

# Leah Briscoe

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/396021/publications.pdf>

Version: 2024-02-01

7

papers

683

citations

1478505

6

h-index

1720034

7

g-index

9

all docs

9

docs citations

9

times ranked

1087

citing authors

#	ARTICLE	IF	CITATIONS
1	FEAST: fast expectation-maximization for microbial source tracking. <i>Nature Methods</i> , 2019, 16, 627-632.	19.0	275
2	Whole Genome Analyses Suggests that <i>Burkholderia</i> sensu lato Contains Two Additional Novel Genera ( <i>Mycetohabitans</i> gen. nov., and <i>Trinickia</i> gen. nov.): Implications for the Evolution of Diazotrophy and Nodulation in the <i>Burkholderiaceae</i> . <i>Genes</i> , 2018, 9, 389.	2.4	252
3	Symbiotic <i>Burkholderia</i> Species Show Diverse Arrangements of <i>nif/fix</i> and <i>nod</i> Genes and Lack Typical High-Affinity Cytochrome <i>cbb3</i> Oxidase Genes. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 609-619.	2.6	62
4	Modeling the temporal dynamics of the gut microbial community in adults and infants. <i>PLoS Computational Biology</i> , 2019, 15, e1006960.	3.2	42
5	SaVanT: a web-based tool for the sample-level visualization of molecular signatures in gene expression profiles. <i>BMC Genomics</i> , 2017, 18, 824.	2.8	32
6	The effect of gastric acid suppression on probiotic colonization in a double blinded randomized clinical trial. <i>Clinical Nutrition ESPEN</i> , 2022, 47, 70-77.	1.2	13
7	Evaluating supervised and unsupervised background noise correction in human gut microbiome data. <i>PLoS Computational Biology</i> , 2022, 18, e1009838.	3.2	6