

Lies Laenen

List of Publications by Year in descending order

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Version: 2024-02-01

126
papers

7,685
citations

76294

40
h-index

64755

79
g-index

137
all docs

137
docs citations

137
times ranked

11658
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Considerable escape of SARS-CoV-2 Omicron to antibody neutralization. <i>Nature</i> , 2022, 602, 671-675. | 13.7 | 1,202 |
| 2 | RotaC: A web-based tool for the complete genome classification of group A rotaviruses. <i>BMC Microbiology</i> , 2009, 9, 238. | 1.3 | 365 |
| 3 | Remdesivir, Molnupiravir and Nirmatrelvir remain active against SARS-CoV-2 Omicron and other variants of concern. <i>Antiviral Research</i> , 2022, 198, 105252. | 1.9 | 302 |
| 4 | The Papillomavirus Episteme: a major update to the papillomavirus sequence database. <i>Nucleic Acids Research</i> , 2017, 45, D499-D506. | 6.5 | 298 |
| 5 | Taxonomy of the order Bunyvirales: update 2019. <i>Archives of Virology</i> , 2019, 164, 1949-1965. | 0.9 | 285 |
| 6 | Modular approach to customise sample preparation procedures for viral metagenomics: a reproducible protocol for virome analysis. <i>Scientific Reports</i> , 2015, 5, 16532. | 1.6 | 277 |
| 7 | Temporal and spatial analysis of the 2014–2015 Ebola virus outbreak in West Africa. <i>Nature</i> , 2015, 524, 97-101. | 13.7 | 272 |
| 8 | Serum neutralization of SARS-CoV-2 Omicron sublineages BA.1 and BA.2 in patients receiving monoclonal antibodies. <i>Nature Medicine</i> , 2022, 28, 1297-1302. | 15.2 | 235 |
| 9 | Taxonomy of the order Mononegavirales: update 2019. <i>Archives of Virology</i> , 2019, 164, 1967-1980. | 0.9 | 224 |
| 10 | Symptomatic Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Reinfection by a Phylogenetically Distinct Strain. <i>Clinical Infectious Diseases</i> , 2021, 73, 354-356. | 2.9 | 218 |
| 11 | 2020 taxonomic update for phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyvirales and Mononegavirales. <i>Archives of Virology</i> , 2020, 165, 3023-3072. | 0.9 | 184 |
| 12 | A Recurrent Mutation at Position 26340 of SARS-CoV-2 Is Associated with Failure of the E Gene Quantitative Reverse Transcription-PCR Utilized in a Commercial Dual-Target Diagnostic Assay. <i>Journal of Clinical Microbiology</i> , 2020, 58, . | 1.8 | 160 |
| 13 | Taxonomy of the family Arenaviridae and the order Bunyvirales: update 2018. <i>Archives of Virology</i> , 2018, 163, 2295-2310. | 0.9 | 157 |
| 14 | Taxonomy of the order Mononegavirales: update 2018. <i>Archives of Virology</i> , 2018, 163, 2283-2294. | 0.9 | 153 |
| 15 | Hantaviruses: Immunology, Treatment, and Prevention. <i>Viral Immunology</i> , 2004, 17, 481-497. | 0.6 | 148 |
| 16 | High-Throughput Analysis of Human Cytomegalovirus Genome Diversity Highlights the Widespread Occurrence of Gene-Disrupting Mutations and Pervasive Recombination. <i>Journal of Virology</i> , 2015, 89, 7673-7695. | 1.5 | 148 |
| 17 | Taxonomy of the order Bunyvirales: second update 2018. <i>Archives of Virology</i> , 2019, 164, 927-941. | 0.9 | 115 |
| 18 | Classify viruses – the gain is worth the pain. <i>Nature</i> , 2019, 566, 318-320. | 13.7 | 104 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | The omicron (B.1.1.529) SARS-CoV-2 variant of concern does not readily infect Syrian hamsters. <i>Antiviral Research</i> , 2022, 198, 105253. | 1.9 | 104 |
| 20 | Track Omicron™s spread with molecular data. <i>Science</i> , 2021, 374, 1454-1455. | 6.0 | 103 |
| 21 | Comparing infectivity and virulence of emerging SARS-CoV-2 variants in Syrian hamsters. <i>EBioMedicine</i> , 2021, 68, 103403. | 2.7 | 102 |
| 22 | Molnupiravir Inhibits Replication of the Emerging SARS-CoV-2 Variants of Concern in a Hamster Infection Model. <i>Journal of Infectious Diseases</i> , 2021, 224, 749-753. | 1.9 | 95 |
| 23 | Hantaviridae: Current Classification and Future Perspectives. <i>Viruses</i> , 2019, 11, 788. | 1.5 | 94 |
| 24 | The SARS-CoV-2 and other human coronavirus spike proteins are fine-tuned towards temperature and proteases of the human airways. <i>PLoS Pathogens</i> , 2021, 17, e1009500. | 2.1 | 91 |
| 25 | Cameroonian fruit bats harbor divergent viruses, including rotavirus H, bastroviruses, and picobirnaviruses using an alternative genetic code. <i>Virus Evolution</i> , 2018, 4, vey008. | 2.2 | 90 |
| 26 | Considerable escape of SARS-CoV-2 Omicron to antibody neutralization. <i>Nature</i> , 0, , . | 13.7 | 88 |
| 27 | A Phylodynamic Workflow to Rapidly Gain Insights into the Dispersal History and Dynamics of SARS-CoV-2 Lineages. <i>Molecular Biology and Evolution</i> , 2021, 38, 1608-1613. | 3.5 | 79 |
| 28 | A proposal for new criteria for the classification of hantaviruses, based on S and M segment protein sequences. <i>Infection, Genetics and Evolution</i> , 2009, 9, 813-820. | 1.0 | 71 |
| 29 | Taxonomy of the order Mononegavirales: second update 2018. <i>Archives of Virology</i> , 2019, 164, 1233-1244. | 0.9 | 70 |
| 30 | 2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2021, 166, 3513-3566. | 0.9 | 62 |
| 31 | Recent approaches in hantavirus vaccine development. <i>Expert Review of Vaccines</i> , 2009, 8, 67-76. | 2.0 | 59 |
| 32 | Nanopore sequencing as a revolutionary diagnostic tool for porcine viral enteric disease complexes identifies porcine kobuvirus as an important enteric virus. <i>Scientific Reports</i> , 2018, 8, 9830. | 1.6 | 59 |
| 33 | Gut Virome Analysis of Cameroonians Reveals High Diversity of Enteric Viruses, Including Potential Interspecies Transmitted Viruses. <i>MSphere</i> , 2019, 4, . | 1.3 | 57 |
| 34 | Genomic and Functional Characteristics of Human Cytomegalovirus Revealed by Next-Generation Sequencing. <i>Viruses</i> , 2014, 6, 1049-1072. | 1.5 | 53 |
| 35 | Convalescent plasma treatment of persistent severe acute respiratory syndrome coronavirusâ€2 (SARSâ€CoVâ€2) infection in patients with lymphoma with impaired humoral immunity and lack of neutralising antibodies. <i>British Journal of Haematology</i> , 2021, 192, 1100-1105. | 1.2 | 51 |
| 36 | Organ-specific genome diversity of replication-competent SARS-CoV-2. <i>Nature Communications</i> , 2021, 12, 6612. | 5.8 | 49 |

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|----|---|-----|-----------|
| 37 | Beechnuts and outbreaks of nephropathia epidemica (NE): of mast, mice and men. <i>Nephrology Dialysis Transplantation</i> , 2010, 25, 1740-1746. | 0.4 | 47 |
| 38 | Low eukaryotic viral richness is associated with faecal microbiota transplantation success in patients with UC. <i>Gut</i> , 2018, 67, 1558-1559. | 6.1 | 46 |
| 39 | Case Report: Convalescent Plasma, a Targeted Therapy for Patients with COVID and Severe COVID-19. <i>Frontiers in Immunology</i> , 2020, 11, 596761. | 2.2 | 45 |
| 40 | Another case of “European hantavirus pulmonary syndrome” with severe lung, prior to kidney, involvement, and diagnosed by viral inclusions in lung macrophages. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2013, 32, 1341-1345. | 1.3 | 44 |
| 41 | Novel highly divergent reassortant bat rotaviruses in Cameroon, without evidence of zoonosis. <i>Scientific Reports</i> , 2016, 6, 34209. | 1.6 | 44 |
| 42 | Novel highly divergent sapoviruses detected by metagenomics analysis in straw-colored fruit bats in Cameroon. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-7. | 3.0 | 44 |
| 43 | Highly diverse population of Picornaviridae and other members of the Picornavirales, in Cameroonian fruit bats. <i>BMC Genomics</i> , 2017, 18, 249. | 1.2 | 42 |
| 44 | Successful double-lung transplantation from a donor previously infected with SARS-CoV-2. <i>Lancet Respiratory Medicine</i> , 2021, 9, 315-318. | 5.2 | 41 |
| 45 | An affinity-enhanced, broadly neutralizing heavy chain “only antibody protects against SARS-CoV-2 infection in animal models. <i>Science Translational Medicine</i> , 2021, 13, eabi7826. | 5.8 | 41 |
| 46 | Human cytomegalovirus genomics and transcriptomics through the lens of next-generation sequencing: revision and future challenges. <i>Virus Genes</i> , 2019, 55, 138-164. | 0.7 | 39 |
| 47 | Early high antibody titre convalescent plasma for hospitalised COVID-19 patients: DAWn-plasma. <i>European Respiratory Journal</i> , 2022, 59, 2101724. | 3.1 | 38 |
| 48 | Honey-bee “associated prokaryotic viral communities reveal wide viral diversity and a profound metabolic coding potential. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10511-10519. | 3.3 | 36 |
| 49 | Discovery and genome characterization of three new Jeilongviruses, a lineage of paramyxoviruses characterized by their unique membrane proteins. <i>BMC Genomics</i> , 2018, 19, 617. | 1.2 | 35 |
| 50 | Dynamic changes in paediatric invasive pneumococcal disease after sequential switches of conjugate vaccine in Belgium: a national retrospective observational study. <i>Lancet Infectious Diseases</i> , 2021, 21, 127-136. | 4.6 | 34 |
| 51 | Tumor Necrosis Factor- α Genetic Predisposing Factors Can Influence Clinical Severity in Nephropathia Epidemica. <i>Viral Immunology</i> , 2006, 19, 558-564. | 0.6 | 33 |
| 52 | 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 |
| 53 | SARS-CoV-2 neutralising antibody testing in Europe: towards harmonisation of neutralising antibody titres for better use of convalescent plasma and comparability of trial data. <i>Eurosurveillance</i> , 2021, 26, . | 3.9 | 31 |
| 54 | The virota and its transkingdom interactions in the healthy infant gut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2114619119. | 3.3 | 30 |

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|----|---|-----|-----------|
| 55 | Spatio-temporal analysis of Nova virus, a divergent hantavirus circulating in the European mole in Belgium. <i>Molecular Ecology</i> , 2016, 25, 5994-6008. | 2.0 | 28 |
| 56 | Viral gut metagenomics of sympatric wild and domestic canids, and monitoring of viruses: Insights from an endangered wolf population. <i>Ecology and Evolution</i> , 2017, 7, 4135-4146. | 0.8 | 28 |
| 57 | Longitudinal antibody and T cell responses in Ebola virus disease survivors and contacts: an observational cohort study. <i>Lancet Infectious Diseases</i> , The, 2021, 21, 507-516. | 4.6 | 26 |
| 58 | Genomic Diversity of Hepatitis B Virus Infection Associated With Fulminant Hepatitis B Development. <i>Hepatitis Monthly</i> , 2015, 15, e29477. | 0.1 | 26 |
| 59 | A Novel Hantavirus of the European Mole, Bruges Virus, Is Involved in Frequent Nova Virus Coinfections. <i>Genome Biology and Evolution</i> , 2018, 10, 45-55. | 1.1 | 23 |
| 60 | A Method Enabling High-Throughput Sequencing of Human Cytomegalovirus Complete Genomes from Clinical Isolates. <i>PLoS ONE</i> , 2014, 9, e95501. | 1.1 | 23 |
| 61 | Laboratory information system requirements to manage the COVID-19 pandemic: A report from the Belgian national reference testing center. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2020, 27, 1293-1299. | 2.2 | 22 |
| 62 | Glycoprotein-Specific Antibodies Produced by DNA Vaccination Protect Guinea Pigs from Lethal Argentine and Venezuelan Hemorrhagic Fever. <i>Journal of Virology</i> , 2016, 90, 3515-3529. | 1.5 | 21 |
| 63 | Truncated Recombinant Dobrava Hantavirus Nucleocapsid Proteins Induce Strong, Long-Lasting Immune Responses in Mice. <i>Intervirology</i> , 2006, 49, 253-260. | 1.2 | 20 |
| 64 | Antibiotic Resistance Plasmids Cointegrated into a Megaplasmid Harboring the <i>bla</i> _{OXA-427} Carbapenemase Gene. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, . | 1.4 | 20 |
| 65 | Grotenhout Virus, a Novel Nairovirus Found in <i>Ixodes ricinus</i> in Belgium. <i>Genome Announcements</i> , 2017, 5, . | 0.8 | 19 |
| 66 | Truncated Recombinant Puumala Virus Nucleocapsid Proteins Protect Mice Against Challenge in Vivo. <i>Viral Immunology</i> , 2008, 21, 49-60. | 0.6 | 18 |
| 67 | Satellite Derived Forest Phenology and Its Relation with Nephropathia Epidemica in Belgium. <i>International Journal of Environmental Research and Public Health</i> , 2010, 7, 2486-2500. | 1.2 | 18 |
| 68 | Fast detection of SARS-CoV-2 variants including Omicron using one-step RT-PCR and Sanger sequencing. <i>Journal of Virological Methods</i> , 2022, 304, 114512. | 1.0 | 18 |
| 69 | Common occurrence of Belerina virus, a novel paramyxovirus found in Belgian hedgehogs. <i>Scientific Reports</i> , 2020, 10, 19341. | 1.6 | 17 |
| 70 | Identifying the patterns and drivers of Puumala hantavirus enzootic dynamics using reservoir sampling. <i>Virus Evolution</i> , 2019, 5, vez009. | 2.2 | 16 |
| 71 | Novel Filoviruses, Hantavirus, and Rhabdovirus in Freshwater Fish, Switzerland, 2017. <i>Emerging Infectious Diseases</i> , 2021, 27, 3082-3091. | 2.0 | 16 |
| 72 | Hepatitis C Virus NS5B Sequence-Based Genotyping Analysis of Patients From the Sharkia Governorate, Egypt. <i>Hepatitis Monthly</i> , 2013, 13, e12706. | 0.1 | 15 |

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|----|--|-----|-----------|
| 73 | In-depth analysis of pneumococcal serotypes in Belgian children (2015–2018): Diversity, invasive disease potential, and antimicrobial susceptibility in carriage and disease. <i>Vaccine</i> , 2021, 39, 372-379. | 1.7 | 14 |
| 74 | Ecological Niche Modelling of Bank Voles in Western Europe. <i>International Journal of Environmental Research and Public Health</i> , 2013, 10, 499-514. | 1.2 | 13 |
| 75 | Identification of a novel species of papillomavirus in giraffe lesions using nanopore sequencing. <i>Veterinary Microbiology</i> , 2017, 201, 26-31. | 0.8 | 13 |
| 76 | A lethal disease model for New World hantaviruses using immunosuppressed Syrian hamsters. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0006042. | 1.3 | 13 |
| 77 | Nationwide Harmonization Effort for Semi-Quantitative Reporting of SARS-CoV-2 PCR Test Results in Belgium. <i>Viruses</i> , 2022, 14, 1294. | 1.5 | 13 |
| 78 | Complete Genome Sequence of Equid Herpesvirus 3. <i>Genome Announcements</i> , 2014, 2, . | 0.8 | 12 |
| 79 | Identification of the First SARS-CoV-2 Lineage B.1.1.529 Virus Detected in Europe. <i>Microbiology Resource Announcements</i> , 2022, 11, e0116121. | 0.3 | 12 |
| 80 | Phylogenetic analysis of Puumala virus strains from Central Europe highlights the need for a full-genome perspective on hantavirus evolution. <i>Virus Genes</i> , 2017, 53, 913-917. | 0.7 | 11 |
| 81 | Complete Genome Sequence of a New Ebola Virus Strain Isolated during the 2017 Likati Outbreak in the Democratic Republic of the Congo. <i>Microbiology Resource Announcements</i> , 2019, 8, . | 0.3 | 11 |
| 82 | Strengthening the Interaction of the Virology Community with the International Committee on Taxonomy of Viruses (ICTV) by Linking Virus Names and Their Abbreviations to Virus Species. <i>Systematic Biology</i> , 2019, 68, 828-839. | 2.7 | 11 |
| 83 | SARS-CoV-2 Detection for Diagnosis Purposes in the Setting of a Molecular Biology Research Lab. <i>Methods and Protocols</i> , 2020, 3, 59. | 0.9 | 11 |
| 84 | Novel hepatitis B virus subgenotype A8 and quasi-subgenotype D12 in African–Belgian chronic carriers. <i>International Journal of Infectious Diseases</i> , 2020, 93, 98-101. | 1.5 | 11 |
| 85 | Genome Sequence of Ruloma Virus, a Novel Paramyxovirus Clustering Basally to Members of the Genus <i>Jeilongvirus</i> . <i>Microbiology Resource Announcements</i> , 2021, 10, . | 0.3 | 11 |
| 86 | Detection of Puumala Hantavirus Antibody with ELISA Using a Recombinant Truncated Nucleocapsid Protein Expressed in <i>Escherichia coli</i> . <i>Viral Immunology</i> , 2004, 17, 315-321. | 0.6 | 10 |
| 87 | Exploiting genomic surveillance to map the spatio-temporal dispersal of SARS-CoV-2 spike mutations in Belgium across 2020. <i>Scientific Reports</i> , 2021, 11, 18580. | 1.6 | 10 |
| 88 | BKTyper: Free Online Tool for Polyoma BK Virus VP1 and NCCR Typing. <i>Viruses</i> , 2020, 12, 837. | 1.5 | 9 |
| 89 | Convalescent plasma donors show enhanced cross-reactive neutralizing antibody response to antigenic variants of SARS-CoV-2 following immunization. <i>Transfusion</i> , 2022, 62, 1347-1354. | 0.8 | 9 |
| 90 | Modelling seasonal and multi-annual variation in bank vole populations and nephropathia epidemica. <i>Biosystems Engineering</i> , 2014, 121, 25-37. | 1.9 | 8 |

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|-----|---|-----|-----------|
| 91 | A single bat species in Cameroon harbors multiple highly divergent papillomaviruses in stool identified by metagenomics analysis. <i>Virology Reports</i> , 2016, 6, 74-80. | 0.4 | 8 |
| 92 | Accounting for population structure reveals ambiguity in the Zaire Ebolavirus reservoir dynamics. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008117. | 1.3 | 8 |
| 93 | Meeting report: Eleventh International Conference on Hantaviruses. <i>Antiviral Research</i> , 2020, 176, 104733. | 1.9 | 8 |
| 94 | Exploration of the <i>Ixodes ricinus</i> virosphere unveils an extensive virus diversity including novel coltiviruses and other reoviruses. <i>Virus Evolution</i> , 2021, 7, veab066. | 2.2 | 8 |
| 95 | NetoVIR: a reproducible protocol for virome analysis. <i>Protocol Exchange</i> , 0, , . | 0.3 | 8 |
| 96 | Intracellular flow cytometry complements RT-qPCR detection of circulating SARS-CoV-2 variants of concern. <i>BioTechniques</i> , 2022, 72, 245-254. | 0.8 | 8 |
| 97 | Epidemiological history and genomic characterization of non-D1 HBV strains identified in Iran. <i>Journal of Clinical Virology</i> , 2015, 63, 38-41. | 1.6 | 7 |
| 98 | A decade of norovirus genetic diversity in Belgium. <i>Infection, Genetics and Evolution</i> , 2015, 30, 37-44. | 1.0 | 7 |
| 99 | First genomic characterization of a Belgian Enterovirus C104 using sequence-independent Nanopore sequencing. <i>Infection, Genetics and Evolution</i> , 2020, 81, 104267. | 1.0 | 7 |
| 100 | The role of airborne transmission in a large single source outbreak of SARS-CoV-2 in a Belgian nursing home in 2020. <i>Epidemics</i> , 2022, 40, 100589. | 1.5 | 7 |
| 101 | Expanding the Arterivirus Host Spectrum: Olivier's Shrew Virus 1, A Novel Arterivirus Discovered in African Giant Shrews. <i>Scientific Reports</i> , 2018, 8, 11171. | 1.6 | 6 |
| 102 | Advancing Marburg virus antiviral screening: Optimization of a novel T7 polymerase-independent minigenome system. <i>Antiviral Research</i> , 2021, 185, 104977. | 1.9 | 6 |
| 103 | Variant Analysis of SARS-CoV-2 Genomes from Belgian Military Personnel Engaged in Overseas Missions and Operations. <i>Viruses</i> , 2021, 13, 1359. | 1.5 | 6 |
| 104 | A rare case of HBV genotype fluctuation (shifting and reversion) after liver transplantation. <i>Journal of Clinical Virology</i> , 2015, 71, 93-97. | 1.6 | 5 |
| 105 | Acute hantavirus infection presenting as haemolytic-uraemic syndrome (HUS): the importance of early clinical diagnosis. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2018, 37, 135-140. | 1.3 | 5 |
| 106 | Chloroquine, an Anti-Malaria Drug as Effective Prevention for Hantavirus Infections. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 580532. | 1.8 | 5 |
| 107 | Genomic characterization of <i>Erethizon dorsatum</i> papillomavirus 2, a new papillomavirus species marked by its exceptional genome size. <i>Journal of General Virology</i> , 2018, 99, 1699-1704. | 1.3 | 5 |
| 108 | Identification of novel Ebola virus inhibitors using biologically contained virus. <i>Antiviral Research</i> , 2022, 200, 105294. | 1.9 | 5 |

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|-----|--|-----|-----------|
| 109 | Phylogenomic Characterization of Lopma Virus and Praja Virus, Two Novel Rodent-Borne Arteriviruses. <i>Viruses</i> , 2021, 13, 1842. | 1.5 | 4 |
| 110 | New approach for genomic characterisation of equine sarcoid-derived BPV-1/-2 using nanopore-based sequencing. <i>Virology Journal</i> , 2022, 19, 8. | 1.4 | 4 |
| 111 | Two Separate Clusters of SARS-CoV-2 Delta Variant Infections in a Group of 41 Students Travelling from India: An Illustration of the Need for Rigorous Testing and Quarantine. <i>Viruses</i> , 2022, 14, 1198. | 1.5 | 4 |
| 112 | Complete Genome Sequence of Nova Virus, a Hantavirus Circulating in the European Mole in Belgium. <i>Genome Announcements</i> , 2015, 3, . | 0.8 | 3 |
| 113 | Comment on "A Cluster of Three Cases of Hantavirus Pulmonary Syndrome among Canadian Military Personnel": <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2016, 2016, 1-3. | 0.7 | 3 |
| 114 | Virus Hunting: Discovery of New Episomal Circular Viruses by Rolling Circle Techniques. <i>Current Protocols in Microbiology</i> , 2017, 44, 1E.12.1-1E.12.18. | 6.5 | 3 |
| 115 | Poliovirus sampling by using sodium dodecyl sulfate/EDTA-pretreated chromatography paper strips. <i>Biochemical and Biophysical Research Communications</i> , 2004, 325, 711-715. | 1.0 | 2 |
| 116 | Host switching pathogens, infectious outbreaks and zoonosis: A Marie Skłodowska-Curie innovative training network (HONOURs). <i>Virus Research</i> , 2018, 257, 120-124. | 1.1 | 2 |
| 117 | 128 days of SARS-CoV-2 viral shedding in a haemodialysis patient. <i>CKJ: Clinical Kidney Journal</i> , 2021, 14, 1284-1286. | 1.4 | 2 |
| 118 | Symptomatic severe acute respiratory syndrome coronavirus-2 reinfection in a lupus patient treated with hydroxychloroquine: a case report. <i>Journal of Medical Case Reports</i> , 2021, 15, 572. | 0.4 | 2 |
| 119 | Reliable and Scalable SARS-CoV-2 qPCR Testing at a High Sample Throughput: Lessons Learned from the Belgian Initiative. <i>Life</i> , 2022, 12, 159. | 1.1 | 2 |
| 120 | Multidrug-resistant tuberculosis control in Rwanda overcomes a successful clone that causes most disease over a quarter century. <i>Journal of Clinical Tuberculosis and Other Mycobacterial Diseases</i> , 2022, 27, 100299. | 0.6 | 2 |
| 121 | Antiviral treatment with fluoxetine for rituximab-associated chronic echovirus 13 meningoencephalitis and myofasciitis. <i>European Journal of Neurology</i> , 0, , . | 1.7 | 2 |
| 122 | Complete Genome Sequence of a Papillomavirus Isolated from the European Mole. <i>Genome Announcements</i> , 2013, 1, . | 0.8 | 1 |
| 123 | Common Occurrence of Belerina Virus, a Novel Paramyxovirus Found in Belgian Hedgehogs. <i>Proceedings (mdpi)</i> , 2020, 50, 40. | 0.2 | 1 |
| 124 | Detection of Known and Novel Viral Pathogens in Belgian Ixodes ricinus Ticks. <i>Proceedings (mdpi)</i> , 2020, 50, . | 0.2 | 0 |
| 125 | A confirmed case of COVID-19 reinfection with a genetically distinct strain: a case report from Belgium. <i>Acta Clinica Belgica</i> , 2021, , 1-2. | 0.5 | 0 |
| 126 | Commentary: Development of a Comparative European Orthohantavirus Microneutralization Assay With Multi-Species Validation and Evaluation in a Human Diagnostic Cohort. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 702709. | 1.8 | 0 |