

Martin Häglzer

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

1,336
citations

430874

18
h-index

414414

32
g-index

60
all docs

60
docs citations

60
times ranked

2170
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	5.5	178
2	De novo transcriptome assembly: A comprehensive cross-species comparison of short-read RNA-Seq assemblers. <i>GigaScience</i> , 2019, 8, .	6.4	150
3	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.	6.5	110
4	Integrating cultivation and metagenomics for a multi-kingdom view of skin microbiome diversity and functions. <i>Nature Microbiology</i> , 2022, 7, 169-179.	13.3	58
5	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.	8.5	56
6	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, .	3.4	53
7	Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells. <i>Scientific Reports</i> , 2016, 6, 34589.	3.3	47
8	<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.	2.8	45
9	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.	3.8	42
10	Virus- and Interferon Alpha-Induced Transcriptomes of Cells from the Microbat <i>Myotis daubentonii</i> . <i>IScience</i> , 2019, 19, 647-661.	4.1	37
11	The economical lifestyle of CPR bacteria in groundwater allows little preference for environmental drivers. <i>Environmental Microbiomes</i> , 2021, 16, 24.	5.0	36
12	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.	3.3	34
13	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, evv154.	2.5	31
14	Carbon fixation rates in groundwater similar to those in oligotrophic marine systems. <i>Nature Geoscience</i> , 2022, 15, 561-567.	12.9	28
15	Evaluation of Sequencing Library Preparation Protocols for Viral Metagenomic Analysis from Pristine Aquifer Groundwaters. <i>Viruses</i> , 2019, 11, 484.	3.3	27
16	Differential Effects of Vitamins A and D on the Transcriptional Landscape of Human Monocytes during Infection. <i>Scientific Reports</i> , 2017, 7, 40599.	3.3	25
17	Comparative Genome Analysis of 33 <i>Chlamydia</i> Strains Reveals Characteristic Features of <i>Chlamydia psittaci</i> and Closely Related Species. <i>Pathogens</i> , 2020, 9, 899.	2.8	24
18	Evidence for the existence of a new genus <i>Chlamydiifrater</i> gen. nov. inside the family <i>Chlamydiaceae</i> 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, 126200.	2.8	24

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19	poreCov-An Easy to Use, Fast, and Robust Workflow for SARS-CoV-2 Genome Reconstruction via Nanopore Sequencing. <i>Frontiers in Genetics</i> , 2021, 12, 711437.	2.3	24
20	Towards a comprehensive picture of alloacceptor tRNA remodeling in metazoan mitochondrial genomes. <i>Nucleic Acids Research</i> , 2015, 43, 8044-8056.	14.5	22
21	Complete Genome Sequence of JII-1961, a Bovine <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> Field Isolate from Germany. <i>Genome Announcements</i> , 2017, 5, .	0.8	19
22	Software Dedicated to Virus Sequence Analysis –Bioinformatics Goes Viral–. <i>Advances in Virus Research</i> , 2017, 99, 233-257.	2.1	19
23	RNAflow: An Effective and Simple RNA-Seq Differential Gene Expression Pipeline Using Nextflow. <i>Genes</i> , 2020, 11, 1487.	2.4	18
24	Metagenomics workflow for hybrid assembly, differential coverage binning, metatranscriptomics and pathway analysis (MUFFIN). <i>PLoS Computational Biology</i> , 2021, 17, e1008716.	3.2	18
25	Investigation of a Limited but Explosive COVID-19 Outbreak in a German Secondary School. <i>Viruses</i> , 2022, 14, 87.	3.3	16
26	SLC35F2, a Transporter Sporadically Mutated in the Untranslated Region, Promotes Growth, Migration, and Invasion of Bladder Cancer Cells. <i>Cells</i> , 2021, 10, 80.	4.1	12
27	Whole-Genome Sequence of <i>Chlamydia gallinacea</i> Type Strain 08-1274/3. <i>Genome Announcements</i> , 2016, 4, .	0.8	9
28	Rise and Fall of SARS-CoV-2 Lineage A.27 in Germany. <i>Viruses</i> , 2021, 13, 1491.	3.3	9
29	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.	2.9	9
30	Comparative Study of Ten Thogotovirus Isolates and Their Distinct <i>In Vivo</i> Characteristics. <i>Journal of Virology</i> , 2022, 96, JVI0155621.	3.4	9
31	Context-aware genomic surveillance reveals hidden transmission of a carbapenemase-producing <i>Klebsiella pneumoniae</i> . <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
32	Structure and Hierarchy of Influenza Virus Models Revealed by Reaction Network Analysis. <i>Viruses</i> , 2019, 11, 449.	3.3	8
33	A decade of de novo transcriptome assembly: Are we there yet?. <i>Molecular Ecology Resources</i> , 2021, 21, 11-13.	4.8	6
34	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.	2.2	5
35	RUNX3 Transcript Variants Have Distinct Roles in Ovarian Carcinoma and Differently Influence Platinum Sensitivity and Angiogenesis. <i>Cancers</i> , 2021, 13, 476.	3.7	5
36	Evaluation of associations between genotypes of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> and presence of intestinal lesions characteristic of paratuberculosis. <i>Veterinary Microbiology</i> , 2017, 201, 188-194.	1.9	4

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37	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.	3.2	4
38	BAFFR activates PI3K/AKT signaling in human naive but not in switched memory B cells through direct interactions with B cell antigen receptors. <i>Cell Reports</i> , 2022, 39, 111019.	6.4	4
39	CovRadar: continuously tracking and filtering SARS-CoV-2 mutations for genomic surveillance. <i>Bioinformatics</i> , 2022, 38, 4223-4225.	4.1	4
40	A marine <i>Chlamydomonas</i> sp. emerging as an algal model. <i>Journal of Phycology</i> , 2021, 57, 54-69.	2.3	3
41	DarkQ: continuous genomic monitoring using message queues. <i>F1000Research</i> , 0, 10, 998.	1.6	1
42	Near Chromosome-Level Genome Assembly and Annotation of <i>Rhodotorula babjevae</i> Strains Reveals High Intraspecific Divergence. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 323.	3.5	1