

# 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  | Unravelling the Diversity of Grapevine Microbiome. PLoS ONE, 2014, 9, e85622.   | 2.5 | 268       |
| 2  | Wine fermentation microbiome: a landscape from different Portuguese wine appellations. Frontiers in Microbiology, 2015, 6, 905.   | 3.5 | 170       |
| 3  | Taking Root: Enduring Effect of Rhizosphere Bacterial Colonization in Mangroves. PLoS ONE, 2010, 5, e14065.   | 2.5 | 121       |
| 4  | 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       |
| 5  | 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       |
| 6  | 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       |
| 7  | The draft genome sequence of cork oak. Scientific Data, 2018, 5, 180069.  | 5.3 | 98        |
| 8  | Habitat- and host-related variation in sponge bacterial symbiont communities in Indonesian waters. FEMS Microbiology Ecology, 2013, 85, 465-482.  | 2.7 | 87        |
| 9  | Parallel DNA pyrosequencing unveils new zebrafish microRNAs. BMC Genomics, 2009, 10, 195.   | 2.8 | 65        |
| 10 | 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        |
| 11 | Comparative transcriptomic analysis of male and female flowers of monoecious <i>Quercus suber</i> . Frontiers in Plant Science, 2014, 5, 599.   | 3.6 | 59        |
| 12 | Searching for resistance genes to <i>Bursaphelenchus xylophilus</i> using high throughput screening. BMC Genomics, 2012, 13, 599.   | 2.8 | 53        |
| 13 | A comprehensive assessment of the transcriptome of cork oak ( <i>Quercus suber</i> ) through EST sequencing. BMC Genomics, 2014, 15, 371.   | 2.8 | 53        |
| 14 | Extracellular $\alpha$ -amylase from <i>Thermus filiformis</i> Ork A2: purification and biochemical characterization. Extremophiles, 1998, 2, 23-32.  | 2.3 | 52        |
| 15 | 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        |
| 16 | Microbial diversity in deep-sea sediments from the Menez Gwen hydrothermal vent system of the Mid-Atlantic Ridge. Marine Genomics, 2015, 24, 343-355.   | 1.1 | 46        |
| 17 | Complete genome sequence of the Radiation-Resistant bacterium <i>Rubrobacter radiotolerans</i> RSPS-4. Standards in Genomic Sciences, 2014, 9, 1062-1075.   | 1.5 | 43        |
| 18 | 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> . MicrobiologyOpen, 2019, 8, e00840. | 3.0 | 38        |

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|----|---|------|-----------|
| 19 | 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        |
| 20 | Lactation as a programming window for metabolic syndrome. <i>European Journal of Clinical Investigation</i> , 2021, 51, e13482.   | 3.4  | 32        |
| 21 | Biometrical, Biochemical, and Molecular Diagnosis of Portuguese <i>Meloidogyne hispanica</i> Isolates. <i>Plant Disease</i> , 2012, 96, 865-874.  | 1.4  | 31        |
| 22 | Sediment Microbial Diversity of Three Deep-Sea Hydrothermal Vents Southwest of the Azores. <i>Microbial Ecology</i> , 2017, 74, 332-349.  | 2.8  | 31        |
| 23 | Expression of Genes Encoding Extracellular Matrix Macromolecules and Metalloproteinases in Avian Tibial Dyschondroplasia. <i>Journal of Comparative Pathology</i> , 2011, 145, 174-186.   | 0.4  | 28        |
| 24 | 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        |
| 25 | Assessment of the Geographic Origins of Pinewood Nematode Isolates via Single Nucleotide Polymorphism in Effector Genes. <i>PLoS ONE</i> , 2013, 8, e83542.   | 2.5  | 27        |
| 26 | <i>Bursaphelenchus xylophilus</i> and <i>B. mucronatus</i> secretomes: a comparative proteomic analysis. <i>Scientific Reports</i> , 2016, 6, 39007.  | 3.3  | 25        |
| 27 | 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        |
| 28 | 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        |
| 29 | 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        |
| 30 | The Transcriptome of <i>Bathymodiolus azoricus</i> Gill Reveals Expression of Genes from Endosymbionts and Free-Living Deep-Sea Bacteria. <i>Marine Drugs</i> , 2012, 10, 1765-1783.  | 4.6  | 21        |
| 31 | 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        |
| 32 | 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        |
| 33 | 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        |
| 34 | <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        |
| 35 | <i>Raineya orbicola</i> gen. nov., sp. nov. a slightly thermophilic bacterium of the phylum Bacteroidetes 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        |
| 36 | Rethinking water treatment targets: Bacteria regrowth under unprovable conditions. <i>Water Research</i> , 2021, 201, 117374.   | 11.3 | 17        |

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|----|---|-----|-----------|
| 37 | 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        |
| 38 | 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        |
| 39 | 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        |
| 40 | Linking Tree Health, Rhizosphere Physicochemical Properties, and Microbiome in Acute Oak Decline. <i>Forests</i> , 2020, 11, 1153.  | 2.1 | 12        |
| 41 | Potato cyst nematodes: New solutions to an old problem. <i>Crop Protection</i> , 2020, 137, 105303.   | 2.1 | 11        |
| 42 | <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        |
| 43 | 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        |
| 44 | Doxorubicin persistently rewires cardiac circadian homeostasis in mice. <i>Archives of Toxicology</i> , 2020, 94, 257-271.  | 4.2 | 8         |
| 45 | 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         |
| 46 | Draft Genome Sequence of <i>Serratia fonticola</i> UTAD54, a Carbapenem-Resistant Strain Isolated from Drinking Water. <i>Genome Announcements</i> , 2013, 1, .   | 0.8 | 7         |
| 47 | 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         |
| 48 | Molecular characterization and functional analysis of a calponin gene from the pinewood nematode. <i>Forest Pathology</i> , 2015, 45, 467-473.  | 1.1 | 4         |
| 49 | Draft Genome Sequence of <i>Serratia fonticola</i> LMG 7882 T Isolated from Freshwater. <i>Genome Announcements</i> , 2013, 1, .  | 0.8 | 3         |
| 50 | Metatranscriptomics profile of the gill microbial community during <i>Bathymodiolus azoricus</i> ; aquarium acclimatization at atmospheric pressure. <i>AIMS Microbiology</i> , 2018, 4, 240-260.   | 2.2 | 3         |
| 51 | <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         |
| 52 | An Insightful Model to Study Innate Immunity and Stress Response in Deep-Sea Vent Animals: Profiling the Mussel <i>Bathymodiolus azoricus</i> . , 0, , .  |     | 2         |
| 53 | <i>Salmonella</i> 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         |
| 54 | Flow-based method for biofilm microbiota enrichment and exploration of metagenomes. <i>AMB Express</i> , 2022, 12, 36.  | 3.0 | 1         |

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|----|--|-----|-----------|
| 55 | 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         |