

Helisson Faoro

List of Publications by Citations

Source: <https://exaly.com/author-pdf/2464805/helisson-faoro-publications-by-citations.pdf>
Version: 2024-04-05

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

55 papers	1,296 citations	20 h-index	35 g-index
62 ext. papers	1,668 ext. citations	4.3 avg, IF	3.89 L-index

#	Paper	IF	Citations
55	Genome of <i>Herbaspirillum seropedicae</i> strain SmR1, a specialized diazotrophic endophyte of tropical grasses. <i>PLoS Genetics</i> , 2011 , 7, e1002064	6	151
54	Influence of soil characteristics on the diversity of bacteria in the Southern Brazilian Atlantic Forest. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 4744-9	4.8	135
53	Identification and characterization of a new true lipase isolated through metagenomic approach. <i>Microbial Cell Factories</i> , 2011 , 10, 54	6.4	127
52	Dual RNA-seq transcriptional analysis of wheat roots colonized by <i>Azospirillum brasilense</i> reveals up-regulation of nutrient acquisition and cell cycle genes. <i>BMC Genomics</i> , 2014 , 15, 378	4.5	96
51	An improved protocol for intact chloroplasts and cpDNA isolation in conifers. <i>PLoS ONE</i> , 2014 , 9, e84792	3.7	54
50	The complete chloroplast genome sequence of <i>Podocarpus lambertii</i> : genome structure, evolutionary aspects, gene content and SSR detection. <i>PLoS ONE</i> , 2014 , 9, e90618	3.7	47
49	FGAP: an automated gap closing tool. <i>BMC Research Notes</i> , 2014 , 7, 371	2.3	45
48	RNA-seq transcriptional profiling of <i>Herbaspirillum seropedicae</i> colonizing wheat (<i>Triticum aestivum</i>) roots. <i>Plant Molecular Biology</i> , 2016 , 90, 589-603	4.6	44
47	Isolation of a novel lipase from a metagenomic library derived from mangrove sediment from the south Brazilian coast. <i>Genetics and Molecular Research</i> , 2010 , 9, 514-23	1.2	44
46	Diversity of 16S rRNA genes from bacteria of sugarcane rhizosphere soil. <i>Brazilian Journal of Medical and Biological Research</i> , 2011 , 44, 1215-21	2.8	40
45	Naringenin regulates expression of genes involved in cell wall synthesis in <i>Herbaspirillum seropedicae</i> . <i>Applied and Environmental Microbiology</i> , 2011 , 77, 2180-3	4.8	38
44	Molecular adaptations of <i>Herbaspirillum seropedicae</i> during colonization of the maize rhizosphere. <i>Environmental Microbiology</i> , 2016 , 18, 2343-56	5.2	32
43	Genomic comparison of the endophyte <i>Herbaspirillum seropedicae</i> SmR1 and the phytopathogen <i>Herbaspirillum rubrisubalbicans</i> M1 by suppressive subtractive hybridization and partial genome sequencing. <i>FEMS Microbiology Ecology</i> , 2012 , 80, 441-51	4.3	31
42	Characterization of a new Acidobacteria-derived moderately thermostable lipase from a Brazilian Atlantic Forest soil metagenome. <i>FEMS Microbiology Ecology</i> , 2012 , 81, 386-94	4.3	27
41	The oil-contaminated soil diazotroph <i>Azoarcus olearius</i> DQS-4 is genetically and phenotypically similar to the model grass endophyte <i>Azoarcus</i> sp. BH72. <i>Environmental Microbiology Reports</i> , 2017 , 9, 223-238	3.7	25
40	Comparison of the RNA Content of Extracellular Vesicles Derived from and. <i>Cells</i> , 2019 , 8,	7.9	25
39	The type III secretion system is necessary for the development of a pathogenic and endophytic interaction between <i>Herbaspirillum rubrisubalbicans</i> and Poaceae. <i>BMC Microbiology</i> , 2012 , 12, 98	4.5	25

38	Phylogenetic inference and SSR characterization of tropical woody bamboos tribe Bambuseae (Poaceae: Bambusoideae) based on complete plastid genome sequences. <i>Current Genetics</i> , 2016 , 62, 443-53	2.9	23
37	RNA-binding proteins and their role in the regulation of gene expression in <i>Trypanosoma cruzi</i> and <i>Saccharomyces cerevisiae</i> . <i>Genetics and Molecular Biology</i> , 2017 , 40, 22-30	2	20
36	Culture-independent analysis of endophytic bacterial communities associated with Brazilian sugarcane. <i>Genetics and Molecular Research</i> , 2013 , 12, 4549-58	1.2	20
35	The plastome sequence of the endemic Amazonian conifer, <i>Retrophyllum piresii</i> (Silba) C.N.Page, reveals different recombination events and plastome isoforms. <i>Tree Genetics and Genomes</i> , 2016 , 12, 1	2.1	19
34	Draft genome sequence of <i>Herbaspirillum lusitanum</i> P6-12, an endophyte isolated from root nodules of <i>Phaseolus vulgaris</i> . <i>Journal of Bacteriology</i> , 2012 , 194, 4136-7	3.5	18
33	Comparative Genomics of Sibling Species of Associated with Human Chromoblastomycosis. <i>Frontiers in Microbiology</i> , 2017 , 8, 1924	5.7	17
32	Metataxonomic and metagenomic analysis of mangrove microbiomes reveals community patterns driven by salinity and pH gradients in Paranaguá Bay, Brazil. <i>Science of the Total Environment</i> , 2019 , 694, 133609	10.2	16
31	Genome wide transcriptional profiling of <i>Herbaspirillum seropedicae</i> SmR1 grown in the presence of naringenin. <i>Frontiers in Microbiology</i> , 2015 , 6, 491	5.7	16
30	A broad pH range and processive chitinase from a metagenome library. <i>Brazilian Journal of Medical and Biological Research</i> , 2017 , 50, e5658	2.8	15
29	Emended description of the genus <i>Phytobacter</i> , its type species <i>Phytobacter diazotrophicus</i> (Zhang 2008) and description of <i>Phytobacter ursingii</i> sp. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018 , 68, 176-184	2.2	14
28	Identification of a new lipase family in the Brazilian Atlantic Forest soil metagenome. <i>Environmental Microbiology Reports</i> , 2011 , 3, 750-5	3.7	13
27	The <i>Herbaspirillum seropedicae</i> SmR1 Fnr orthologs controls the cytochrome composition of the electron transport chain. <i>Scientific Reports</i> , 2013 , 3, 2544	4.9	12
26	Cross-Kingdom Extracellular Vesicles EV-RNA Communication as a Mechanism for Host-Pathogen Interaction. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020 , 10, 593160	5.9	11
25	Genome sequence of the diazotrophic Gram-positive rhizobacterium <i>Paenibacillus riograndensis</i> SBR5(T). <i>Journal of Bacteriology</i> , 2011 , 193, 6391-2	3.5	11
24	Identification of insect-specific flaviviruses in areas of Brazil and Paraguay experiencing endemic arbovirus transmission and the description of a novel flavivirus infecting <i>Sabethes belisarioi</i> . <i>Virology</i> , 2019 , 527, 98-106	3.6	10
23	Genome Sequence of <i>Bacillus mycoides</i> B38V, a Growth-Promoting Bacterium of Sunflower. <i>Genome Announcements</i> , 2015 , 3,		7
22	Genetic and biological characterisation of Zika virus isolates from different Brazilian regions. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2019 , 114, e190150	2.6	7
21	Modulation of defence and iron homeostasis genes in rice roots by the diazotrophic endophyte <i>Herbaspirillum seropedicae</i> . <i>Scientific Reports</i> , 2019 , 9, 10573	4.9	6

20	Distinct grazing pressure loads generate different impacts on bacterial community in a long-term experiment in Pampa biome. <i>Applied Soil Ecology</i> , 2019 , 137, 167-177	5	5
19	Whole-Genome Shotgun Sequence of the Keratinolytic Bacterium <i>Lysobacter</i> sp. A03, Isolated from the Antarctic Environment. <i>Genome Announcements</i> , 2015 , 3,		5
18	Genome comparison between clinical and environmental strains of <i>Herbaspirillum seropedicae</i> reveals a potential new emerging bacterium adapted to human hosts. <i>BMC Genomics</i> , 2019 , 20, 630	4.5	5
17	Genome of <i>Rhizobium</i> sp. UR51a, Isolated from Rice Cropped in Southern Brazilian Fields. <i>Genome Announcements</i> , 2015 , 3,		4
16	Draft Genome Sequence of <i>Herbaspirillum huttiense</i> subsp. <i>putei</i> IAM 15032, a Strain Isolated from Well Water. <i>Genome Announcements</i> , 2013 , 1,		4
15	Molecular relationships of <i>Campomanesia xanthocarpa</i> within Myrtaceae based on the complete plastome sequence and on the plastid <i>ycf2</i> gene. <i>Genetics and Molecular Biology</i> , 2020 , 43, e20180377	2	4
14	Metagenomic evaluation of the effects of storage conditions on the bacterial microbiota of oysters <i>Crassostrea gasar</i> (Adanson, 1757). <i>Journal of Applied Microbiology</i> , 2018 , 125, 1435-1443	4.7	3
13	Draft Genome Sequence of <i>Aeromonas caviae</i> 8LM, Isolated from Stool Culture of a Child with Diarrhea. <i>Genome Announcements</i> , 2015 , 3,		3
12	Comparative Genomics Provides Insights into the Taxonomy of and Reveals Separate Origins of Genes in the Proposed and Genera. <i>Genes</i> , 2021 , 12,	4.2	3
11	Genome Sequence of Type Strain CBS 980.96, a Causal Agent of Feline Cerebral Phaeohyphomycosis. <i>Genome Announcements</i> , 2017 , 5,		2
10	Identification of a novel alphavirus related to the encephalitis complexes circulating in southern Brazil. <i>Emerging Microbes and Infections</i> , 2019 , 8, 920-933	18.9	2
9	Genome Analysis of Entomopathogenic <i>Bacillus</i> sp. ABP14 Isolated from a Lignocellulosic Compost. <i>Genome Biology and Evolution</i> , 2019 , 11, 1658-1662	3.9	2
8	Genome of <i>Pseudomonas</i> sp. FeS53a, a Putative Plant Growth-Promoting Bacterium Associated with Rice Grown in Iron-Stressed Soils. <i>Genome Announcements</i> , 2015 , 3,		2
7	Metagenomic analysis of the bacterial microbiota associated with cultured oysters (<i>Crassostrea</i> sp.) in estuarine environments. <i>Anais Da Academia Brasileira De Ciencias</i> , 2020 , 92, e20180432	1.4	2
6	Re-emergence of Gamma-like-II and emergence of Gamma-S:E661D SARS-CoV-2 lineages in the south of Brazil after the 2021 outbreak. <i>Virology Journal</i> , 2021 , 18, 222	6.1	2
5	Development and validation of the first SSR markers for <i>Mimosa scabrella</i> Benth. <i>Genetics and Molecular Research</i> , 2017 , 16,	1.2	2
4	Phylogenetic-based inference reveals distinct transmission dynamics of SARS-CoV-2 lineages Gamma and P.2 in Brazil.. <i>IScience</i> , 2022 , 25, 104156	6.1	2
3	Complete Genome Sequence of <i>Herbaspirillum hiltneri</i> N3 (DSM 17495), Isolated from Surface-Sterilized Wheat Roots. <i>Genome Announcements</i> , 2015 , 3,		1

- 2 Verrucomicrobia in Brazilian Atlantic forest soil. *Applied and Environmental Microbiology*, **2011**, 77, 3903-4.8 1
- 1 Resistome analysis of bloodstream infection bacterial genomes reveals a specific set of proteins involved in antibiotic resistance and drug efflux. *NAR Genomics and Bioinformatics*, **2020**, 2, lqaa055 3.7 0