

# Conceição Egas

## List of Publications by Year in descending order

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Version: 2024-02-01

55  
papers

2,168  
citations

257450

24  
h-index

243625

44  
g-index

68  
all docs

68  
docs citations

68  
times ranked

3402  
citing authors

#	ARTICLE	IF	CITATIONS
1	Flow-based method for biofilm microbiota enrichment and exploration of metagenomes. <i>AMB Express</i> , 2022, 12, 36.	3.0	1
2	Lactation as a programming window for metabolic syndrome. <i>European Journal of Clinical Investigation</i> , 2021, 51, e13482.	3.4	32
3	Rethinking water treatment targets: Bacteria regrowth under unprovable conditions. <i>Water Research</i> , 2021, 201, 117374.	11.3	17
4	Doxorubicin persistently rewires cardiac circadian homeostasis in mice. <i>Archives of Toxicology</i> , 2020, 94, 257-271.	4.2	8
5	Potato cyst nematodes: New solutions to an old problem. <i>Crop Protection</i> , 2020, 137, 105303.	2.1	11
6	Linking Tree Health, Rhizosphere Physicochemical Properties, and Microbiome in Acute Oak Decline. <i>Forests</i> , 2020, 11, 1153.	2.1	12
7	Comparative genome sequence analysis of several species in the genus <i>Tepidimonas</i> and the description of a novel species <i>Tepidimonas charontis</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1596-1604.	1.7	8
8	Combining an innovative non-invasive sampling method and high-throughput sequencing to characterize fungal communities on a canvas painting. <i>International Biodeterioration and Biodegradation</i> , 2019, 145, 104816.	3.9	20
9	High-quality draft genome sequence of <i>Gaiella occulta</i> isolated from a 150 meter deep mineral water borehole and comparison with the genome sequences of other deep-branching lineages of the phylum <i>Actinobacteria</i> . <i>MicrobiologyOpen</i> , 2019, 8, e00840.	3.0	38
10	Comparative genomics reveals a novel genetic organization of the sad cluster in the sulfonamide-degrader <i>Candidatus Leucobacter sulfamidivorax</i> ™ strain GP. <i>BMC Genomics</i> , 2019, 20, 885.	2.8	13
11	Transfer of <i>Meiothermus chliarophilus</i> (Tenreiro et al. 1995) Nobre et al. 1996, <i>Meiothermus roseus</i> Ming et al. 2016, <i>Meiothermus terrae</i> Yu et al. 2014 and <i>Meiothermus timidus</i> Pires et al. 2005, to <i>Calidithermus</i> gen. nov., as <i>Calidithermus chliarophilus</i> comb. nov., <i>Calidithermus roseus</i> comb. nov., <i>Calidithermus terrae</i> comb. nov. and <i>Calidithermus timidus</i> comb. nov., respectively, and emended description of the genus <i>Meiothermus</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1060-1069.	1.7	28
12	Bacterial Communities in Serpa Cheese by Culture Dependent Techniques, 16S rRNA Gene Sequencing and High-throughput Sequencing Analysis. <i>Journal of Food Science</i> , 2018, 83, 1333-1341.	3.1	24
13	Metagenomic Signatures of Microbial Communities in Deep-Sea Hydrothermal Sediments of Azores Vent Fields. <i>Microbial Ecology</i> , 2018, 76, 387-403.	2.8	25
14	Draft genome sequence of <i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> strain Fito_F321, an endophyte microorganism from <i>Vitis vinifera</i> with biocontrol potential. <i>Standards in Genomic Sciences</i> , 2018, 13, 30.	1.5	25
15	Cysteine proteases secreted by the pinewood nematode, <i>Bursaphelenchus xylophilus</i> : In silico analysis. <i>Computational Biology and Chemistry</i> , 2018, 77, 291-296.	2.3	16
16	The draft genome sequence of cork oak. <i>Scientific Data</i> , 2018, 5, 180069.	5.3	98
17	<i>Raineya orbicola</i> gen. nov., sp. nov. a slightly thermophilic bacterium of the phylum <i>Bacteroidetes</i> and the description of <i>Raineyaceae</i> fam. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 982-989.	1.7	19
18	<i>Lysobacter silvestris</i> sp. nov., isolated from alpine forest soil, and reclassification of <i>Luteimonas tolerans</i> as <i>Lysobacter tolerans</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1571-1577.	1.7	20

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19	<i>Solimicrobium silvestre</i> gen. nov., sp. nov., isolated from alpine forest soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2491-2498.	1.7	11
20	Metatranscriptomics profile of the gill microbial community during & Bathymodiolus azoricus& aquarium acclimatization at atmospheric pressure. <i>AIMS Microbiology</i> , 2018, 4, 240-260.	2.2	3
21	<i>CYP1B1</i> mutational screening in a Portuguese cohort of primary congenital glaucoma patients. <i>Ophthalmic Genetics</i> , 2017, 38, 197-199.	1.2	2
22	Significant effects of RNAi silencing of the venom allergen-like protein ( <i>Mhi-1</i> ) of the root-knot nematode <i>Meloidogyne hispanica</i> in the early events of infection. <i>Plant Pathology</i> , 2017, 66, 1329-1337.	2.4	10
23	Sediment Microbial Diversity of Three Deep-Sea Hydrothermal Vents Southwest of the Azores. <i>Microbial Ecology</i> , 2017, 74, 332-349.	2.8	31
24	Novel de novo <i>FOXC1</i> nonsense mutation in an Axenfeld-Rieger syndrome patient. <i>American Journal of Medical Genetics, Part A</i> , 2017, 173, 1607-1610.	1.2	6
25	Priming of a DNA metabarcoding approach for species identification and inventory in marine macrobenthic communities. <i>Genome</i> , 2017, 60, 260-271.	2.0	16
26	Salmonella Enteritidis Isolate Harboring Multiple Efflux Pumps and Pathogenicity Factors, Shows Absence of O Antigen Polymerase Gene. <i>Frontiers in Microbiology</i> , 2016, 7, 1130.	3.5	1
27	<i>Bursaphelenchus xylophilus</i> and <i>B. mucronatus</i> secretomes: a comparative proteomic analysis. <i>Scientific Reports</i> , 2016, 6, 39007.	3.3	25
28	Molecular characterization and functional analysis of a calponin gene from the pinewood nematode. <i>Forest Pathology</i> , 2015, 45, 467-473.	1.1	4
29	Wine fermentation microbiome: a landscape from different Portuguese wine appellations. <i>Frontiers in Microbiology</i> , 2015, 6, 905.	3.5	170
30	New splicing mutation in the choline kinase beta (CHKB) gene causing a muscular dystrophy detected by whole-exome sequencing. <i>Journal of Human Genetics</i> , 2015, 60, 305-312.	2.3	33
31	Microbial diversity in deep-sea sediments from the Menez Gwen hydrothermal vent system of the Mid-Atlantic Ridge. <i>Marine Genomics</i> , 2015, 24, 343-355.	1.1	46
32	Comparative transcriptomic analysis of male and female flowers of monoecious <i>Quercus suber</i> . <i>Frontiers in Plant Science</i> , 2014, 5, 599.	3.6	59
33	Complete genome sequence of the Radiation-Resistant bacterium <i>Rubrobacter radiotolerans</i> RSPS-4. <i>Standards in Genomic Sciences</i> , 2014, 9, 1062-1075.	1.5	43
34	Genetic Variants in ICAM1, PPARGC1A and MTHFR Are Potentially Associated with Different Phenotypes of Diabetic Retinopathy. <i>Ophthalmologica</i> , 2014, 232, 156-162.	1.9	20
35	A comprehensive assessment of the transcriptome of cork oak ( <i>Quercus suber</i> ) through EST sequencing. <i>BMC Genomics</i> , 2014, 15, 371.	2.8	53
36	Site-related differences in gene expression and bacterial densities in the mussel <i>Bathymodiolus azoricus</i> from the Menez Gwen and Lucky Strike deep-sea hydrothermal vent sites. <i>Fish and Shellfish Immunology</i> , 2014, 39, 343-353.	3.6	21

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37	Unravelling the Diversity of Grapevine Microbiome. PLoS ONE, 2014, 9, e85622.	2.5	268
38	Bacterial diversity from the source to the tap: a comparative study based on 16S rRNA gene-DGGE and culture-dependent methods. FEMS Microbiology Ecology, 2013, 83, 361-374.	2.7	104
39	Draft Genome Sequence of <i>Serratia fonticola</i> UTAD54, a Carbapenem-Resistant Strain Isolated from Drinking Water. Genome Announcements, 2013, 1, .	0.8	7
40	Draft Genome Sequence of <i>Serratia fonticola</i> LMG 7882 T Isolated from Freshwater. Genome Announcements, 2013, 1, .	0.8	3
41	Identification of DLEC1 D215N Somatic Mutation in Formalin Fixed Paraffin Embedded Melanoma and Melanocytic Nevi Specimens. Journal of Skin Cancer, 2013, 2013, 1-4.	1.2	0
42	Habitat- and host-related variation in sponge bacterial symbiont communities in Indonesian waters. FEMS Microbiology Ecology, 2013, 85, 465-482.	2.7	87
43	Assessment of the Geographic Origins of Pinewood Nematode Isolates via Single Nucleotide Polymorphism in Effector Genes. PLoS ONE, 2013, 8, e83542.	2.5	27
44	Biometrical, Biochemical, and Molecular Diagnosis of Portuguese <i>Meloidogyne hispanica</i> Isolates. Plant Disease, 2012, 96, 865-874.	1.4	31
45	Liver hepcidin mRNA expression is inappropriately low in alcoholic patients compared with healthy controls. European Journal of Gastroenterology and Hepatology, 2012, 24, 1158-1165.	1.6	50
46	The Transcriptome of <i>Bathymodiolus azoricus</i> Gill Reveals Expression of Genes from Endosymbionts and Free-Living Deep-Sea Bacteria. Marine Drugs, 2012, 10, 1765-1783.	4.6	21
47	Searching for resistance genes to <i>Bursaphelenchus xylophilus</i> using high throughput screening. BMC Genomics, 2012, 13, 599.	2.8	53
48	Expression of Genes Encoding Extracellular Matrix Macromolecules and Metalloproteinases in Avian Tibial Dyschondroplasia. Journal of Comparative Pathology, 2011, 145, 174-186.	0.4	28
49	Culture-dependent and culture-independent diversity surveys target different bacteria: a case study in a freshwater sample. Antonie Van Leeuwenhoek, 2011, 100, 245-257.	1.7	100
50	High-throughput sequencing and analysis of the gill tissue transcriptome from the deep-sea hydrothermal vent mussel <i>Bathymodiolus azoricus</i> . BMC Genomics, 2010, 11, 559.	2.8	114
51	Taking Root: Enduring Effect of Rhizosphere Bacterial Colonization in Mangroves. PLoS ONE, 2010, 5, e14065.	2.5	121
52	Parallel DNA pyrosequencing unveils new zebrafish microRNAs. BMC Genomics, 2009, 10, 195.	2.8	65
53	The Saposin-like Domain of the Plant Aspartic Proteinase Precursor Is a Potent Inducer of Vesicle Leakage. Journal of Biological Chemistry, 2000, 275, 38190-38196.	3.4	59
54	Extracellular $\alpha$ -amylase from <i>Thermus filiformis</i> Ork A2: purification and biochemical characterization. Extremophiles, 1998, 2, 23-32.	2.3	52

#	ARTICLE	IF	CITATIONS
55	An Insightful Model to Study Innate Immunity and Stress Response in Deep-Sea Vent Animals: Profiling the Mussel <i>Bathymodiolus azoricus</i> . , 0, , .		2