

Germán Bonilla-Rosso

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7626186/publications.pdf>

Version: 2024-02-01

23
papers

2,904
citations

430874

18
h-index

713466

21
g-index

27
all docs

27
docs citations

27
times ranked

4280
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | The Sorcerer II Global Ocean Sampling Expedition: Northwest Atlantic through Eastern Tropical Pacific. <i>PLoS Biology</i> , 2007, 5, e77. | 5.6 | 1,757 |
| 2 | The <i>Plasmodiophora brassicae</i> genome reveals insights in its life cycle and ancestry of chitin synthases. <i>Scientific Reports</i> , 2015, 5, 11153. | 3.3 | 202 |
| 3 | Functional roles and metabolic niches in the honey bee gut microbiota. <i>Current Opinion in Microbiology</i> , 2018, 43, 69-76. | 5.1 | 133 |
| 4 | The genome of <i>Bacillus coahuilensis</i> reveals adaptations essential for survival in the relic of an ancient marine environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5803-5808. | 7.1 | 94 |
| 5 | Comparative Metagenomics of Two Microbial Mats at Cuatro Ciénegas Basin I: Ancient Lessons on How to Cope with an Environment Under Severe Nutrient Stress. <i>Astrobiology</i> , 2012, 12, 648-658. | 3.0 | 85 |
| 6 | High dietary fat intake induces a microbiota signature that promotes food allergy. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 157-170.e8. | 2.9 | 84 |
| 7 | Comparative Metagenomics of Two Microbial Mats at Cuatro Ciénegas Basin II: Community Structure and Composition in Oligotrophic Environments. <i>Astrobiology</i> , 2012, 12, 659-673. | 3.0 | 83 |
| 8 | Bacterial Communities and the Nitrogen Cycle in the Gypsum Soils of Cuatro Ciénegas Basin, Coahuila: A Mars Analogue. <i>Astrobiology</i> , 2012, 12, 699-709. | 3.0 | 59 |
| 9 | Water-sediment niche differentiation in ancient marine lineages of <i>Exiguobacterium</i> endemic to the Cuatro Cienegas Basin. <i>Environmental Microbiology</i> , 2012, 14, 2323-2333. | 3.8 | 48 |
| 10 | Genomic changes underlying host specialization in the bee gut symbiont <i>Lactobacillus</i> Firm5. <i>Molecular Ecology</i> , 2019, 28, 2224-2237. | 3.9 | 45 |
| 11 | Habitat partitioning of marine benthic denitrifier communities in response to oxygen availability. <i>Environmental Microbiology Reports</i> , 2016, 8, 486-492. | 2.4 | 42 |
| 12 | Design and evaluation of primers targeting genes encoding NO-forming nitrite reductases: implications for ecological inference of denitrifying communities. <i>Scientific Reports</i> , 2016, 6, 39208. | 3.3 | 37 |
| 13 | Honey bees harbor a diverse gut virome engaging in nested strain-level interactions with the microbiota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7355-7362. | 7.1 | 37 |
| 14 | Expression of nirK and nirS genes in two strains of <i>Pseudomonas stutzeri</i> harbouring both types of NO-forming nitrite reductases. <i>Research in Microbiology</i> , 2018, 169, 343-347. | 2.1 | 35 |
| 15 | External carbon addition for enhancing denitrification modifies bacterial community composition and affects CH ₄ and N ₂ O production in sub-arctic mining pond sediments. <i>Water Research</i> , 2019, 158, 22-33. | 11.3 | 32 |
| 16 | A prevalent and culturable microbiota links ecological balance to clinical stability of the human lung after transplantation. <i>Nature Communications</i> , 2021, 12, 2126. | 12.8 | 31 |
| 17 | Mesocosms of Aquatic Bacterial Communities from the Cuatro Cienegas Basin (Mexico): A Tool to Test Bacterial Community Response to Environmental Stress. <i>Microbial Ecology</i> , 2012, 64, 346-358. | 2.8 | 23 |
| 18 | Structure and species composition of ectomycorrhizal fungal communities colonizing seedlings and adult trees of <i>Pinus montezumae</i> in Mexican neotropical forests. <i>FEMS Microbiology Ecology</i> , 2012, 80, 479-487. | 2.7 | 21 |

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|----|--|-----|-----------|
| 19 | Suppression of High-Fat Diet-Induced Obesity by Platycodon Grandiflorus in Mice Is Linked to Changes in the Gut Microbiota. <i>Journal of Nutrition</i> , 2020, 150, 2364-2374. | 2.9 | 17 |
| 20 | Drastic changes in aquatic bacterial populations from the Cuatro Ciénegas Basin (Mexico) in response to long-term environmental stress. <i>Antonie Van Leeuwenhoek</i> , 2013, 104, 1159-1175. | 1.7 | 16 |
| 21 | Understanding microbial community diversity metrics derived from metagenomes: performance evaluation using simulated data sets. <i>FEMS Microbiology Ecology</i> , 2012, 82, 37-49. | 2.7 | 9 |
| 22 | Lessons Learned from Simulated Metagenomic Datasets. , 2013, , 1-8. | | 1 |
| 23 | Lessons Learned from Simulated Metagenomic Datasets. , 2015, , 353-359. | | 0 |