

Martin Hlzer

List of Publications by Citations

Source: <https://exaly.com/author-pdf/1000691/martin-holzer-publications-by-citations.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	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
43	De novo transcriptome assembly: A comprehensive cross-species comparison of short-read RNA-Seq assemblers. <i>GigaScience</i> , 2019 , 8,	7.6	78
42	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
41	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
40	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
39	Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells. <i>Scientific Reports</i> , 2016 , 6, 34589	4.9	30
38	<i>Chlamydia buteonis</i> , a new <i>Chlamydia</i> species isolated from a red-shouldered hawk. <i>Systematic and Applied Microbiology</i> , 2019 , 42, 125997	4.2	28
37	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
36	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
35	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
34	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
33	Towards a comprehensive picture of alloacceptor tRNA remodeling in metazoan mitochondrial genomes. <i>Nucleic Acids Research</i> , 2015 , 43, 8044-56	20.1	16
32	Evaluation of Sequencing Library Preparation Protocols for Viral Metagenomic Analysis from Pristine Aquifer Groundwaters. <i>Viruses</i> , 2019 , 11,	6.2	15
31	Comprehensive insights in the <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> 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
30	Software Dedicated to Virus Sequence Analysis "Bioinformatics Goes Viral". <i>Advances in Virus Research</i> , 2017 , 99, 233-257	10.7	12
29	Direct RNA nanopore sequencing of full-length coronavirus genomes provides novel insights into structural variants and enables modification analysis		12
28	Comparative Genome Analysis of 33 Strains Reveals Characteristic Features of and Closely Related Species. <i>Pathogens</i> , 2020 , 9,	4.5	9

27	Whole-Genome Sequence of Chlamydia gallinacea Type Strain 08-1274/3. <i>Genome Announcements</i> , 2016 , 4,		7
26	Complete Genome Sequence of JII-1961, a Bovine subsp. Field Isolate from Germany. <i>Genome Announcements</i> , 2017 , 5,		7
25	Structure and Hierarchy of Influenza Virus Models Revealed by Reaction Network Analysis. <i>Viruses</i> , 2019 , 11,	6.2	6
24	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
23	Metagenomics workflow for hybrid assembly, differential coverage binning, metatranscriptomics and pathway analysis (MUFFIN). <i>PLoS Computational Biology</i> , 2021 , 17, e1008716	5	6
22	Integrating cultivation and metagenomics for a multi-kingdom view of skin microbiome diversity and functions.. <i>Nature Microbiology</i> , 2021 ,	26.6	6
21	What the Phage: A scalable workflow for the identification and analysis of phage sequences		5
20	Evidence for the existence of a new genus Chlamydiifrater gen. nov. inside the family Chlamydiaceae with two new species isolated from flamingo (<i>Phoenicopterus roseus</i>): Chlamydiifrater phoenicopteri sp. nov. and Chlamydiifrater volucris sp. nov. <i>Systematic and Applied Microbiology</i> , 2021 , 44, 126200	4.2	4
19	Molecular epidemiology of SARS-CoV-2 - a regional to global perspective		4
18	Rise and Fall of SARS-CoV-2 Lineage A.27 in Germany. <i>Viruses</i> , 2021 , 13,	6.2	4
17	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
16	The economical lifestyle of CPR bacteria in groundwater allows little preference for environmental drivers.. <i>Environmental Microbiomes</i> , 2021 , 16, 24	5.6	4
15	Inclusion of Oxford Nanopore long reads improves all microbial and phage metagenome-assembled genomes from a complex aquifer system		3
14	PCAGO: An interactive web service to analyze RNA-Seq data with principal component analysis		3
13	RNAflow: An Effective and Simple RNA-Seq Differential Gene Expression Pipeline Using Nextflow. <i>Genes</i> , 2020 , 11,	4.2	3
12	Computational Strategies to Combat COVID-19: Useful Tools to Accelerate SARS-CoV-2 and Coronavirus Research		2
11	poreCov - an easy to use, fast, and robust workflow for SARS-CoV-2 genome reconstruction via nanopore sequencing		2
10	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

9	Comparative study of ten thogotovirus isolates and their distinct characteristics.. <i>Journal of Virology</i> , 2022 , JVI0155621	6.6	1
8	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
7	EpiDope: A Deep neural network for linear B-cell epitope prediction		1
6	Metagenomics workflow for hybrid assembly, differential coverage binning, transcriptomics and pathway analysis (MUFFIN)		1
5	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
4	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
3	A marine <i>Chlamydomonas</i> sp. emerging as an algal model. <i>Journal of Phycology</i> , 2021 , 57, 54-69	3	1
2	Transcript Variants Have Distinct Roles in Ovarian Carcinoma and Differently Influence Platinum Sensitivity and Angiogenesis. <i>Cancers</i> , 2021 , 13,	6.6	1
1	DarkQ: continuous genomic monitoring using message queues. <i>F1000Research</i> , 10, 998	3.6	0