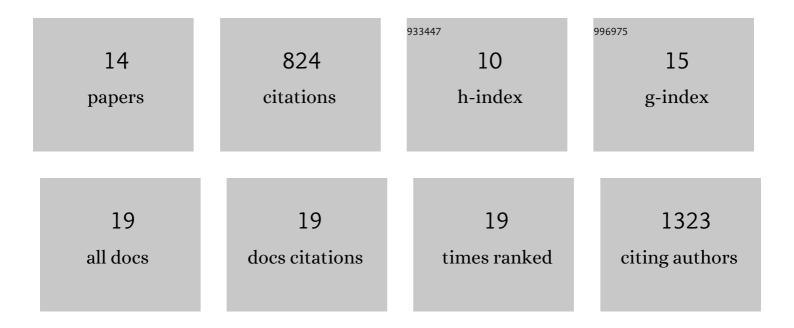
Louis J Taylor

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5742712/publications.pdf Version: 2024-02-01



ΙουιςΙΤλυορ

#	Article	IF	CITATIONS
1	Lack of detection of a human placenta microbiome in samples from preterm and term deliveries. Microbiome, 2018, 6, 196.	11.1	221
2	Sunbeam: an extensible pipeline for analyzing metagenomic sequencing experiments. Microbiome, 2019, 7, 46.	11.1	134
3	Redondoviridae, a Family of Small, Circular DNA Viruses of the Human Oro-Respiratory Tract Associated with Periodontitis and Critical Illness. Cell Host and Microbe, 2019, 25, 719-729.e4.	11.0	83
4	Signatures of COVID-19 Severity and Immune Response in the Respiratory Tract Microbiome. MBio, 2021, 12, e0177721.	4.1	74
5	Detection of SARS-CoV-2 RNA using RT-LAMP and molecular beacons. Genome Biology, 2021, 22, 169.	8.8	61
6	Structural Basis for Inhibitor-Induced Aggregation of HIV Integrase. PLoS Biology, 2016, 14, e1002584.	5.6	56
7	Lifestyle and the presence of helminths is associated with gut microbiome composition in Cameroonians. Genome Biology, 2020, 21, 122.	8.8	48
8	Epidermal closure regulates histolysis during mammalian (<i>Mus</i>) digit regeneration. Regeneration (Oxford, England), 2015, 2, 106-119.	6.3	46
9	A specific sequence in the genome of respiratory syncytial virus regulates the generation of copy-back defective viral genomes. PLoS Pathogens, 2019, 15, e1007707.	4.7	33
10	Redondovirus Diversity and Evolution on Global, Individual, and Molecular Scales. Journal of Virology, 2021, 95, e0081721.	3.4	12
11	grabseqs: simple downloading of reads and metadata from multiple next-generation sequencing data repositories. Bioinformatics, 2020, 36, 3607-3609.	4.1	11
12	ICTV Virus Taxonomy Profile: Redondoviridae. Journal of General Virology, 2021, 102, .	2.9	9
13	Pyviko: an automated Python tool to design gene knockouts in complex viruses with overlapping genes. BMC Microbiology, 2017, 17, 12.	3.3	7
14	Rengasvirus, a Circular Replication-Associated Protein-Encoding Single-Stranded DNA Virus-Related Genome That Is a Common Contaminant in Metagenomic Data. Microbiology Resource Announcements, 2021, 10, .	0.6	1