Serena Manara

List of Publications by Year in descending order

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| # | Article | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Coronaviruses and SARS-CoV-2 in sewerage and their removal: Step by step in wastewater treatment plants. Environmental Research, 2022, 207, 112204. | 7.5 | 27 |
| 2 | The wave of the SARS-CoV-2 Omicron variant resulted in a rapid spike and decline as highlighted by municipal wastewater surveillance. Environmental Technology and Innovation, 2022, 28, 102667. | 6.1 | 22 |
| 3 | Route of SARS-CoV-2 in sewerage and wastewater treatment plants. , 2021, , 145-176. | | 4 |
| 4 | Genomic diversity and ecology of human-associated Akkermansia species in the gut microbiome revealed by extensive metagenomic assembly. Genome Biology, 2021, 22, 209. | 8.8 | 65 |
| 5 | Surveillance of SARS-CoV-2 in extensive monitoring of municipal wastewater: key issues to yield reliable results. Water Science and Technology, 2021, 84, 3508-3514. | 2.5 | 6 |
| 6 | Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. Nature Communications, 2020, 11, 2500. | 12.8 | 368 |
| 7 | Analysis of 1321 Eubacterium rectale genomes from metagenomes uncovers complex phylogeographic population structure and subspecies functional adaptations. Genome Biology, 2020, 21, 138. | 8.8 | 72 |
| 8 | SARS-CoV-2 from faeces to wastewater treatment: What do we know? A review. Science of the Total Environment, 2020, 743, 140444. | 8.0 | 321 |
| 9 | Methicillin-resistant Staphylococcus aureus eradication in cystic fibrosis patients: A randomized multicenter study. PLoS ONE, 2019, 14, e0213497. | 2.5 | 22 |
| 10 | Metagenomic analysis of colorectal cancer datasets identifies cross-cohort microbial diagnostic signatures and a link with choline degradation. Nature Medicine, 2019, 25, 667-678. | 30.7 | 602 |
| 11 | Microbial genomes from non-human primate gut metagenomes expand the primate-associated bacterial tree of life with over 1000 novel species. Genome Biology, 2019, 20, 299. | 8.8 | 58 |
| 12 | Extensive Unexplored Human Microbiome Diversity Revealed by Over 150,000 Genomes from Metagenomes Spanning Age, Geography, and Lifestyle. Cell, 2019, 176, 649-662.e20. | 28.9 | 1,087 |
| 13 | Whole-genome epidemiology, characterisation, and phylogenetic reconstruction of Staphylococcus aureus strains in a paediatric hospital. Genome Medicine, 2018, 10, 82. | 8.2 | 54 |
| 14 | Mother-to-Infant Microbial Transmission from Different Body Sites Shapes the Developing Infant Gut Microbiome. Cell Host and Microbe, 2018, 24, 133-145.e5. | 11.0 | 822 |
| 15 | Studying Vertical Microbiome Transmission from Mothers to Infants by Strain-Level Metagenomic Profiling. MSystems, 2017, 2, . | 3.8 | 329 |