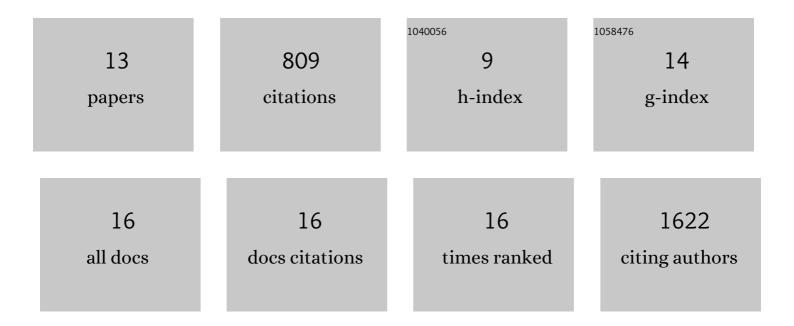
Sébastien Matamoros

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/541825/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Global phylogenetic analysis of Escherichia coli and plasmids carrying the mcr-1 gene indicates bacterial diversity but plasmid restriction. Scientific Reports, 2017, 7, 15364.	3.3	230
2	Dissemination of the mcr-1 colistin resistance gene. Lancet Infectious Diseases, The, 2016, 16, 147-149.	9.1	172
3	The dynamics of the pulmonary microbiome during mechanical ventilation in the intensive care unit and the association with occurrence of pneumonia. Thorax, 2017, 72, 803-810.	5.6	118
4	Zoonotic Transmission of <i>mcr-1</i> Colistin Resistance Gene from Small-Scale Poultry Farms, Vietnam. Emerging Infectious Diseases, 2017, 23, 529-532.	4.3	91
5	Recommendations for the introduction of metagenomic next-generation sequencing in clinical virology, part II: bioinformatic analysis and reporting. Journal of Clinical Virology, 2021, 138, 104812.	3.1	39
6	Serologic Surveillance and Phylogenetic Analysis of SARS-CoV-2 Infection Among Hospital Health Care Workers. JAMA Network Open, 2021, 4, e2118554.	5.9	36
7	Limited contribution of non-intensive chicken farming to ESBL-producing Escherichia coli colonization in humans in Vietnam: an epidemiological and genomic analysis. Journal of Antimicrobial Chemotherapy, 2019, 74, 561-570.	3.0	35
8	Quantifying the contribution of four resistance mechanisms to ciprofloxacin MIC in <i>Escherichia coli</i> : a systematic review. Journal of Antimicrobial Chemotherapy, 2019, 74, 298-310.	3.0	31
9	Understanding and predicting ciprofloxacin minimum inhibitory concentration in Escherichia coli with machine learning. Scientific Reports, 2020, 10, 15026.	3.3	24
10	Thermus thermophilus DNA can be used as internal control for process monitoring of clinical metagenomic next-generation sequencing of urine samples. Journal of Microbiological Methods, 2020, 176, 106005.	1.6	8
11	Proficiency Testing of Metagenomics-Based Detection of Food-Borne Pathogens Using a Complex Artificial Sequencing Dataset. Frontiers in Microbiology, 2020, 11, 575377.	3.5	7
12	Amplified fragment length polymorphism and whole genome sequencing: a comparison of methods in the investigation of a nosocomial outbreak with vancomycin resistant enterococci. Antimicrobial Resistance and Infection Control, 2019, 8, 153.	4.1	5
13	Accelerating surveillance and research of antimicrobial resistance – an online repository for sharing of antimicrobial susceptibility data associated with whole-genome sequences. Microbial Genomics, 2020. 6	2.0	5