

# Ulrik FahnÃe

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3605922/publications.pdf>

Version: 2024-02-01

51  
papers

800  
citations

567247

15  
h-index

580810

25  
g-index

55  
all docs

55  
docs citations

55  
times ranked

1206  
citing authors

#	ARTICLE	IF	CITATIONS
1	HCV genome-wide analysis for development of efficient culture systems and unravelling of antiviral resistance in genotype 4. <i>Gut</i> , 2022, 71, 627-642.	12.1	7
2	Analysis of Neutralization Titers against SARS-CoV-2 in Health-Care Workers Vaccinated with Prime-Boost mRNA mRNA or Vector mRNA COVID-19 Vaccines. <i>Vaccines</i> , 2022, 10, 75.	4.4	8
3	Versatile SARS-CoV-2 Reverse-Genetics Systems for the Study of Antiviral Resistance and Replication. <i>Viruses</i> , 2022, 14, 172.	3.3	18
4	High recombination rate of hepatitis C virus revealed by a green fluorescent protein reconstitution cell system. <i>Virus Evolution</i> , 2022, 8, veab106.	4.9	1
5	Neutralization and receptor use of infectious culture-derived rat hepacivirus as a model for HCV. <i>Hepatology</i> , 2022, 76, 1506-1519.	7.3	8
6	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.	3.1	2
7	A Distinct Dexamethasone-Dependent Gene Expression Profile in the Lungs of COVID-19 Patients. <i>Journal of Infectious Diseases</i> , 2022, 226, 2137-2141.	4.0	3
8	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.	2.0	7
9	SARS-CoV-2 Production in a Scalable High Cell Density Bioreactor. <i>Vaccines</i> , 2021, 9, 706.	4.4	14
10	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.	3.2	58
11	Pathogenesis, MicroRNA-122 Gene Regulation, and Protective Immune Responses After Acute Equine Hepacivirus Infection. <i>Hepatology</i> , 2021, 74, 1148-1163.	7.3	14
12	In vitro efficacy of artemisinin-based treatments against SARS-CoV-2. <i>Scientific Reports</i> , 2021, 11, 14571.	3.3	53
13	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.	3.9	9
14	Hepatitis C Virus Protease Inhibitors Show Differential Efficacy and Interactions with Remdesivir for Treatment of SARS-CoV-2 <i>In Vitro</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0268020.	3.2	28
15	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.	6.1	13
16	Efficacy of Ion-Channel Inhibitors Amantadine, Memantine and Rimantadine for the Treatment of SARS-CoV-2 <i>In Vitro</i> . <i>Viruses</i> , 2021, 13, 2082.	3.3	18
17	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.	0.6	2
18	Ribavirin inhibition of cell-culture infectious hepatitis C genotype 1-3 viruses is strain-dependent. <i>Virology</i> , 2020, 540, 132-140.	2.4	10

#	ARTICLE	IF	CITATIONS
19	Development of a downstream process for the production of an inactivated whole hepatitis C virus vaccine. <i>Scientific Reports</i> , 2020, 10, 16261.	3.3	23
20	Equine pegiviruses cause persistent infection of bone marrow and are not associated with hepatitis. <i>PLoS Pathogens</i> , 2020, 16, e1008677.	4.7	17
21	Analysis of Virus Population Profiles within Pigs Infected with Virulent Classical Swine Fever Viruses: Evidence for Bottlenecks in Transmission but Absence of Tissue-Specific Virus Variants. <i>Journal of Virology</i> , 2020, 94, .	3.4	2
22	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, .	3.2	7
23	Influence of baseline resistance on treatment outcome in patients treated for chronic hepatitis C in Denmark: a nationwide study. <i>Journal of Hepatology</i> , 2020, 73, S335.	3.7	0
24	Identification of Novel Determinants of Neutralization Epitope Shielding for Hepatitis C Virus in Vitro. <i>Proceedings (mdpi)</i> , 2020, 50, .	0.2	0
25	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.	2.9	2
26	Virus Adaptation and Selection Following Challenge of Animals Vaccinated against Classical Swine Fever Virus. <i>Viruses</i> , 2019, 11, 932.	3.3	8
27	Evolutionary Pathways to Persistence of Highly Fit and Resistant Hepatitis C Virus Protease Inhibitor Escape Variants. <i>Hepatology</i> , 2019, 70, 771-787.	7.3	46
28	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.	3.7	34
29	Full-Length Open Reading Frame Amplification of Hepatitis C Virus. <i>Methods in Molecular Biology</i> , 2019, 1911, 85-91.	0.9	16
30	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.	1.5	16
31	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.	1.3	41
32	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.	1.6	7
33	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.	3.3	10
34	Strategy for efficient generation of numerous full-length cDNA clones of classical swine fever virus for haplotyping. <i>BMC Genomics</i> , 2018, 19, 600.	2.8	3
35	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.	3.1	9
36	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.	2.9	12

#	ARTICLE	IF	CITATIONS
37	Distinct roles for the III <sub>d</sub> 2 sub-domain in pestivirus and picornavirus internal ribosome entry sites. <i>Nucleic Acids Research</i> , 2017, 45, 13016-13028.	14.5	14
38	Mouse models of acute and chronic hepatitis C virus infection. <i>Science</i> , 2017, 357, 204-208.	12.6	99
39	Deoxynucleoside Salvage in Fission Yeast Allows Rescue of Ribonucleotide Reductase Deficiency but Not Spd1-Mediated Inhibition of Replication. <i>Genes</i> , 2017, 8, 128.	2.4	5
40	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.	2.9	16
41	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.	2.1	8
42	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.	1.9	3
43	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.	2.5	15
44	Spd2 assists Spd1 in modulation of RNR architecture but does not regulate deoxynucleotide pools. <i>Journal of Cell Science</i> , 2014, 127, 2460-70.	2.0	11
45	Complete Genome Sequence of Classical Swine Fever Virus Genotype 2.2 Strain Bergen. <i>Genome Announcements</i> , 2014, 2, .	0.8	0
46	Complete Genome Sequence of Border Disease Virus Genotype 3 Strain Gifhorn. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
47	Studies on genetic diversity of bovine viral diarrhoea viruses in Danish cattle herds. <i>Virus Genes</i> , 2014, 48, 376-380.	1.6	4
48	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.	2.4	18
49	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.	2.8	9
50	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.	2.1	27
51	Analysis of classical swine fever virus RNA replication determinants using replicons. <i>Journal of General Virology</i> , 2013, 94, 1739-1748.	2.9	24