

# Jacobo de la Cuesta-Zuluaga

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

18  
papers

802  
citations

9  
h-index

22  
g-index

22  
ext. papers

1,154  
ext. citations

6.9  
avg, IF

4.42  
L-index

#	Paper	IF	Citations
18	Metformin Is Associated With Higher Relative Abundance of Mucin-Degrading Akkermansia muciniphila and Several Short-Chain Fatty Acid-Producing Microbiota in the Gut. <i>Diabetes Care</i> , <b>2017</b> , 40, 54-62	14.6	325
17	Higher Fecal Short-Chain Fatty Acid Levels Are Associated with Gut Microbiome Dysbiosis, Obesity, Hypertension and Cardiometabolic Disease Risk Factors. <i>Nutrients</i> , <b>2018</b> , 11,	6.7	166
16	Age- and Sex-Dependent Patterns of Gut Microbial Diversity in Human Adults. <i>MSystems</i> , <b>2019</b> , 4,	7.6	110
15	Gut microbiota is associated with obesity and cardiometabolic disease in a population in the midst of Westernization. <i>Scientific Reports</i> , <b>2018</b> , 8, 11356	4.9	48
14	Syntrophy via Interspecies H Transfer between and Underlies Their Global Cooccurrence in the Human Gut. <i>MBio</i> , <b>2020</b> , 11,	7.8	43
13	Impact of DNA extraction, sample dilution, and reagent contamination on 16S rRNA gene sequencing of human feces. <i>Applied Microbiology and Biotechnology</i> , <b>2018</b> , 102, 403-411	5.7	31
12	Large-Scale Metagenome Assembly Reveals Novel Animal-Associated Microbial Genomes, Biosynthetic Gene Clusters, and Other Genetic Diversity. <i>MSystems</i> , <b>2020</b> , 5,	7.6	21
11	Considerations For Optimizing Microbiome Analysis Using a Marker Gene. <i>Frontiers in Nutrition</i> , <b>2016</b> , 3, 26	6.2	18
10	Struo: a pipeline for building custom databases for common metagenome profilers. <i>Bioinformatics</i> , <b>2020</b> , 36, 2314-2315	7.2	16
9	Genomic Insights into Adaptations of Trimethylamine-Utilizing Methanogens to Diverse Habitats, Including the Human Gut. <i>MSystems</i> , <b>2021</b> , 6,	7.6	5
8	Variants in genes of innate immunity, appetite control and energy metabolism are associated with host cardiometabolic health and gut microbiota composition. <i>Gut Microbes</i> , <b>2020</b> , 11, 556-568	8.8	4
7	Gut microbiota composition explains more variance in the host cardiometabolic risk than genetic ancestry. <i>Gut Microbes</i> , <b>2020</b> , 11, 191-204	8.8	4
6	Gut microbiota composition explains more variance in the host cardiometabolic risk than genetic ancestry		3
5	Genomic insights into adaptations of TMA-utilizing methanogens to diverse habitats including the human gut		2
4	Large scale metagenome assembly reveals novel animal-associated microbial genomes, biosynthetic gene clusters, and other genetic diversity		2
3	Incorporating genome-based phylogeny and functional similarity into diversity assessments helps to resolve a global collection of human gut metagenomes		1
2	Age and sex-dependent patterns of gut microbial diversity in human adults		1

1      Reclassification of *as comb. nov.* based on whole genome analysis. *International Journal of Systematic and Evolutionary Microbiology*, **2021**, 71, 2.2      1