

Ulrik Fahne

List of Publications by Citations

Source: <https://exaly.com/author-pdf/3605922/ulrik-fahnoe-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.

48
papers

460
citations

12
h-index

19
g-index

55
ext. papers

663
ext. citations

6.4
avg, IF

3.69
L-index

#	Paper	IF	Citations
48	Mouse models of acute and chronic hepatitis C virus infection. <i>Science</i> , 2017 , 357, 204-208	33.3	74
47	HCV Genotype 6a Escape From and Resistance to Velpatasvir, Pibrentasvir, and Sofosbuvir in Robust Infectious Cell Culture Models. <i>Gastroenterology</i> , 2018 , 154, 2194-2208.e12	13.3	34
46	Evolutionary Pathways to Persistence of Highly Fit and Resistant Hepatitis C Virus Protease Inhibitor Escape Variants. <i>Hepatology</i> , 2019 , 70, 771-787	11.2	28
45	HCV genotype 1-6 NS3 residue 80 substitutions impact protease inhibitor activity and promote viral escape. <i>Journal of Hepatology</i> , 2019 , 70, 388-397	13.4	25
44	A fast and robust method for full genome sequencing of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) Type 1 and Type 2. <i>Journal of Virological Methods</i> , 2013 , 193, 697-705	2.6	24
43	Overcoming Culture Restriction for SARS-CoV-2 in Human Cells Facilitates the Screening of Compounds Inhibiting Viral Replication. <i>Antimicrobial Agents and Chemotherapy</i> , 2021 , 65, e0009721	5.9	20
42	Analysis of classical swine fever virus RNA replication determinants using replicons. <i>Journal of General Virology</i> , 2013 , 94, 1739-1748	4.9	19
41	In vitro efficacy of artemisinin-based treatments against SARS-CoV-2. <i>Scientific Reports</i> , 2021 , 11, 14571	4.9	18
40	Rescue of the highly virulent classical swine fever virus strain "Koslov" from cloned cDNA and first insights into genome variations relevant for virulence. <i>Virology</i> , 2014 , 468-470, 379-387	3.6	15
39	Creation of Functional Viruses from Non-Functional cDNA Clones Obtained from an RNA Virus Population by the Use of Ancestral Reconstruction. <i>PLoS ONE</i> , 2015 , 10, e0140912	3.7	13
38	Determinants of the VP1/2A junction cleavage by the 3C protease in foot-and-mouth disease virus-infected cells. <i>Journal of General Virology</i> , 2017 , 98, 385-395	4.9	13
37	Hepatitis C Virus Protease Inhibitors Show Differential Efficacy and Interactions with Remdesivir for Treatment of SARS-CoV-2. <i>Antimicrobial Agents and Chemotherapy</i> , 2021 , 65, e0268020	5.9	13
36	Direct acting antiviral treatment of chronic hepatitis C in Denmark: factors associated with and barriers to treatment initiation. <i>Scandinavian Journal of Gastroenterology</i> , 2018 , 53, 849-856	2.4	12
35	Full-Length Open Reading Frame Amplification of Hepatitis C Virus. <i>Methods in Molecular Biology</i> , 2019 , 1911, 85-91	1.4	12
34	Development of a downstream process for the production of an inactivated whole hepatitis C virus vaccine. <i>Scientific Reports</i> , 2020 , 10, 16261	4.9	11
33	Spd2 assists Spd1 in the modulation of ribonucleotide reductase architecture but does not regulate deoxynucleotide pools. <i>Journal of Cell Science</i> , 2014 , 127, 2460-70	5.3	9
32	Ribavirin-induced mutagenesis across the complete open reading frame of hepatitis C virus genotypes 1a and 3a. <i>Journal of General Virology</i> , 2018 , 99, 1066-1077	4.9	9

31	Distinct roles for the III _d 2 sub-domain in pestivirus and picornavirus internal ribosome entry sites. <i>Nucleic Acids Research</i> , 2017 , 45, 13016-13028	20.1	8
30	Efficient generation of recombinant RNA viruses using targeted recombination-mediated mutagenesis of bacterial artificial chromosomes containing full-length cDNA. <i>BMC Genomics</i> , 2013 , 14, 819	4.5	8
29	In vitro efficacy of Artemisinin-based treatments against SARS-CoV-2		7
28	A fast and robust method for whole genome sequencing of the Aleutian Mink Disease Virus (AMDV) genome. <i>Journal of Virological Methods</i> , 2016 , 234, 43-51	2.6	7
27	Ribavirin inhibition of cell-culture infectious hepatitis C genotype 1-3 viruses is strain-dependent. <i>Virology</i> , 2020 , 540, 132-140	3.6	7
26	A near full-length open reading frame next generation sequencing assay for genotyping and identification of resistance-associated variants in hepatitis C virus. <i>Journal of Clinical Virology</i> , 2018 , 105, 49-56	14.5	6
25	Equine pegiviruses cause persistent infection of bone marrow and are not associated with hepatitis. <i>PLoS Pathogens</i> , 2020 , 16, e1008677	7.6	6
24	Efficacy of Ion-Channel Inhibitors Amantadine, Memantine and Rimantadine for the Treatment of SARS-CoV-2 In Vitro. <i>Viruses</i> , 2021 , 13,	6.2	5
23	Mutations Identified in the Hepatitis C Virus (HCV) Polymerase of Patients with Chronic HCV Treated with Ribavirin Cause Resistance and Affect Viral Replication Fidelity. <i>Antimicrobial Agents and Chemotherapy</i> , 2020 , 64,	5.9	5
22	Outcome and adverse events in patients with chronic hepatitis C treated with direct-acting antivirals: a clinical randomized study. <i>European Journal of Gastroenterology and Hepatology</i> , 2018 , 30, 1177-1186	2.2	5
21	High density Huh7.5 cell hollow fiber bioreactor culture for high-yield production of hepatitis C virus and studies of antivirals. <i>Scientific Reports</i> , 2018 , 8, 17505	4.9	5
20	Virus Adaptation and Selection Following Challenge of Animals Vaccinated against Classical Swine Fever Virus. <i>Viruses</i> , 2019 , 11,	6.2	4
19	Studies on genetic diversity of bovine viral diarrhea viruses in Danish cattle herds. <i>Virus Genes</i> , 2014 , 48, 376-80	2.3	4
18	Complete genome sequence of border disease virus genotype 3 strain gifhorn. <i>Genome Announcements</i> , 2014 , 2,		4
17	Versatile SARS-CoV-2 Reverse-Genetics Systems for the Study of Antiviral Resistance and Replication.. <i>Viruses</i> , 2022 , 14,	6.2	3
16	Efficient culture of SARS-CoV-2 in human hepatoma cells enhances viability of the virus in human lung cancer cell lines permitting the screening of antiviral compounds		3
15	SARS-CoV-2 Production in a Scalable High Cell Density Bioreactor. <i>Vaccines</i> , 2021 , 9,	5.3	3
14	Sequence adaptations during growth of rescued classical swine fever viruses in cell culture and within infected pigs. <i>Veterinary Microbiology</i> , 2016 , 192, 123-134	3.3	3

13	Global evolutionary analysis of chronic hepatitis C patients revealed significant effect of baseline viral resistance, including novel non-target sites, for DAA-based treatment and retreatment outcome. <i>Journal of Viral Hepatitis</i> , 2021 , 28, 302-316	3.4	3
12	Deoxynucleoside Salvage in Fission Yeast Allows Rescue of Ribonucleotide Reductase Deficiency but Not Spd1-Mediated Inhibition of Replication. <i>Genes</i> , 2017 , 8,	4.2	2
11	Hepatitis C Virus Protease Inhibitors Show Differential Efficacy and Interactions with Remdesivir for Treatment of SARS-CoV-2 in Vitro		2
10	HCV genome-wide analysis for development of efficient culture systems and unravelling of antiviral resistance in genotype 4. <i>Gut</i> , 2021 ,	19.2	2
9	Pathogenesis, MicroRNA-122 Gene-Regulation, and Protective Immune Responses After Acute Equine Hepacivirus Infection. <i>Hepatology</i> , 2021 , 74, 1148-1163	11.2	2
8	Inferior cure rate in pilot study of 4-week glecaprevir/pibrentasvir treatment with or without ribavirin of chronic hepatitis C. <i>Liver International</i> , 2021 , 41, 2601-2610	7.9	2
7	Identification of specific amino acid residues in the border disease virus glycoprotein E2 that modify virus growth in pig cells but not in sheep cells. <i>Journal of General Virology</i> , 2020 , 101, 1170-1181	4.9	1
6	Neutralisation titres against SARS-CoV-2 are sustained 6 months after onset of symptoms in individuals with mild COVID-19. <i>EBioMedicine</i> , 2021 , 71, 103519	8.8	1
5	High recombination rate of hepatitis C virus revealed by a green fluorescent protein reconstitution cell system.. <i>Virus Evolution</i> , 2022 , 8, veab106	3.7	1
4	Novel hepatitis B virus reverse transcriptase mutations in patients with sustained viremia despite long-term tenofovir treatment.. <i>Journal of Clinical Virology</i> , 2022 , 150-151, 105159	14.5	1
3	Strategy for efficient generation of numerous full-length cDNA clones of classical swine fever virus for haplotyping. <i>BMC Genomics</i> , 2018 , 19, 600	4.5	0
2	Characterization of a Novel Hepatitis C Virus Genotype 1 Subtype from a Patient Failing 4 Weeks of Glecaprevir-Pibrentasvir Treatment. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0075521	1.3	0
1	Identification of Novel Determinants of Neutralization Epitope Shielding for Hepatitis C Virus in Vitro. <i>Proceedings (mdpi)</i> , 2020 , 50, 5	0.3	