

Martin Hlzer

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

44
papers

621
citations

14
h-index

23
g-index

60
ext. papers

1,042
ext. citations

7.2
avg, IF

4.49
L-index

#	Paper	IF	Citations
44	Comparative study of ten thogotovirus isolates and their distinct characteristics.. <i>Journal of Virology</i> , 2022 , JVI0155621	6.6	1
43	Chromosome-level genome assembly and transcriptome-based annotation of the oleaginous yeast <i>Rhodotorula toruloides</i> CBS 14. <i>Genomics</i> , 2021 , 113, 4022-4027	4.3	1
42	Evidence for the existence of a new genus <i>Chlamydiifrater</i> gen. nov. inside the family Chlamydiaceae with two new species isolated from flamingo (<i>Phoenicopterus roseus</i>): <i>Chlamydiifrater phoenicopteri</i> sp. nov. and <i>Chlamydiifrater volucris</i> sp. nov. <i>Systematic and Applied Microbiology</i> , 2021 , 44, 1212-1220	4.2	4
41	poreCov-An Easy to Use, Fast, and Robust Workflow for SARS-CoV-2 Genome Reconstruction Nanopore Sequencing. <i>Frontiers in Genetics</i> , 2021 , 12, 711437	4.5	6
40	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. <i>Briefings in Bioinformatics</i> , 2021 , 22, 642-663	13.4	56
39	A marine <i>Chlamydomonas</i> sp. emerging as an algal model. <i>Journal of Phycology</i> , 2021 , 57, 54-69	3	1
38	Metagenomics workflow for hybrid assembly, differential coverage binning, metatranscriptomics and pathway analysis (MUFFIN). <i>PLoS Computational Biology</i> , 2021 , 17, e1008716	5	6
37	Rise and Fall of SARS-CoV-2 Lineage A.27 in Germany. <i>Viruses</i> , 2021 , 13,	6.2	4
36	Transcript Variants Have Distinct Roles in Ovarian Carcinoma and Differently Influence Platinum Sensitivity and Angiogenesis. <i>Cancers</i> , 2021 , 13,	6.6	1
35	SLC35F2, a Transporter Sporadically Mutated in the Untranslated Region, Promotes Growth, Migration, and Invasion of Bladder Cancer Cells. <i>Cells</i> , 2021 , 10,	7.9	4
34	Integrating cultivation and metagenomics for a multi-kingdom view of skin microbiome diversity and functions.. <i>Nature Microbiology</i> , 2021 ,	26.6	6
33	The economical lifestyle of CPR bacteria in groundwater allows little preference for environmental drivers.. <i>Environmental Microbiomes</i> , 2021 , 16, 24	5.6	4
32	Comparative Genome Analysis of 33 Strains Reveals Characteristic Features of and Closely Related Species. <i>Pathogens</i> , 2020 , 9,	4.5	9
31	Inclusion of Oxford Nanopore long reads improves all microbial and viral metagenome-assembled genomes from a complex aquifer system. <i>Environmental Microbiology</i> , 2020 , 22, 4000-4013	5.2	17
30	RNAflow: An Effective and Simple RNA-Seq Differential Gene Expression Pipeline Using Nextflow. <i>Genes</i> , 2020 , 11,	4.2	3
29	A comprehensive annotation and differential expression analysis of short and long non-coding RNAs in 16 bat genomes. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqz006	3.7	1
28	Virus- and Interferon Alpha-Induced Transcriptomes of Cells from the Microbat <i>Myotis daubentonii</i> . <i>IScience</i> , 2019 , 19, 647-661	6.1	17

27	Chlamydia buteonis, a new Chlamydia species isolated from a red-shouldered hawk. <i>Systematic and Applied Microbiology</i> , 2019 , 42, 125997	4.2	28
26	Evaluation of Sequencing Library Preparation Protocols for Viral Metagenomic Analysis from Pristine Aquifer Groundwaters. <i>Viruses</i> , 2019 , 11,	6.2	15
25	Structure and Hierarchy of Influenza Virus Models Revealed by Reaction Network Analysis. <i>Viruses</i> , 2019 , 11,	6.2	6
24	De novo transcriptome assembly: A comprehensive cross-species comparison of short-read RNA-Seq assemblers. <i>GigaScience</i> , 2019 , 8,	7.6	78
23	Direct RNA nanopore sequencing of full-length coronavirus genomes provides novel insights into structural variants and enables modification analysis. <i>Genome Research</i> , 2019 , 29, 1545-1554	9.7	112
22	SilentMutations (SIM): A tool for analyzing long-range RNA-RNA interactions in viral genomes and structured RNAs. <i>Virus Research</i> , 2019 , 260, 135-141	6.4	1
21	Cohesin-mediated NF- κ B signaling limits hematopoietic stem cell self-renewal in aging and inflammation. <i>Journal of Experimental Medicine</i> , 2019 , 216, 152-175	16.6	39
20	Differential Effects of Vitamins A and D on the Transcriptional Landscape of Human Monocytes during Infection. <i>Scientific Reports</i> , 2017 , 7, 40599	4.9	16
19	Massive Effect on LncRNAs in Human Monocytes During Fungal and Bacterial Infections and in Response to Vitamins A and D. <i>Scientific Reports</i> , 2017 , 7, 40598	4.9	23
18	Evaluation of associations between genotypes of Mycobacterium avium subsp. paratuberculosis and presence of intestinal lesions characteristic of paratuberculosis. <i>Veterinary Microbiology</i> , 2017 , 201, 188-194	3.34	1
17	Evolution and Antiviral Specificities of Interferon-Induced Mx Proteins of Bats against Ebola, Influenza, and Other RNA Viruses. <i>Journal of Virology</i> , 2017 , 91,	6.6	34
16	Complete Genome Sequence of JII-1961, a Bovine subsp. Field Isolate from Germany. <i>Genome Announcements</i> , 2017 , 5,		7
15	Software Dedicated to Virus Sequence Analysis "Bioinformatics Goes Viral". <i>Advances in Virus Research</i> , 2017 , 99, 233-257	10.7	12
14	Whole-Genome Sequence of Chlamydia gallinacea Type Strain 08-1274/3. <i>Genome Announcements</i> , 2016 , 4,		7
13	Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells. <i>Scientific Reports</i> , 2016 , 6, 34589	4.9	30
12	Towards a comprehensive picture of alloacceptor tRNA remodeling in metazoan mitochondrial genomes. <i>Nucleic Acids Research</i> , 2015 , 43, 8044-56	20.1	16
11	Comprehensive insights in the Mycobacterium avium subsp. paratuberculosis genome using new WGS data of sheep strain JIII-386 from Germany. <i>Genome Biology and Evolution</i> , 2015 , 7, 2585-2601	3.9	15
10	Computational Strategies to Combat COVID-19: Useful Tools to Accelerate SARS-CoV-2 and Coronavirus Research		2

9	EpiDope: A Deep neural network for linear B-cell epitope prediction	1
8	Inclusion of Oxford Nanopore long reads improves all microbial and phage metagenome-assembled genomes from a complex aquifer system	3
7	Metagenomics workflow for hybrid assembly, differential coverage binning, transcriptomics and pathway analysis (MUFFIN)	1
6	What the Phage: A scalable workflow for the identification and analysis of phage sequences	5
5	PCAGO: An interactive web service to analyze RNA-Seq data with principal component analysis	3
4	Direct RNA nanopore sequencing of full-length coronavirus genomes provides novel insights into structural variants and enables modification analysis	12
3	poreCov - an easy to use, fast, and robust workflow for SARS-CoV-2 genome reconstruction via nanopore sequencing	2
2	Molecular epidemiology of SARS-CoV-2 - a regional to global perspective	4
1	DarkQ: continuous genomic monitoring using message queues. <i>F1000Research</i> ,10, 998	3.6 0