

Rodrigo Bacigalupe

List of Publications by Year in descending order

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Version: 2024-02-01

15
papers

1,447
citations

840776

11
h-index

996975

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docs citations

18
times ranked

1755
citing authors

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