Leen Beller

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5186243/publications.pdf

Version: 2024-02-01

17	956	14	17
papers	citations	h-index	g-index
18	18	18	1862
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	The virota and its transkingdom interactions in the healthy infant gut. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2114619119.	3.3	30
2	Benchmark of thirteen bioinformatic pipelines for metagenomic virus diagnostics using datasets from clinical samples. Journal of Clinical Virology, 2021, 141, 104908.	1.6	28
3	High Prevalence of Coinfecting Enteropathogens in Suspected Rotavirus Vaccine Breakthrough Cases. Journal of Clinical Microbiology, 2021, 59, e0123621.	1.8	9
4	At Least Seven Distinct Rotavirus Genotype Constellations in Bats with Evidence of Reassortment and Zoonotic Transmissions. MBio, 2021, 12, .	1.8	31
5	A Previously Undescribed Highly Prevalent Phage Identified in a Danish Enteric Virome Catalog. MSystems, 2021, 6, e0038221.	1.7	22
6	Successional Stages in Infant Gut Microbiota Maturation. MBio, 2021, 12, e0185721.	1.8	48
7	Clinical relevance of plasma virome dynamics in liver transplant recipients. EBioMedicine, 2020, 60, 103009.	2.7	21
8	Honey-bee–associated prokaryotic viral communities reveal wide viral diversity and a profound metabolic coding potential. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10511-10519.	3.3	36
9	What is (not) known about the dynamics of the human gut virome in health and disease. Current Opinion in Virology, 2019, 37, 52-57.	2.6	47
10	A decade of enterovirus genetic diversity in Belgium. Journal of Clinical Virology, 2019, 121, 104205.	1.6	9
11	Stable distinct core eukaryotic viromes in different mosquito species from Guadeloupe, using single mosquito viral metagenomics. Microbiome, 2019, 7, 121.	4.9	109
12	Gut Virome Analysis of Cameroonians Reveals High Diversity of Enteric Viruses, Including Potential Interspecies Transmitted Viruses. MSphere, 2019, 4, .	1.3	57
13	Discovery and genome characterization of three new Jeilongviruses, a lineage of paramyxoviruses characterized by their unique membrane proteins. BMC Genomics, 2018, 19, 617.	1.2	35
14	Nanopore sequencing as a revolutionary diagnostic tool for porcine viral enteric disease complexes identifies porcine kobuvirus as an important enteric virus. Scientific Reports, 2018, 8, 9830.	1.6	59
15	Cameroonian fruit bats harbor divergent viruses, including rotavirus H, bastroviruses, and picobirnaviruses using an alternative genetic code. Virus Evolution, 2018, 4, vey008.	2.2	90
16	Novel highly divergent reassortant bat rotaviruses in Cameroon, without evidence of zoonosis. Scientific Reports, 2016, 6, 34209.	1.6	44
17	Modular approach to customise sample preparation procedures for viral metagenomics: a reproducible protocol for virome analysis. Scientific Reports, 2015, 5, 16532.	1.6	277