

# Leen Beller

## List of Publications by Year in descending order

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

Version: 2024-02-01

17  
papers

956  
citations

623188

14  
h-index

887659

17  
g-index

18  
all docs

18  
docs citations

18  
times ranked

1862  
citing authors

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