	1.4	29
29	Recruitment and Rearrangement of Three Different Genetic Determinants into a Conjugative Plasmid Increase Copper Resistance in <i>Pseudomonas syringae</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 1028-1033.	1.4	46
30	A <i>Pseudomonas syringae</i> Diversity Survey Reveals a Differentiated Phylotype of the Pathovar <i>syringae</i> Associated with the Mango Host and Mangotoxin Production. <i>Phytopathology</i> , 2013, 103, 1115-1129.	1.1	30
31	Characterisation of the mgo operon in <i>Pseudomonas syringae</i> pv. <i>syringae</i> UMAF0158 that is required for mangotoxin production. <i>BMC Microbiology</i> , 2012, 12, 10.	1.3	32
32	The mbo Operon Is Specific and Essential for Biosynthesis of Mangotoxin in <i>Pseudomonas syringae</i> . <i>PLoS ONE</i> , 2012, 7, e36709.	1.1	35