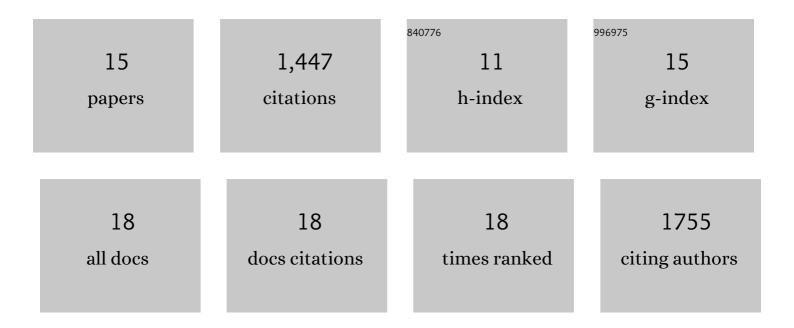
Rodrigo Bacigalupe

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1106083/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	From Roots to Leaves: The Capacity of <i>Micromonospora</i> to Colonize Different Legume Tissues. Phytobiomes Journal, 2022, 6, 35-44.	2.7	7
2	Variation and transmission of the human gut microbiota across multiple familial generations. Nature Microbiology, 2022, 7, 87-96.	13.3	32
3	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	21.4	676
4	Treponema peruense sp. nov., a commensal spirochaete isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	1.7	10
5	Lateral transduction is inherent to the life cycle of the archetypical Salmonella phage P22. Nature Communications, 2021, 12, 6510.	12.8	30
6	GWAS of stool frequency provides insights into gastrointestinal motility and irritable bowel syndrome. Cell Genomics, 2021, 1, 100069.	6.5	15
7	Genome-wide associations of human gut microbiome variation and implications for causal inference analyses. Nature Microbiology, 2020, 5, 1079-1087.	13.3	144
8	Metagenomic sequencing of clinical samples reveals a single widespread clone of Lawsonia intracellularis responsible for porcine proliferative enteropathy. Microbial Genomics, 2020, 6, .	2.0	2
9	Microbiota of human precolostrum and its potential role as a source of bacteria to the infant mouth. Scientific Reports, 2019, 9, 8435.	3.3	51
10	A multihost bacterial pathogen overcomes continuous population bottlenecks to adapt to new host species. Science Advances, 2019, 5, eaax0063.	10.3	20
11	Genome hypermobility by lateral transduction. Science, 2018, 362, 207-212.	12.6	187
12	Gene exchange drives the ecological success of a multi-host bacterial pathogen. Nature Ecology and Evolution, 2018, 2, 1468-1478.	7.8	156
13	Population Genomics of <i>Legionella longbeachae</i> and Hidden Complexities of Infection Source Attribution. Emerging Infectious Diseases, 2017, 23, 750-757.	4.3	16
14	Genome Features of the Endophytic Actinobacterium Micromonospora lupini Strain Lupac 08: On the Process of Adaptation to an Endophytic Life Style?. PLoS ONE, 2014, 9, e108522.	2.5	74
15	Genome Sequence of Micromonospora lupini Lupac 08, Isolated from Root Nodules of Lupinus angustifolius. Journal of Bacteriology, 2012, 194, 4135-4135.	2.2	14