

Evelien M Adriaenssens

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

4,839
citations

168829

31
h-index

134545

62
g-index

79
all docs

79
docs citations

79
times ranked

5236
citing authors

#	ARTICLE	IF	CITATIONS
1	Highly diverse flavobacterial phages isolated from North Sea spring blooms. <i>ISME Journal</i> , 2022, 16, 555-568.	4.4	32
2	Differentiating between viruses and virus species by writing their names correctly. <i>Archives of Virology</i> , 2022, 167, 1231-1234.	0.9	33
3	Genomic Diversity of Bacteriophages Infecting the Genus <i>Acinetobacter</i> . <i>Viruses</i> , 2022, 14, 181.	1.5	12
4	RNA-viromics reveals diverse communities of soil RNA viruses with the potential to affect grassland ecosystems across multiple trophic levels. <i>ISME Communications</i> , 2022, 2, .	1.7	32
5	Metagenomic investigation of the equine faecal microbiome reveals extensive taxonomic diversity. <i>PeerJ</i> , 2022, 10, e13084.	0.9	18
6	Mobility of antimicrobial resistance across serovars and disease presentations in non-typhoidal <i>Salmonella</i> from animals and humans in Vietnam. <i>Microbial Genomics</i> , 2022, 8, .	1.0	2
7	Detection of Bacteriophages: Sequence-Based Systems. , 2021, , 621-644.		3
8	CoronaHiT: high-throughput sequencing of SARS-CoV-2 genomes. <i>Genome Medicine</i> , 2021, 13, 21.	3.6	94
9	A Roadmap for Genome-Based Phage Taxonomy. <i>Viruses</i> , 2021, 13, 506.	1.5	268
10	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. <i>PeerJ</i> , 2021, 9, e10941.	0.9	79
11	ICTV Virus Taxonomy Profile: Plectroviridae. <i>Journal of General Virology</i> , 2021, 102, .	1.3	1
12	Large-scale sequencing of SARS-CoV-2 genomes from one region allows detailed epidemiology and enables local outbreak management. <i>Microbial Genomics</i> , 2021, 7, .	1.0	31
13	Changes to virus taxonomy and to the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2021). <i>Archives of Virology</i> , 2021, 166, 2633-2648.	0.9	219
14	ICTV Virus Taxonomy Profile: Inoviridae. <i>Journal of General Virology</i> , 2021, 102, .	1.3	13
15	Bacterial Viruses Subcommittee and Archaeal Viruses Subcommittee of the ICTV: update of taxonomy changes in 2021. <i>Archives of Virology</i> , 2021, 166, 3239-3244.	0.9	24
16	Phage Diversity in the Human Gut Microbiome: a Taxonomist's Perspective. <i>MSystems</i> , 2021, 6, e0079921.	1.7	15
17	Tracing the fate of wastewater viruses reveals catchment-scale virome diversity and connectivity. <i>Water Research</i> , 2021, 203, 117568.	5.3	17
18	Comparison of PCR versus PCR-Free DNA Library Preparation for Characterising the Human Faecal Virome. <i>Viruses</i> , 2021, 13, 2093.	1.5	9

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19	Leviviricetes: expanding and restructuring the taxonomy of bacteria-infecting single-stranded RNA viruses. <i>Microbial Genomics</i> , 2021, 7, .	1.0	18
20	Perspective on taxonomic classification of uncultivated viruses. <i>Current Opinion in Virology</i> , 2021, 51, 207-215.	2.6	31
21	Phage Annotation Guide: Guidelines for Assembly and High-Quality Annotation. <i>Phage</i> , 2021, 2, 170-182.	0.8	24
22	Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Phages. <i>Systematic Biology</i> , 2020, 69, 110-123.	2.7	89
23	From Orphan Phage to a Proposed New Familyâ€”The Diversity of N4-Like Viruses. <i>Antibiotics</i> , 2020, 9, 663.	1.5	39
24	Changes to virus taxonomy and the Statutes ratified by the International Committee on Taxonomy of Viruses (2020). <i>Archives of Virology</i> , 2020, 165, 2737-2748.	0.9	202
25	The Site-Specific Recombination System of the Escherichia coli Bacteriophage Î¶24B. <i>Frontiers in Microbiology</i> , 2020, 11, 578056.	1.5	6
26	Viral indicators for tracking domestic wastewater contamination in the aquatic environment. <i>Water Research</i> , 2020, 181, 115926.	5.3	97
27	Phages Actively Challenge Niche Communities in Antarctic Soils. <i>MSystems</i> , 2020, 5, .	1.7	17
28	Differences in Compositions of Gut Bacterial Populations and Bacteriophages in 5â€”11 Year-Olds Born Preterm Compared to Full Term. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 276.	1.8	9
29	Evolution of Salmonella enterica serotype Typhimurium driven by anthropogenic selection and niche adaptation. <i>PLoS Genetics</i> , 2020, 16, e1008850.	1.5	48
30	Taxonomy of prokaryotic viruses: 2018-2019 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , 2020, 165, 1253-1260.	0.9	144
31	ICTV Virus Taxonomy Profile: Herelleviridae. <i>Journal of General Virology</i> , 2020, 101, 362-363.	1.3	37
32	Still Something to Discover: Novel Insights into Escherichia coli Phage Diversity and Taxonomy. <i>Viruses</i> , 2019, 11, 454.	1.5	77
33	Taxonomic assignment of uncultivated prokaryotic virus genomes is enabled by gene-sharing networks. <i>Nature Biotechnology</i> , 2019, 37, 632-639.	9.4	569
34	Critical Evaluation of CrAssphage as a Molecular Marker for Human-Derived Wastewater Contamination in the Aquatic Environment. <i>Food and Environmental Virology</i> , 2019, 11, 113-119.	1.5	77
35	5. Metagenomics of extreme environments: methods and applications. , 2019, , 93-126.		0
36	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414

#	ARTICLE	IF	CITATIONS
37	Detection of Bacteriophages: Sequence-Based Systems. , 2019, , 1-25.		1
38	Taxonomy of prokaryotic viruses: 2017 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. Archives of Virology, 2018, 163, 1125-1129.	0.9	172
39	Exploring Viral Diversity in a Unique South African Soil Habitat. Scientific Reports, 2018, 8, 111.	1.6	23
40	Namib Desert Soil Microbial Community Diversity, Assembly, and Function Along a Natural Xeric Gradient. Microbial Ecology, 2018, 75, 193-203.	1.4	60
41	Purification of Bacteriophages Using Anion-Exchange Chromatography. Methods in Molecular Biology, 2018, 1681, 59-69.	0.4	8
42	Evaluation of the genomic diversity of viruses infecting bacteria, archaea and eukaryotes using a common bioinformatic platform: steps towards a unified taxonomy. Journal of General Virology, 2018, 99, 1331-1343.	1.3	72
43	Viromic Analysis of Wastewater Input to a River Catchment Reveals a Diverse Assemblage of RNA Viruses. MSystems, 2018, 3, .	1.7	59
44	Genomics of Viruses of Microorganisms. , 2018, , .		0
45	Metaviromes of Extracellular Soil Viruses along a Namib Desert Aridity Gradient. Genome Announcements, 2017, 5, .	0.8	18
46	Taxonomy of prokaryotic viruses: 2016 update from the ICTV bacterial and archaeal viruses subcommittee. Archives of Virology, 2017, 162, 1153-1157.	0.9	57
47	How to Name and Classify Your Phage: An Informal Guide. Viruses, 2017, 9, 70.	1.5	323
48	Environmental drivers of viral community composition in Antarctic soils identified by viromics. Microbiome, 2017, 5, 83.	4.9	94
49	Metaviromics of Namib Desert Salt Pans: A Novel Lineage of Haloarchaeal Salterproviruses and a Rich Source of ssDNA Viruses. Viruses, 2016, 8, 14.	1.5	24
50	Taxonomy of prokaryotic viruses: update from the ICTV bacterial and archaeal viruses subcommittee. Archives of Virology, 2016, 161, 1095-1099.	0.9	83
51	Diversity and Ecology of Viruses in Hyperarid Desert Soils. Applied and Environmental Microbiology, 2016, 82, 770-777.	1.4	89
52	Genetic signatures indicate widespread antibiotic resistance and phage infection in microbial communities of the McMurdo Dry Valleys, East Antarctica. Polar Biology, 2015, 38, 919-925.	0.5	28
53	Metagenomic analysis of the viral community in <sc>N</sc>amib <sc>D</sc>esert hypoliths. Environmental Microbiology, 2015, 17, 480-495.	1.8	83
54	Integration of genomic and proteomic analyses in the classification of the Siphoviridae family. Virology, 2015, 477, 144-154.	1.1	52

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55	Niche-dependent genetic diversity in Antarctic metaviromes. <i>Bacteriophage</i> , 2014, 4, e980125.	1.9	12
56	Draft Genome Sequence of the Aromatic Hydrocarbon-Degrading Bacterium <i>Sphingobium</i> sp. Strain Ant17, Isolated from Antarctic Soil. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
57	Three proposed new bacteriophage genera of staphylococcal phages: <i>3alikevirus</i> , <i>77likevirus</i> and <i>Phietalikevirus</i> . <i>Archives of Virology</i> , 2014, 159, 389-398.	0.9	22
58	High-Level Diversity of Tailed Phages, Eukaryote-Associated Viruses, and Virophage-Like Elements in the Metaviromes of Antarctic Soils. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6888-6897.	1.4	121
59	Using Signature Genes as Tools To Assess Environmental Viral Ecology and Diversity. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4470-4480.	1.4	141
60	Complete Genome Sequence of the Novel <i>Escherichia coli</i> Phage phAPEC8. <i>Journal of Virology</i> , 2012, 86, 13117-13118.	1.5	22
61	Complete Genome Sequence of the Giant <i>Pseudomonas</i> Phage Lu11. <i>Journal of Virology</i> , 2012, 86, 6369-6370.	1.5	25
62	A suggested new bacteriophage genus: <i>Viunalikevirus</i> . <i>Archives of Virology</i> , 2012, 157, 2035-2046.	0.9	77
63	CIM [®] monolithic anion-exchange chromatography as a useful alternative to CsCl gradient purification of bacteriophage particles. <i>Virology</i> , 2012, 434, 265-270.	1.1	65
64	T4-Related Bacteriophage LIMEstone Isolates for the Control of Soft Rot on Potato Caused by <i>Dickeya solani</i> . <i>PLoS ONE</i> , 2012, 7, e33227.	1.1	169
65	Bacteriophages LIMelight and LIMZero of <i>Pantoea agglomerans</i> , Belonging to the <i>phiKMV</i> -Like Viruses. <i>Applied and Environmental Microbiology</i> , 2011, 77, 3443-3450.	1.4	51