

Andreas Nitsche

List of Publications by Year in descending order

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Version: 2024-02-01

195
papers

26,652
citations

46984

47
h-index

7340

152
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218
all docs

218
docs citations

218
times ranked

48165
citing authors

#	ARTICLE	IF	CITATIONS
1	Deep Time Course Proteomics of SARS-CoV- and SARS-CoV-2-Infected Human Lung Epithelial Cells (Calu-3) Reveals Strong Induction of Interferon-Stimulated Gene Expression by SARS-CoV-2 in Contrast to SARS-CoV. <i>Journal of Proteome Research</i> , 2022, 21, 459-469.	1.8	16
2	Longitudinal SARS-CoV-2 seroepidemiological investigation among healthcare workers at a tertiary care hospital in Germany. <i>BMC Infectious Diseases</i> , 2022, 22, 80.	1.3	6
3	Lateral flow-based nucleic acid detection of SARS-CoV-2 using enzymatic incorporation of biotin-labeled dUTP for POCT use. <i>Analytical and Bioanalytical Chemistry</i> , 2022, 414, 3177-3186.	1.9	33
4	RNA reference materials with defined viral RNA loads of SARS-CoV-2—A useful tool towards a better PCR assay harmonization. <i>PLoS ONE</i> , 2022, 17, e0262656.	1.1	29
5	Full Genome of batCoV/MinFul/2018/SriLanka, a Novel Alpha-Coronavirus Detected in <i>Miniopterus fuliginosus</i> , Sri Lanka. <i>Viruses</i> , 2022, 14, 337.	1.5	8
6	Evaluation of a commercial ELISA as alternative to plaque reduction neutralization test to detect neutralizing antibodies against SARS-CoV-2. <i>Scientific Reports</i> , 2022, 12, 3549.	1.6	34
7	RespiCoV: Simultaneous identification of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) and 46 respiratory tract viruses and bacteria by amplicon-based Oxford-Nanopore MinION sequencing. <i>PLoS ONE</i> , 2022, 17, e0264855.	1.1	3
8	Paramyxovirus Diversity within One Population of <i>Miniopterus fuliginosus</i> Bats in Sri Lanka. <i>Pathogens</i> , 2022, 11, 434.	1.2	4
9	Genomic Sequencing and Analysis of a Novel Human Cowpox Virus With Mosaic Sequences From North America and Old World Orthopoxvirus. <i>Frontiers in Microbiology</i> , 2022, 13, 868887.	1.5	13
10	First Complete Cytochrome B Sequences and Molecular Taxonomy of Bat Species from Sri Lanka. <i>Animals</i> , 2022, 12, 1674.	1.0	3
11	Olfactory transmucosal SARS-CoV-2 invasion as a port of central nervous system entry in individuals with COVID-19. <i>Nature Neuroscience</i> , 2021, 24, 168-175.	7.1	991
12	Utility of a Sequence-Independent, Single-Primer-Amplification (SISPA) and Nanopore Sequencing Approach for Detection and Characterization of Tick-Borne Viral Pathogens. <i>Viruses</i> , 2021, 13, 203.	1.5	5
13	Morphometry of SARS-CoV and SARS-CoV-2 particles in ultrathin plastic sections of infected Vero cell cultures. <i>Scientific Reports</i> , 2021, 11, 3515.	1.6	107
14	Amantadine Inhibits SARS-CoV-2 In Vitro. <i>Viruses</i> , 2021, 13, 539.	1.5	38
15	Application of spectral library prediction for parallel reaction monitoring of viral peptides. <i>Proteomics</i> , 2021, 21, 2000226.	1.3	3
16	The virome of German bats: comparing virus discovery approaches. <i>Scientific Reports</i> , 2021, 11, 7430.	1.6	21
17	Generalized cowpox virus infection in an immunosuppressed patient. <i>International Journal of Infectious Diseases</i> , 2021, 106, 276-278.	1.5	12
18	Strengthening the United Nations Secretary-General's Mechanism to an alleged use of bioweapons through a quality-assured laboratory response. <i>Nature Communications</i> , 2021, 12, 3078.	5.8	7

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19	Detection of Alpha- and Betacoronaviruses in <i>Miniopterus fuliginosus</i> and <i>Rousettus leschenaultii</i> , two species of Sri Lankan Bats. <i>Vaccines</i> , 2021, 9, 650.	2.1	9
20	Resource-efficient internally controlled in-house real-time PCR detection of SARS-CoV-2. <i>Virology Journal</i> , 2021, 18, 110.	1.4	42
21	First Serological Evidence of Crimean-Congo Hemorrhagic Fever Virus and Rift Valley Fever Virus in Ruminants in Tunisia. <i>Pathogens</i> , 2021, 10, 769.	1.2	14
22	An intra-host SARS-CoV-2 dynamics model to assess testing and quarantine strategies for incoming travelers, contact management, and de-isolation. <i>Patterns</i> , 2021, 2, 100262.	3.1	15
23	Update on Potentially Zoonotic Viruses of European Bats. <i>Vaccines</i> , 2021, 9, 690.	2.1	21
24	AmpliCoV: Rapid Whole-Genome Sequencing Using Multiplex PCR Amplification and Real-Time Oxford Nanopore MinION Sequencing Enables Rapid Variant Identification of SARS-CoV-2. <i>Frontiers in Microbiology</i> , 2021, 12, 651151.	1.5	25
25	Replication of cowpox virus in macrophages is dependent on the host range factor p28/N1R. <i>Virology Journal</i> , 2021, 18, 173.	1.4	4
26	Sensitive on-site detection of SARS-CoV-2 by ID NOW COVID-19. <i>Molecular and Cellular Probes</i> , 2021, 58, 101742.	0.9	7
27	Delayed Antibody and T-Cell Response to BNT162b2 Vaccination in the Elderly, Germany. <i>Emerging Infectious Diseases</i> , 2021, 27, 2174-2178.	2.0	67
28	Inactivation of Coronaviruses during Sample Preparation for Proteomics Experiments. <i>Journal of Proteome Research</i> , 2021, 20, 4598-4602.	1.8	2
29	Self-collected oral, nasal and saliva samples yield sensitivity comparable to professionally collected oro-nasopharyngeal swabs in SARS-CoV-2 diagnosis among symptomatic outpatients. <i>International Journal of Infectious Diseases</i> , 2021, 110, 261-266.	1.5	15
30	Establishment of a specimen panel for the decentralised technical evaluation of the sensitivity of 31 rapid diagnostic tests for SARS-CoV-2 antigen, Germany, September 2020 to April 2021. <i>Eurosurveillance</i> , 2021, 26, .	3.9	14
31	Comparative sensitivity evaluation for 122 CE-marked rapid diagnostic tests for SARS-CoV-2 antigen, Germany, September 2020 to April 2021. <i>Eurosurveillance</i> , 2021, 26, .	3.9	94
32	Comparative Pathogenesis, Genomics and Phylogeography of Mousepox. <i>Viruses</i> , 2021, 13, 1146.	1.5	4
33	Discrimination of SARS-CoV-2 Infections From Other Viral Respiratory Infections by Scent Detection Dogs. <i>Frontiers in Medicine</i> , 2021, 8, 749588.	1.2	17
34	Seroepidemiological study on the spread of SARS-CoV-2 in Germany: Study protocol of the CORONA-MONITORING bundesweit' study (RKI-SOEP study).. , 2021, 6, 2-16.		4
35	Predicting bacterial virulence factors – evaluation of machine learning and negative data strategies. <i>Briefings in Bioinformatics</i> , 2020, 21, 1596-1608.	3.2	14
36	Metagenomics-Based Proficiency Test of Smoked Salmon Spiked with a Mock Community. <i>Microorganisms</i> , 2020, 8, 1861.	1.6	4

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37	Description of <i>Sarcocystis scandentiborneensis</i> sp. nov. from treeshrews (<i>Tupaia minor</i> , <i>T. tana</i>) in northern Borneo with annotations on the utility of COI and 18S rDNA sequences for species delineation. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2020, 12, 220-231.	0.6	8
38	Perspective on Proteomics for Virus Detection in Clinical Samples. <i>Journal of Proteome Research</i> , 2020, 19, 4380-4388.	1.8	30
39	Setting a baseline for global urban virome surveillance in sewage. <i>Scientific Reports</i> , 2020, 10, 13748.	1.6	39
40	Re-assembly of nineteenth-century smallpox vaccine genomes reveals the contemporaneous use of horsepox and horsepox-related viruses in the USA. <i>Genome Biology</i> , 2020, 21, 286.	3.8	13
41	Proficiency Testing of Metagenomics-Based Detection of Food-Borne Pathogens Using a Complex Artificial Sequencing Dataset. <i>Frontiers in Microbiology</i> , 2020, 11, 575377.	1.5	7
42	Stable Isotope-Triggered Offset Fragmentation Allows Massively Multiplexed Target Profiling on Quadrupole-Orbitrap Mass Spectrometers. <i>Journal of Proteome Research</i> , 2020, 19, 2854-2862.	1.8	5
43	TaxIt: An Iterative Computational Pipeline for Untargeted Strain-Level Identification Using MS/MS Spectra from Pathogenic Single-Organism Samples. <i>Journal of Proteome Research</i> , 2020, 19, 2501-2510.	1.8	11
44	Multiple orthonairoviruses including Crimean-Congo hemorrhagic fever virus, Tamdy virus and the novel Meram virus in Anatolia. <i>Ticks and Tick-borne Diseases</i> , 2020, 11, 101448.	1.1	16
45	Early smallpox vaccine manufacturing in the United States: Introduction of the "animal vaccine" in 1870, establishment of "vaccine farms", and the beginnings of the vaccine industry. <i>Vaccine</i> , 2020, 38, 4773-4779.	1.7	16
46	SARS-CoV-2 Cell Entry Depends on ACE2 and TMPRSS2 and Is Blocked by a Clinically Proven Protease Inhibitor. <i>Cell</i> , 2020, 181, 271-280.e8.	13.5	16,161
47	Severe Multiorgan Failure Following Yellow Fever Vaccination. <i>Vaccines</i> , 2020, 8, 249.	2.1	7
48	Travel-associated neurological disease terminated in a postmortem diagnosed atypical HSV-1 encephalitis after high-dose steroid therapy "a case report. <i>BMC Infectious Diseases</i> , 2020, 20, 150.	1.3	3
49	Utility of primary cells to examine NPC1 receptor expression in <i>Mops condylurus</i> , a potential Ebola virus reservoir. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0007952.	1.3	7
50	Zwiesel bat banyangvirus, a potentially zoonotic Huaiyangshan banyangvirus (Formerly known as) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	1.6	24
51	Monkeypox virus emergence in wild chimpanzees reveals distinct clinical outcomes and viral diversity. <i>Nature Microbiology</i> , 2020, 5, 955-965.	5.9	86
52	Infectious KoRV-related retroviruses circulating in Australian bats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9529-9536.	3.3	31
53	First detection of bat-borne Issyk-Kul virus in Europe. <i>Scientific Reports</i> , 2020, 10, 22384.	1.6	13
54	Seroepidemiological study on the spread of SARS-CoV-2 in populations in especially affected areas in Germany - Study protocol of the CORONA-MONITORING lokal study.., 2020, 5, 2-16.		12

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55	Serology- and PCR-based cumulative incidence of SARS-CoV-2 infection in adults in a successfully contained early hotspot (CoMoLo study), Germany, May to June 2020. <i>Eurosurveillance</i> , 2020, 25, .	3.9	65
56	Multi-assay investigation of viral etiology in pediatric central nervous system infections. <i>Journal of Infection in Developing Countries</i> , 2020, 14, 572-579.	0.5	1
57	Probable alterations in fecal bacterial microbiota by somatostatin receptor analogs in acromegaly. <i>Turkish Journal of Biochemistry</i> , 2020, 45, 695-700.	0.3	0
58	Novel Tick Phlebovirus Genotypes Lacking Evidence for Vertebrate Infections in Anatolia and Thrace, Turkey. <i>Viruses</i> , 2019, 11, 703.	1.5	8
59	Feasibility study for the use of self-collected nasal swabs to identify pathogens among participants of a population-based surveillance system for acute respiratory infections (GrippeWeb-Plus) Germany, 2016. <i>Influenza and Other Respiratory Viruses</i> , 2019, 13, 319-330.	1.5	19
60	Effects of Regular Kefir Consumption on Gut Microbiota in Patients with Metabolic Syndrome: A Parallel-Group, Randomized, Controlled Study. <i>Nutrients</i> , 2019, 11, 2089.	1.7	77
61	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, .	1.8	34
62	Purple: A Computational Workflow for Strategic Selection of Peptides for Viral Diagnostics Using MS-Based Targeted Proteomics. <i>Viruses</i> , 2019, 11, 536.	1.5	4
63	Arboviral screening of invasive <i>Aedes</i> species in northeastern Turkey: West Nile virus circulation and detection of insect-only viruses. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007334.	1.3	31
64	Survey and Characterization of Jingmen Tick Virus Variants. <i>Viruses</i> , 2019, 11, 1071.	1.5	38
65	A novel genetic lineage of Tula orthohantavirus in Altai voles (<i>Microtus obscurus</i>) from Turkey. <i>Infection, Genetics and Evolution</i> , 2019, 67, 150-158.	1.0	12
66	A cross-sectional screening by next-generation sequencing reveals <i>Rickettsia</i> , <i>Coxiella</i> , <i>Francisella</i> , <i>Borrelia</i> , <i>Babesia</i> , <i>Theileria</i> and <i>Hemolivia</i> species in ticks from Anatolia. <i>Parasites and Vectors</i> , 2019, 12, 26.	1.0	25
67	PriLive: privacy-preserving real-time filtering for next-generation sequencing. <i>Bioinformatics</i> , 2018, 34, 2376-2383.	1.8	5
68	Global ubiquitination analysis reveals extensive modification and proteasomal degradation of cowpox virus proteins, but preservation of viral cores. <i>Scientific Reports</i> , 2018, 8, 1807.	1.6	21
69	A metagenomic survey identifies Tamdy orthonairovirus as well as divergent phlebo-, rhabdo-, chu- and flavi-like viruses in Anatolia, Turkey. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 1173-1183.	1.1	48
70	<i>DMSO</i> as a mobile phase additive enhances detection of ubiquitination sites by nano-ESI-MS/MS. <i>Journal of Mass Spectrometry</i> , 2018, 53, 183-187.	0.7	4
71	A novel three-dimensional cell culture method enhances antiviral drug screening in primary human cells. <i>Antiviral Research</i> , 2018, 150, 20-29.	1.9	25
72	West Nile virus, <i>Anopheles flavivirus</i> , a novel flavivirus as well as Merida-like rhabdovirus Turkey in field-collected mosquitoes from Thrace and Anatolia. <i>Infection, Genetics and Evolution</i> , 2018, 57, 36-45.	1.0	23

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73	Need for additional capacity and improved capability for molecular detection of yellow fever virus in European Expert Laboratories: External Quality Assessment, March 2018. <i>Eurosurveillance</i> , 2018, 23, .	3.9	6
74	Whole Genome Characterization of Orthopoxvirus (OPV) Abatino, a Zoonotic Virus Representing a Putative Novel Clade of Old World Orthopoxviruses. <i>Viruses</i> , 2018, 10, 546.	1.5	17
75	PAIPline: pathogen identification in metagenomic and clinical next generation sequencing samples. <i>Bioinformatics</i> , 2018, 34, i715-i721.	1.8	27
76	Beyond the myths: Novel findings for old paradigms in the history of the smallpox vaccine. <i>PLoS Pathogens</i> , 2018, 14, e1007082.	2.1	19
77	LiveKrakenâ€“real-time metagenomic classification of illumina data. <i>Bioinformatics</i> , 2018, 34, 3750-3752.	1.8	25
78	HiLive: real-time mapping of illumina reads while sequencing. <i>Bioinformatics</i> , 2017, 33, 917-319.	1.8	18
79	A novel rhabdovirus, related to Merida virus, in field-collected mosquitoes from Anatolia and Thrace. <i>Archives of Virology</i> , 2017, 162, 1903-1911.	0.9	18
80	An Early American Smallpox Vaccine Based on Horsepox. <i>New England Journal of Medicine</i> , 2017, 377, 1491-1492.	13.9	56
81	Equination (inoculation of horsepox): An early alternative to vaccination (inoculation of cowpox) and the potential role of horsepox virus in the origin of the smallpox vaccine. <i>Vaccine</i> , 2017, 35, 7222-7230.	1.7	50
82	Co-circulation of West Nile virus and distinct insect-specific flaviviruses in Turkey. <i>Parasites and Vectors</i> , 2017, 10, 149.	1.0	24
83	Generalised cowpox virus infection. <i>Lancet, The</i> , 2017, 390, 1769.	6.3	11
84	A Cross-Sectional Serosurvey of Anti-Orthopoxvirus Antibodies in Central and Western Africa. <i>Viruses</i> , 2017, 9, 278.	1.5	20
85	A Next-Generation Sequencing Approach Uncovers Viral Transcripts Incorporated in Poxvirus Virions. <i>Viruses</i> , 2017, 9, 296.	1.5	10
86	Combined Proteomics/Genomics Approach Reveals Proteomic Changes of Mature Virions as a Novel Poxvirus Adaptation Mechanism. <i>Viruses</i> , 2017, 9, 337.	1.5	6
87	Use of RNALaterÂ® Preservation for Virome Sequencing in Outbreak Settings. <i>Frontiers in Microbiology</i> , 2017, 8, 1888.	1.5	9
88	Seasonal recurrence of cowpox virus outbreaks in captive cheetahs (<i>Acinonyx jubatus</i>). <i>PLoS ONE</i> , 2017, 12, e0187089.	1.1	15
89	Development and preliminary evaluation of a multiplexed amplification and next generation sequencing method for viral hemorrhagic fever diagnostics. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0006075.	1.3	29
90	Generic amplification and next generation sequencing reveal Crimean-Congo hemorrhagic fever virus AP92-like strain and distinct tick phleboviruses in Anatolia, Turkey. <i>Parasites and Vectors</i> , 2017, 10, 335.	1.0	37

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91	Berlin Squirrelpox Virus, a New Poxvirus in Red Squirrels, Berlin, Germany. <i>Emerging Infectious Diseases</i> , 2017, 23, 1726-1729.	2.0	9
92	Comparing Viral Metagenomic Extraction Methods. <i>Current Issues in Molecular Biology</i> , 2017, 24, 59-70.	1.0	25
93	Viral Metagenomics on Blood-Feeding Arthropods as a Tool for Human Disease Surveillance. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1743.	1.8	46
94	Rapid and sensitive point-of-care detection of Orthopoxviruses by ABICAP immunofiltration. <i>Virology Journal</i> , 2016, 13, 207.	1.4	25
95	Infection of human airway epithelial cells by different subtypes of Dobrava-Belgrade virus reveals gene expression patterns corresponding to their virulence potential. <i>Virology</i> , 2016, 493, 189-201.	1.1	11
96	In vivo evidence for ribavirin-induced mutagenesis of the hepatitis E virus genome. <i>Gut</i> , 2016, 65, 1733-1743.	6.1	145
97	Highly Efficient Multivalent 2D Nanosystems for Inhibition of Orthopoxvirus Particles. <i>Advanced Healthcare Materials</i> , 2016, 5, 2922-2930.	3.9	57
98	Analysis of Diagnostic Findings From the European Mobile Laboratory in Guã©ckÃ©dou, Guinea, March 2014 Through March 2015. <i>Journal of Infectious Diseases</i> , 2016, 214, S250-S257.	1.9	32
99	Isolation and genomic characterization of <i>Culex theileri</i> flaviviruses in field-collected mosquitoes from Turkey. <i>Infection, Genetics and Evolution</i> , 2016, 46, 138-147.	1.0	13
100	Pitfalls in PCR troubleshooting: Expect the unexpected?. <i>Biomolecular Detection and Quantification</i> , 2016, 6, 1-3.	7.0	5
101	Rapid characterisation of <i>Klebsiella oxytoca</i> isolates from contaminated liquid hand soap using mass spectrometry, FTIR and Raman spectroscopy. <i>Faraday Discussions</i> , 2016, 187, 353-375.	1.6	29
102	Development of a Genus-Specific Antigen Capture ELISA for Orthopoxviruses â€” Target Selection and Optimized Screening. <i>PLoS ONE</i> , 2016, 11, e0150110.	1.1	21
103	Isolation and Functional Characterization of the Novel <i>Clostridium botulinum</i> Neurotoxin A8 Subtype. <i>PLoS ONE</i> , 2015, 10, e0116381.	1.1	59
104	Comparative Genomic Analysis of Two Novel Sporadic Shiga Toxin-Producing <i>Escherichia coli</i> O104:H4 Strains Isolated 2011 in Germany. <i>PLoS ONE</i> , 2015, 10, e0122074.	1.1	14
105	Comparison of 454 Ultra-Deep Sequencing and Allele-Specific Real-Time PCR with Regard to the Detection of Emerging Drug-Resistant Minor HIV-1 Variants after Antiretroviral Prophylaxis for Vertical Transmission. <i>PLoS ONE</i> , 2015, 10, e0140809.	1.1	5
106	Comparison of the Cowpox Virus and Vaccinia Virus Mature Virion Proteome: Analysis of the Species- and Strain-Specific Proteome. <i>PLoS ONE</i> , 2015, 10, e0141527.	1.1	26
107	SuRankCo: supervised ranking of contigs in de novo assemblies. <i>BMC Bioinformatics</i> , 2015, 16, 240.	1.2	13
108	Investigating the zoonotic origin of the West African Ebola epidemic. <i>EMBO Molecular Medicine</i> , 2015, 7, 17-23.	3.3	347

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109	Evaluation of Virus Inactivation by Formaldehyde to Enhance Biosafety of Diagnostic Electron Microscopy. <i>Viruses</i> , 2015, 7, 666-679.	1.5	51
110	Temporal and spatial analysis of the 2014–2015 Ebola virus outbreak in West Africa. <i>Nature</i> , 2015, 524, 97-101.	13.7	272
111	Comprehensive molecular, genomic and phenotypic analysis of a major clone of <i>Enterococcus faecalis</i> MLST ST40. <i>BMC Genomics</i> , 2015, 16, 175.	1.2	33
112	Hantavirus-induced pathogenesis in mice with a humanized immune system. <i>Journal of General Virology</i> , 2015, 96, 1258-1263.	1.3	20
113	What caused the outbreak of ESBL-producing <i>Klebsiella pneumoniae</i> in a neonatal intensive care unit, Germany 2009 to 2012? Reconstructing transmission with epidemiological analysis and whole-genome sequencing. <i>BMJ Open</i> , 2015, 5, e007397-e007397.	0.8	62
114	Genomic Analysis, Phenotype, and Virulence of the Historical Brazilian Smallpox Vaccine Strain IOC: Implications for the Origins and Evolutionary Relationships of Vaccinia Virus. <i>Journal of Virology</i> , 2015, 89, 11909-11925.	1.5	32
115	Rat cytomegalovirus (RCMV) English isolate and a newly identified Berlin isolate share similarities with but are separate as an anciently diverged clade from Mouse CMV and the Maastricht isolate of RCMV. <i>Journal of General Virology</i> , 2015, 96, 1873-1882.	1.3	15
116	RAMBO-K: Rapid and Sensitive Removal of Background Sequences from Next Generation Sequencing Data. <i>PLoS ONE</i> , 2015, 10, e0137896.	1.1	18
117	Tracing the Spread of <i>Clostridium difficile</i> Ribotype 027 in Germany Based on Bacterial Genome Sequences. <i>PLoS ONE</i> , 2015, 10, e0139811.	1.1	40
118	Protocol for Metagenomic Virus Detection in Clinical Specimens ¹ . <i>Emerging Infectious Diseases</i> , 2015, 21, 48-57.	2.0	90
119	Cowpox after a cat scratch – case report from Poland. <i>Annals of Agricultural and Environmental Medicine</i> , 2015, 22, 456-458.	0.5	18
120	Multiplex Pyrosequencing [®] : Simultaneous Genotyping Based on SNPs from Distant Genomic Regions. <i>Methods in Molecular Biology</i> , 2015, 1315, 337-347.	0.4	0
121	Human Metapneumovirus: Insights from a Ten-Year Molecular and Epidemiological Analysis in Germany. <i>PLoS ONE</i> , 2014, 9, e88342.	1.1	52
122	Fatal Monkeypox in Wild-Living Sooty Mangabey, Côte d'Ivoire, 2012. <i>Emerging Infectious Diseases</i> , 2014, 20, 1009-1011.	2.0	100
123	Identification and characterization of a phage display-derived peptide for orthopoxvirus detection. <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 7611-7621.	1.9	11
124	Pipasic: similarity and expression correction for strain-level identification and quantification in metaproteomics. <i>Bioinformatics</i> , 2014, 30, i149-i156.	1.8	32
125	Comparison of host cell gene expression in cowpox, monkeypox or vaccinia virus-infected cells reveals virus-specific regulation of immune response genes. <i>Virology Journal</i> , 2013, 10, 61.	1.4	43
126	Cowpox virus but not Vaccinia virus induces secretion of CXCL1, IL-8 and IL-6 and chemotaxis of monocytes in vitro. <i>Virus Research</i> , 2013, 171, 161-167.	1.1	10

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127	Novel <i>Mycobacterium tuberculosis</i> Complex Isolate from a Wild Chimpanzee. <i>Emerging Infectious Diseases</i> , 2013, 19, 969-976.	2.0	100
128	Clinicopathological Findings in Persistent Corneal Cowpox Infection. <i>JAMA Ophthalmology</i> , 2013, 131, 1089.	1.4	22
129	MultiPSQ: A Software Solution for the Analysis of Diagnostic n-Plexed Pyrosequencing Reactions. <i>PLoS ONE</i> , 2013, 8, e60055.	1.1	4
130	Genome-Wide Comparison of Cowpox Viruses Reveals a New Clade Related to Variola Virus. <i>PLoS ONE</i> , 2013, 8, e79953.	1.1	55
131	Complete Genome Sequence of the English Isolate of Rat Cytomegalovirus (<i>Murid Herpesvirus 8</i>) Tj ETQq1 1.0.784314.rgBT / Ov	1.5	22
132	Complete Genome Sequence of the Porcine Isolate <i>Enterococcus faecalis</i> D32. <i>Journal of Bacteriology</i> , 2012, 194, 5490-5491.	1.0	16
133	Genome Analysis of Bat Adenovirus 2: Indications of Interspecies Transmission. <i>Journal of Virology</i> , 2012, 86, 1888-1892.	1.5	74
134	Inactivation Effect of Standard and Fractionated Electron Beam Irradiation on Enveloped and Non-Enveloped Viruses in a Tendon Transplant Model. <i>Transfusion Medicine and Hemotherapy</i> , 2012, 39, 29-35.	0.7	17
135	Generation and characterization of a Cowpox virus mutant lacking host range factor CP77. <i>Virus Research</i> , 2012, 168, 23-32.	1.1	2
136	Direct Optical Detection of Viral Nucleoprotein Binding to an Anti-Influenza Aptamer. <i>Analytical Chemistry</i> , 2012, 84, 5501-5508.	3.2	61
137	Cowpox in Zoo Animals. , 2012, , 32-37.		2
138	Comparison of real-time PCR and MassTag PCR for the multiplex detection of highly pathogenic agents. <i>Molecular and Cellular Probes</i> , 2012, 26, 177-181.	0.9	6
139	Single-Nucleotide Polymorphism Genotyping Identifies a Locally Endemic Clone of Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2012, 7, e32698.	1.1	12
140	mPSQed: A Software for the Design of Multiplex Pyrosequencing Assays. <i>PLoS ONE</i> , 2012, 7, e38140.	1.1	6
141	Isolation and Characterization of Three Mammalian Orthoreoviruses from European Bats. <i>PLoS ONE</i> , 2012, 7, e43106.	1.1	72
142	Comparison of Shedding Characteristics of Seasonal Influenza Virus (Sub)Types and Influenza A(H1N1)pdm09; Germany, 2007-2011. <i>PLoS ONE</i> , 2012, 7, e51653.	1.1	98
143	Features of All LNA-Duplexes Showing a New Type of Nucleic Acid Geometry. <i>Journal of Nucleic Acids</i> , 2012, 2012, 1-8.	0.8	3
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