

# Dirk Häpfer

## List of Publications by Year in descending order

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Version: 2024-02-01

150  
papers

6,187  
citations

76326

40  
h-index

88630

70  
g-index

164  
all docs

164  
docs citations

164  
times ranked

7275  
citing authors

#	ARTICLE	IF	CITATIONS
1	Novel Orthobunyavirus in Cattle, Europe, 2011. <i>Emerging Infectious Diseases</i> , 2012, 18, 469-472.	4.3	553
2	A Variegated Squirrel Bornavirus Associated with Fatal Human Encephalitis. <i>New England Journal of Medicine</i> , 2015, 373, 154-162.	27.0	217
3	2020 taxonomic update for phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2020, 165, 3023-3072.	2.1	184
4	Extracellular proteins of <i>Staphylococcus aureus</i> and the role of SarA and $\sigma^B$ . <i>Proteomics</i> , 2001, 1, 480-493.	2.2	178
5	Influence of the Two-Component System SaeRS on Global Gene Expression in Two Different <i>Staphylococcus aureus</i> Strains. <i>Journal of Bacteriology</i> , 2006, 188, 7742-7758.	2.2	164
6	Influenza A viruses escape from MxA restriction at the expense of efficient nuclear vRNP import. <i>Scientific Reports</i> , 2016, 6, 23138.	3.3	146
7	Epizootic Emergence of Usutu Virus in Wild and Captive Birds in Germany. <i>PLoS ONE</i> , 2012, 7, e32604.	2.5	129
8	Deletion at the 5' end of Estonian ASFV strains associated with an attenuated phenotype. <i>Scientific Reports</i> , 2018, 8, 6510.	3.3	118
9	West Nile virus epizootic in Germany, 2018. <i>Antiviral Research</i> , 2019, 162, 39-43.	4.1	117
10	Comparison of Porcine Epidemic Diarrhea Viruses from Germany and the United States, 2014. <i>Emerging Infectious Diseases</i> , 2015, 21, 493-496.	4.3	111
11	Comprehensive Characterization of the Contribution of Individual SigB-Dependent General Stress Genes to Stress Resistance of <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2005, 187, 2810-2826.	2.2	110
12	Schmallenberg Virus as Possible Ancestor of Shamonda Virus. <i>Emerging Infectious Diseases</i> , 2012, 18, 1644-6.	4.3	107
13	Fatal Encephalitic Borna Disease Virus 1 in Solid-Organ Transplant Recipients. <i>New England Journal of Medicine</i> , 2018, 379, 1377-1379.	27.0	106
14	A Versatile Sample Processing Workflow for Metagenomic Pathogen Detection. <i>Scientific Reports</i> , 2018, 8, 13108.	3.3	106
15	Related strains of African swine fever virus with different virulence: genome comparison and analysis. <i>Journal of General Virology</i> , 2015, 96, 408-419.	2.9	98
16	Salt stress adaptation of <i>Bacillus subtilis</i> : A physiological proteomics approach. <i>Proteomics</i> , 2006, 6, 1550-1562.	2.2	96
17	Zoonotic spillover infections with Borna disease virus 1 leading to fatal human encephalitis, 1999-2019: an epidemiological investigation. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 467-477.	9.1	96
18	Outbreaks among Wild Birds and Domestic Poultry Caused by Reassorted Influenza A(H5N8) Clade 2.3.4.4 Viruses, Germany, 2016. <i>Emerging Infectious Diseases</i> , 2017, 23, 633-636.	4.3	89

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19	West Nile Virus Epidemic in Germany Triggered by Epizootic Emergence, 2019. <i>Viruses</i> , 2020, 12, 448.	3.3	85
20	Classification of Cowpox Viruses into Several Distinct Clades and Identification of a Novel Lineage. <i>Viruses</i> , 2017, 9, 142.	3.3	81
21	Bluetongue virus serotype 27: detection and characterization of two novel variants in Corsica, France. <i>Journal of General Virology</i> , 2016, 97, 2073-2083.	2.9	81
22	An infectious bat-derived chimeric influenza virus harbouring the entry machinery of an influenza A virus. <i>Nature Communications</i> , 2014, 5, 4448.	12.8	80
23	Complete Coding Genome Sequence of Putative Novel Bluetongue Virus Serotype 27. <i>Genome Announcements</i> , 2015, 3, .	0.8	74
24	RIEMS: a software pipeline for sensitive and comprehensive taxonomic classification of reads from metagenomics datasets. <i>BMC Bioinformatics</i> , 2015, 16, 69.	2.6	73
25	Influenza A(H5N8) Virus Similar to Strain in Korea Causing Highly Pathogenic Avian Influenza in Germany. <i>Emerging Infectious Diseases</i> , 2015, 21, 860-863.	4.3	73
26	High yields of influenza A virus in Madin-Darby canine kidney cells are promoted by an insufficient interferon-induced antiviral state. <i>Journal of General Virology</i> , 2010, 91, 1754-1763.	2.9	68
27	Molecular epidemiology of current classical swine fever virus isolates of wild boar in Germany. <i>Journal of General Virology</i> , 2010, 91, 2687-2697.	2.9	67
28	New Chimeric Porcine Coronavirus in Swine Feces, Germany, 2012. <i>Emerging Infectious Diseases</i> , 2016, 22, 1314-1315.	4.3	64
29	Toward Animal Cell Culture-Based Influenza Vaccine Design: Viral Hemagglutinin N-Glycosylation Markedly Impacts Immunogenicity. <i>Journal of Immunology</i> , 2013, 190, 220-230.	0.8	59
30	Relatives of rubella virus in diverse mammals. <i>Nature</i> , 2020, 586, 424-428.	27.8	58
31	Swarm incursions of reassortants of highly pathogenic avian influenza virus strains H5N8 and H5N5, clade 2.3.4.4b, Germany, winter 2016/17. <i>Scientific Reports</i> , 2018, 8, 15.	3.3	57
32	Porcine Epidemic Diarrhea in Europe: In-Detail Analyses of Disease Dynamics and Molecular Epidemiology. <i>Viruses</i> , 2017, 9, 177.	3.3	56
33	Avian bornaviruses are widely distributed in canary birds ( <i>Serinus canaria f. domestica</i> ). <i>Veterinary Microbiology</i> , 2013, 165, 287-295.	1.9	55
34	Design and Validation of a Microarray for Detection, Hemagglutinin Subtyping, and Pathotyping of Avian Influenza Viruses. <i>Journal of Clinical Microbiology</i> , 2009, 47, 327-334.	3.9	52
35	A Comprehensive Deep Sequencing Strategy for Full-Length Genomes of Influenza A. <i>PLoS ONE</i> , 2011, 6, e19075.	2.5	51
36	DNase SISPA-Next Generation Sequencing Confirms Schmallenberg Virus in Belgian Field Samples and Identifies Genetic Variation in Europe. <i>PLoS ONE</i> , 2012, 7, e41967.	2.5	50

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37	Highly Pathogenic Avian Influenza H5N8 Clade 2.3.4.4b in Germany in 2016/2017. <i>Frontiers in Veterinary Science</i> , 2017, 4, 240.	2.2	45
38	Analysis of frozen strawberries involved in a large norovirus gastroenteritis outbreak using next generation sequencing and digital PCR. <i>Food Microbiology</i> , 2018, 76, 390-395.	4.2	45
39	Contributions of Individual $\sigma^B$ -Dependent General Stress Genes to Oxidative Stress Resistance of <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2012, 194, 3601-3610.	2.2	43
40	A mutation "hot spot" in the Schmallenberg virus M segment. <i>Journal of General Virology</i> , 2013, 94, 1161-1167.	2.9	43
41	The Origin of Biased Sequence Depth in Sequence-Independent Nucleic Acid Amplification and Optimization for Efficient Massive Parallel Sequencing. <i>PLoS ONE</i> , 2013, 8, e76144.	2.5	42
42	Recommendations for the introduction of metagenomic high-throughput sequencing in clinical virology, part I: Wet lab procedure. <i>Journal of Clinical Virology</i> , 2021, 134, 104691.	3.1	42
43	The Spx paralogue MgsR (YqgZ) controls a subregulon within the general stress response of <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2008, 69, 1104-1120.	2.5	41
44	Complete genome sequence of virulent duck enteritis virus (DEV) strain 2085 and comparison with genome sequences of virulent and attenuated DEV strains. <i>Virus Research</i> , 2011, 160, 316-325.	2.2	41
45	A Deep-Sequencing Workflow for the Fast and Efficient Generation of High-Quality African Swine Fever Virus Whole-Genome Sequences. <i>Viruses</i> , 2019, 11, 846.	3.3	41
46	Outbreak and Cocirculation of Three Different Usutu Virus Strains in Eastern Germany. <i>Vector-Borne and Zoonotic Diseases</i> , 2017, 17, 662-664.	1.5	40
47	Chimeric Newcastle Disease Virus Protects Chickens against Avian Influenza in the Presence of Maternally Derived NDV Immunity. <i>PLoS ONE</i> , 2013, 8, e72530.	2.5	40
48	Simple, Sensitive, and Swift Sequencing of Complete H5N1 Avian Influenza Virus Genomes. <i>Journal of Clinical Microbiology</i> , 2009, 47, 674-679.	3.9	39
49	Impact of Host Cell Line Adaptation on Quasispecies Composition and Glycosylation of Influenza A Virus Hemagglutinin. <i>PLoS ONE</i> , 2011, 6, e27989.	2.5	39
50	Out of the Reservoir: Phenotypic and Genotypic Characterization of a Novel Cowpox Virus Isolated from a Common Vole. <i>Journal of Virology</i> , 2015, 89, 10959-10969.	3.4	39
51	Recommendations for the introduction of metagenomic next-generation sequencing in clinical virology, part II: bioinformatic analysis and reporting. <i>Journal of Clinical Virology</i> , 2021, 138, 104812.	3.1	39
52	Sequencing approach to analyze the role of quasispecies for classical swine fever. <i>Virology</i> , 2013, 438, 14-19.	2.4	37
53	Comparative Analysis of Whole-Genome Sequence of African Swine Fever Virus Belgium 2018/1. <i>Emerging Infectious Diseases</i> , 2019, 25, 1249-1252.	4.3	36
54	Variegated Squirrel Bornavirus 1 in Squirrels, Germany and the Netherlands. <i>Emerging Infectious Diseases</i> , 2017, 23, 477-481.	4.3	35

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55	Proficiency Testing of Virus Diagnostics Based on Bioinformatics Analysis of Simulated <i>In Silico</i> High-Throughput Sequencing Data Sets. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	34
56	Distantly Related Rotaviruses in Common Shrews, Germany, 2004–2014. <i>Emerging Infectious Diseases</i> , 2019, 25, 2310-2314.	4.3	34
57	Comparative studies on the genetic, antigenic and pathogenic characteristics of Bokeloh bat lyssavirus. <i>Journal of General Virology</i> , 2014, 95, 1647-1653.	2.9	34
58	Spatio-temporal Analysis of the Genetic Diversity of Arctic Rabies Viruses and Their Reservoir Hosts in Greenland. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004779.	3.0	34
59	Mixed Triple: Allied Viruses in Unique Recent Isolates of Highly Virulent Type 2 Bovine Viral Diarrhea Virus Detected by Deep Sequencing. <i>Journal of Virology</i> , 2014, 88, 6983-6992.	3.4	33
60	Next-Generation Sequencing in Veterinary Medicine: How Can the Massive Amount of Information Arising from High-Throughput Technologies Improve Diagnosis, Control, and Management of Infectious Diseases?. <i>Methods in Molecular Biology</i> , 2015, 1247, 415-436.	0.9	33
61	High definition viral vaccine strain identity and stability testing using full-genome population data – The next generation of vaccine quality control. <i>Vaccine</i> , 2015, 33, 5829-5837.	3.8	32
62	Genetic characterization of Arrabida virus, a novel phlebovirus isolated in South Portugal. <i>Virus Research</i> , 2016, 214, 19-25.	2.2	30
63	Metagenomics for broad and improved parasite detection: a proof-of-concept study using swine faecal samples. <i>International Journal for Parasitology</i> , 2019, 49, 769-777.	3.1	29
64	The Transcriptional Landscape of Marek's Disease Virus in Primary Chicken B Cells Reveals Novel Splice Variants and Genes. <i>Viruses</i> , 2019, 11, 264.	3.3	29
65	The COMPARE Data Hubs. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	28
66	Identification of African swine fever virus-like elements in the soft tick genome provides insights into the virus' evolution. <i>BMC Biology</i> , 2020, 18, 136.	3.8	28
67	Complete Genome Sequence of <i>Yersinia enterocolitica</i> subsp. <i>palaearctica</i> Serogroup O:3. <i>Journal of Bacteriology</i> , 2011, 193, 2067-2067.	2.2	27
68	Tandem Repeat Insertion in African Swine Fever Virus, Russia, 2012. <i>Emerging Infectious Diseases</i> , 2015, 21, 731-732.	4.3	27
69	Complete Genome and Molecular Epidemiological Data Infer the Maintenance of Rabies among Kudu ( <i>Tragelaphus strepsiceros</i> ) in Namibia. <i>PLoS ONE</i> , 2013, 8, e58739.	2.5	27
70	Highly Pathogenic Avian Influenza Virus Subtype H5N1 Escaping Neutralization: More than HA Variation. <i>Journal of Virology</i> , 2012, 86, 1394-1404.	3.4	26
71	Pathogenicity and Immunogenicity of Different Recombinant Newcastle Disease Virus Clone 30 Variants After <i>In Ovo</i> Vaccination. <i>Avian Diseases</i> , 2012, 56, 208-217.	1.0	26
72	Coinfections: Simultaneous detections of West Nile virus and Usutu virus in birds from Germany. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 776-792.	3.0	26

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73	Novel hantavirus identified in European bat species <i>Nyctalus noctula</i> . <i>Infection, Genetics and Evolution</i> , 2017, 48, 127-130.	2.3	25
74	Molecular diagnostics for the detection of Bokeloh bat lyssavirus in a bat from Bavaria, Germany. <i>Virus Research</i> , 2013, 177, 201-204.	2.2	24
75	Ngari Virus in Goats during Rift Valley Fever Outbreak, Mauritania, 2010. <i>Emerging Infectious Diseases</i> , 2014, 20, 2174-2176.	4.3	23
76	Hepatitis E virus in feral rabbits along a rural-urban transect in Central Germany. <i>Infection, Genetics and Evolution</i> , 2018, 61, 155-159.	2.3	23
77	African swine fever whole-genome sequencing – Quantity wanted but quality needed. <i>PLoS Pathogens</i> , 2020, 16, e1008779.	4.7	23
78	Next-generation diagnostics: virus capture facilitates a sensitive viral diagnosis for epizootic and zoonotic pathogens including SARS-CoV-2. <i>Microbiome</i> , 2021, 9, 51.	11.1	23
79	Detection of SARS-CoV-2 variant B.1.1.7 in a cat in Germany. <i>Research in Veterinary Science</i> , 2021, 140, 229-232.	1.9	23
80	Borna disease outbreak with high mortality in an alpaca herd in a previously unreported endemic area in Germany. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 2093.	3.0	22
81	Synergistic antiviral activity of ribavirin and interferon- $\beta$ against parrot bornaviruses in avian cells. <i>Journal of General Virology</i> , 2016, 97, 2096-2103.	2.9	22
82	<i>Yersinia enterocolitica</i> palearctica serobiotyp O:3/4 - a successful group of emerging zoonotic pathogens. <i>BMC Genomics</i> , 2011, 12, 348.	2.8	21
83	Full genome sequence analysis of a newly emerged QX-like infectious bronchitis virus from Sudan reveals distinct spots of recombination. <i>Infection, Genetics and Evolution</i> , 2016, 46, 42-49.	2.3	21
84	Camelids and Cattle Are Dead-End Hosts for Peste-des-Petits-Ruminants Virus. <i>Viruses</i> , 2019, 11, 1133.	3.3	21
85	A theoretical and generalized approach for the assessment of the sample-specific limit of detection for clinical metagenomics. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 732-742.	4.1	20
86	Genetic and Antigenetic Characterization of the Novel Kotalahti Bat Lyssavirus (KBLV). <i>Viruses</i> , 2021, 13, 69.	3.3	20
87	Recovery of infectious virus from full-length cowpox virus (CPXV) DNA cloned as a bacterial artificial chromosome (BAC). <i>Veterinary Research</i> , 2011, 42, 3.	3.0	19
88	Investigations into the presence of nidoviruses in pythons. <i>Virology Journal</i> , 2020, 17, 6.	3.4	19
89	Experimental Transmission Studies of SARS-CoV-2 in Fruit Bats, Ferrets, Pigs and Chickens. <i>SSRN Electronic Journal</i> , 0, , .	0.4	19
90	Differential 2-D protein gel electrophoresis analysis of <i>Legionella pneumophila</i> wild type and Tat secretion mutants. <i>International Journal of Medical Microbiology</i> , 2008, 298, 449-461.	3.6	18

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91	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
92	Defining objective clusters for rabies virus sequences using affinity propagation clustering. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006182.	3.0	18
93	The Recently Discovered Bokeloh Bat Lyssavirus: Insights Into Its Genetic Heterogeneity and Spatial Distribution in Europe and the Population Genetics of Its Primary Host. <i>Advances in Virus Research</i> , 2017, 99, 199-232.	2.1	17
94	Experimental screening studies on rabies virus transmission and oral rabies vaccination of the Greater Kudu ( <i>Tragelaphus strepsiceros</i> ). <i>Scientific Reports</i> , 2018, 8, 16599.	3.3	17
95	Full-genome sequencing of German rabbit haemorrhagic disease virus uncovers recombination between RHDV (GI.2) and EBHSV (GII.1). <i>Virus Evolution</i> , 2020, 6, veaa080.	4.9	17
96	Lagos bat virus transmission in an Eidolon helvum bat colony, Ghana. <i>Virus Research</i> , 2015, 210, 42-45.	2.2	16
97	A CRISPR/Cas9 Generated Bovine CD46-knockout Cell Line" A Tool to Elucidate the Adaptability of Bovine Viral Diarrhea Viruses (BVDV). <i>Viruses</i> , 2020, 12, 859.	3.3	15
98	A novel alphaherpesvirus associated with fatal diseases in banded Penguins. <i>Journal of General Virology</i> , 2017, 98, 89-95.	2.9	15
99	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
100	Loeffler 4.0: Diagnostic Metagenomics. <i>Advances in Virus Research</i> , 2017, 99, 17-37.	2.1	14
101	In-depth genome analyses of viruses from vaccine-derived rabies cases and corresponding live-attenuated oral rabies vaccines. <i>Vaccine</i> , 2019, 37, 4758-4765.	3.8	14
102	Untargeted metagenomics shows a reliable performance for synchronous detection of parasites. <i>Parasitology Research</i> , 2020, 119, 2623-2629.	1.6	14
103	Pigeon paramyxovirus type 1 variants with polybasic F protein cleavage site but strikingly different pathogenicity. <i>Virus Genes</i> , 2014, 49, 502-506.	1.6	13
104	Proteogenomics Uncovers Critical Elements of Host Response in Bovine Soft Palate Epithelial Cells Following In Vitro Infection with Foot-And-Mouth Disease Virus. <i>Viruses</i> , 2019, 11, 53.	3.3	13
105	Emerging infectious bronchitis virus (IBV) in Egypt: Evidence for an evolutionary advantage of a new S1 variant with a unique gene 3ab constellation. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104433.	2.3	13
106	Generation of a potential koi herpesvirus live vaccine by simultaneous deletion of the viral thymidine kinase and dUTPase genes. <i>Journal of General Virology</i> , 2019, 100, 642-655.	2.9	13
107	Screening red foxes ( <i>Vulpes vulpes</i> ) for possible viral causes of encephalitis. <i>Virology Journal</i> , 2016, 13, 151.	3.4	12
108	A red squirrel associated adenovirus identified by a combined microarray and deep sequencing approach. <i>Archives of Virology</i> , 2017, 162, 3167-3172.	2.1	12

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109	Comparative analysis of European bat lyssavirus 1 pathogenicity in the mouse model. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005668.	3.0	12
110	Novel Picornavirus in Lambs with Severe Encephalomyelitis. <i>Emerging Infectious Diseases</i> , 2019, 25, 963-967.	4.3	12
111	Isolation and characterization of new Puumala orthohantavirus strains from Germany. <i>Virus Genes</i> , 2020, 56, 448-460.	1.6	12
112	No hints at glyphosate-induced ruminal dysbiosis in cows. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 30.	6.4	12
113	A Novel Squirrel Respirovirus with Putative Zoonotic Potential. <i>Viruses</i> , 2018, 10, 373.	3.3	11
114	Re-emergence of porcine epidemic diarrhea virus in a piglet-producing farm in northwestern Germany in 2019. <i>BMC Veterinary Research</i> , 2020, 16, 329.	1.9	11
115	Comparison of genomic and antigenic properties of Newcastle Disease virus genotypes II, XXI and VII from Egypt do not point to antigenic drift as selection marker. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 849-863.	3.0	11
116	Truncation and Sequence Shuffling of Segment 6 Generate Replication-Competent Neuraminidase-Negative Influenza H5N1 Viruses. <i>Journal of Virology</i> , 2013, 87, 13556-13568.	3.4	10
117	Evaluation of a commercial exogenous internal process control for diagnostic RNA virus metagenomics from different animal clinical samples. <i>Journal of Virological Methods</i> , 2020, 283, 113916.	2.1	10
118	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
119	Classical swine fever virus marker vaccine strain CP7_E2alf: genetic stability in vitro and in vivo. <i>Archives of Virology</i> , 2015, 160, 3121-3125.	2.1	9
120	Characterization of gene deletion mutants of Cyprinid herpesvirus 3 (koi herpesvirus) lacking the immunogenic envelope glycoproteins pORF25, pORF65, pORF148 and pORF149. <i>Virus Research</i> , 2019, 261, 21-30.	2.2	9
121	A Genome-Wide CRISPR/Cas9 Screen Reveals the Requirement of Host Sphingomyelin Synthase 1 for Infection with Pseudorabies Virus Mutant gD <sup>Δ</sup> Pass. <i>Viruses</i> , 2021, 13, 1574.	3.3	9
122	Highly efficient library preparation for Ion Torrent sequencing using Y-adapters. <i>BioTechniques</i> , 2019, 67, 229-237.	1.8	8
123	Virus Adaptation and Selection Following Challenge of Animals Vaccinated against Classical Swine Fever Virus. <i>Viruses</i> , 2019, 11, 932.	3.3	8
124	Sequence Analysis of Egyptian Foot-and-Mouth Disease Virus Field and Vaccine Strains: Intertypic Recombination and Evidence for Accidental Release of Virulent Virus. <i>Viruses</i> , 2020, 12, 990.	3.3	8
125	Population- and Variant-Based Genome Analyses of Viruses from Vaccine-Derived Rabies Cases Demonstrate Product Specific Clusters and Unique Patterns. <i>Viruses</i> , 2020, 12, 115.	3.3	8
126	Revisiting Rustrela Virus: New Cases of Encephalitis and a Solution to the Capsid Enigma. <i>Microbiology Spectrum</i> , 2022, 10, e0010322.	3.0	8



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127	Quasispecies composition and diversity do not reveal any predictors for chronic classical swine fever virus infection. <i>Archives of Virology</i> , 2017, 162, 775-786.	2.1	7
128	Presence of two different bovine hepacivirus clusters in Germany. <i>Transboundary and Emerging Diseases</i> , 2018, 65, 1705-1711.	3.0	7
129	Proficiency Testing of Metagenomics-Based Detection of Food-Borne Pathogens Using a Complex Artificial Sequencing Dataset. <i>Frontiers in Microbiology</i> , 2020, 11, 575377.	3.5	7
130	Full-Genome Sequences and Phylogenetic Analysis of Archived Danish European Bat Lyssavirus 1 (EBLV-1) Emphasize a Higher Genetic Resolution and Spatial Segregation for Sublineage 1a. <i>Viruses</i> , 2021, 13, 634.	3.3	6
131	Point Mutations in the Glycoprotein Ectodomain of Field Rabies Viruses Mediate Cell Culture Adaptation through Improved Virus Release in a Host Cell Dependent and Independent Manner. <i>Viruses</i> , 2021, 13, 1989.	3.3	6
132	Widespread occurrence of squirrel adenovirus 1 in red and grey squirrels in Scotland detected by a novel real-time PCR assay. <i>Virus Research</i> , 2018, 257, 113-118.	2.2	5
133	Whole-Genome Sequence of an African Swine Fever Virus Isolate from the Czech Republic. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	5
134	High-Resolution Composition Analysis of an Inactivated Polyvalent Foot-and-Mouth Disease Vaccine. <i>Pathogens</i> , 2020, 9, 63.	2.8	5
135	Whole-genome analysis of SARS-CoV-2 samples indicate no tissue specific genetic adaptation of the virus in COVID-19 patients'™ upper and lower respiratory tract. <i>Diagnostic Microbiology and Infectious Disease</i> , 2021, 101, 115520.	1.8	5
136	Co-circulation of Orthobunyaviruses and Rift Valley Fever Virus in Mauritania, 2015. <i>Frontiers in Microbiology</i> , 2021, 12, 766977.	3.5	5
137	The Bank Vole ( <i>Clethrionomys glareolus</i> )'™ Small Animal Model for Hepacivirus Infection. <i>Viruses</i> , 2021, 13, 2421.	3.3	5
138	Development of a nonhuman primate model for mammalian bornavirus infection. , 2022, 1, .		5
139	Complete Genome Sequence of Border Disease Virus Genotype 3 Strain Gifhorn. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
140	LVQ-KNN: Composition-based DNA/RNA binning of short nucleotide sequences utilizing a prototype-based k-nearest neighbor approach. <i>Virus Research</i> , 2018, 258, 55-63.	2.2	4
141	Neuraminidase-associated plasminogen recruitment enables systemic spread of natural avian Influenza viruses H3N1. <i>PLoS Pathogens</i> , 2021, 17, e1009490.	4.7	4
142	In action'™ an early warning system for the detection of unexpected or novel pathogens. <i>Virus Evolution</i> , 2021, 7, veab085.	4.9	4
143	Extracellular proteins of <i>Staphylococcus aureus</i> and the role of SarA and B. <i>Proteomics</i> , 2001, 1, 480-493.	2.2	4
144	Draft <i>Anaplasma phagocytophilum</i> Genome Sequences from Five Cows, Two Horses, and One Roe Deer Collected in Europe. <i>Genome Announcements</i> , 2016, 4, .	0.8	3

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145	What can we learn about lyssavirus genomes using 454 sequencing?. Berliner Und Munchener Tierarztliche Wochenschrift, 2012, 125, 242-8.	0.7	3
146	Early Transcriptional Changes in the Midgut of Ornithodoros moubata after Feeding and Infection with Borrelia duttonii. Microorganisms, 2022, 10, 525.	3.6	3
147	Host switching pathogens, infectious outbreaks and zoonosis: A Marie Skłodowska-Curie innovative training network (HONOURS). Virus Research, 2018, 257, 120-124.	2.2	2
148	Meta-Ribosomalomics: RNA Sequencing Is an Unbiased Method for Parasite Detection of Different Sample Types. Frontiers in Microbiology, 2021, 12, 614553.	3.5	2
149	A novel enterovirus in lambs with poliomyelitis and brain stem encephalitis. Transboundary and Emerging Diseases, 2022, 69, 227-234.	3.0	2
150	Rabies in kudu: Revisited. Advances in Virus Research, 2022, , 115-173.	2.1	2