Lies Laenen

List of Publications by Year in descending order

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Version: 2024-02-01

76196 64668 7,685 126 40 79 citations h-index g-index papers 137 137 137 11658 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	Early high antibody titre convalescent plasma for hospitalised COVID-19 patients: DAWn-plasma. European Respiratory Journal, 2022, 59, 2101724.	3.1	38
2	Considerable escape of SARS-CoV-2 Omicron to antibody neutralization. Nature, 2022, 602, 671-675.	13.7	1,202
3	Reliable and Scalable SARS-CoV-2 qPCR Testing at a High Sample Throughput: Lessons Learned from the Belgian Initiative. Life, 2022, 12, 159.	1.1	2
4	New approach for genomic characterisation of equine sarcoid-derived BPV-1/-2 using nanopore-based sequencing. Virology Journal, 2022, 19, 8.	1.4	4
5	The omicron (B.1.1.529) SARS-CoV-2 variant of concern does not readily infect Syrian hamsters. Antiviral Research, 2022, 198, 105253.	1.9	104
6	Remdesivir, Molnupiravir and Nirmatrelvir remain active against SARS-CoV-2 Omicron and other variants of concern. Antiviral Research, 2022, 198, 105252.	1.9	302
7	Multidrug-resistant tuberculosis control in Rwanda overcomes a successful clone that causes most disease over a quarter century. Journal of Clinical Tuberculosis and Other Mycobacterial Diseases, 2022, 27, 100299.	0.6	2
8	Identification of the First SARS-CoV-2 Lineage B.1.1.529 Virus Detected in Europe. Microbiology Resource Announcements, 2022, 11, e0116121.	0.3	12
9	The virota and its transkingdom interactions in the healthy infant gut. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2114619119.	3.3	30
10	Serum neutralization of SARS-CoV-2 Omicron sublineages BA.1 and BA.2 in patients receiving monoclonal antibodies. Nature Medicine, 2022, 28, 1297-1302.	15.2	235
11	Identification of novel Ebola virus inhibitors using biologically contained virus. Antiviral Research, 2022, 200, 105294.	1.9	5
12	Fast detection of SARS-CoV-2 variants including Omicron using one-step RT-PCR and Sanger sequencing. Journal of Virological Methods, 2022, 304, 114512.	1.0	18
13	Intracellular flow cytometry complements RT-qPCR detection of circulating SARS-CoV-2 variants of concern. BioTechniques, 2022, 72, 245-254.	0.8	8
14	Convalescent plasma donors show enhanced crossâ€reactive neutralizing antibody response to antigenic variants of SARS oVâ€2 following immunization. Transfusion, 2022, 62, 1347-1354.	0.8	9
15	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. Viruses, 2022, 14, 1198.	1.5	4
16	The role of airborne transmission in a large single source outbreak of SARS-CoV-2 in a Belgian nursing home in 2020. Epidemics, 2022, 40, 100589.	1.5	7
17	Nationwide Harmonization Effort for Semi-Quantitative Reporting of SARS-CoV-2 PCR Test Results in Belgium. Viruses, 2022, 14, 1294.	1.5	13
18	Symptomatic Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Reinfection by a Phylogenetically Distinct Strain. Clinical Infectious Diseases, 2021, 73, 354-356.	2.9	218

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19	Dynamic changes in paediatric invasive pneumococcal disease after sequential switches of conjugate vaccine in Belgium: a national retrospective observational study. Lancet Infectious Diseases, The, 2021, 21, 127-136.	4.6	34
20	Longitudinal antibody and T cell responses in Ebola virus disease survivors and contacts: an observational cohort study. Lancet Infectious Diseases, The, 2021, 21, 507-516.	4.6	26
21	Successful double-lung transplantation from a donor previously infected with SARS-CoV-2. Lancet Respiratory Medicine, the, 2021, 9, 315-318.	5.2	41
22	In-depth analysis of pneumococcal serotypes in Belgian children (2015–2018): Diversity, invasive disease potential, and antimicrobial susceptibility in carriage and disease. Vaccine, 2021, 39, 372-379.	1.7	14
23	A Phylodynamic Workflow to Rapidly Gain Insights into the Dispersal History and Dynamics of SARS-CoV-2 Lineages. Molecular Biology and Evolution, 2021, 38, 1608-1613.	3.5	79
24	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. British Journal of Haematology, 2021, 192, 1100-1105.	1.2	51
25	Advancing Marburg virus antiviral screening: Optimization of a novel T7 polymerase-independent minigenome system. Antiviral Research, 2021, 185, 104977.	1.9	6
26	128 days of SARS-CoV-2 viral shedding in a haemodialysis patient. CKJ: Clinical Kidney Journal, 2021, 14, 1284-1286.	1.4	2
27	Chloroquine, an Anti-Malaria Drug as Effective Prevention for Hantavirus Infections. Frontiers in Cellular and Infection Microbiology, 2021, 11, 580532.	1.8	5
28	The SARS-CoV-2 and other human coronavirus spike proteins are fine-tuned towards temperature and proteases of the human airways. PLoS Pathogens, 2021, 17, e1009500.	2.1	91
29	Genome Sequence of Ruloma Virus, a Novel Paramyxovirus Clustering Basally to Members of the Genus <i>Jeilongvirus</i> . Microbiology Resource Announcements, 2021, 10, .	0.3	11
30	A confirmed case of COVID-19 reinfection with a genetically distinct strain: a case report from Belgium. Acta Clinica Belgica, 2021, , 1-2.	0.5	0
31	Comparing infectivity and virulence of emerging SARS-CoV-2 variants in Syrian hamsters. EBioMedicine, 2021, 68, 103403.	2.7	102
32	Variant Analysis of SARS-CoV-2 Genomes from Belgian Military Personnel Engaged in Overseas Missions and Operations. Viruses, 2021, 13, 1359.	1.5	6
33	Exploration of the <i>lxodes ricinus</i> virosphere unveils an extensive virus diversity including novel coltiviruses and other reoviruses. Virus Evolution, 2021, 7, veab066.	2.2	8
34	Molnupiravir Inhibits Replication of the Emerging SARS-CoV-2 Variants of Concern in a Hamster Infection Model. Journal of Infectious Diseases, 2021, 224, 749-753.	1.9	95
35	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. Eurosurveillance, 2021, 26, .	3.9	31
36	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. Archives of Virology, 2021, 166, 3513-3566.	0.9	62

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37	Commentary: Development of a Comparative European Orthohantavirus Microneutralization Assay With Multi-Species Validation and Evaluation in a Human Diagnostic Cohort. Frontiers in Cellular and Infection Microbiology, 2021, 11, 702709.	1.8	O
38	Phylogenomic Characterization of Lopma Virus and Praja Virus, Two Novel Rodent-Borne Arteriviruses. Viruses, 2021, 13, 1842.	1.5	4
39	Exploiting genomic surveillance to map the spatio-temporal dispersal of SARS-CoV-2 spike mutations in Belgium across 2020. Scientific Reports, 2021, 11, 18580.	1.6	10
40	An affinity-enhanced, broadly neutralizing heavy chain–only antibody protects against SARS-CoV-2 infection in animal models. Science Translational Medicine, 2021, 13, eabi7826.	5.8	41
41	Symptomatic severe acute respiratory syndrome coronavirusÂ2 reinfection in a lupus patient treated with hydroxychloroquine: a case report. Journal of Medical Case Reports, 2021, 15, 572.	0.4	2
42	Organ-specific genome diversity of replication-competent SARS-CoV-2. Nature Communications, 2021, 12, 6612.	5.8	49
43	Novel Filoviruses, Hantavirus, and Rhabdovirus in Freshwater Fish, Switzerland, 2017. Emerging Infectious Diseases, 2021, 27, 3082-3091.	2.0	16
44	Track Omicron's spread with molecular data. Science, 2021, 374, 1454-1455.	6.0	103
45	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. Journal of Clinical Microbiology, 2020, 58, .	1.8	160
46	Case Report: Convalescent Plasma, a Targeted Therapy for Patients with CVID and Severe COVID-19. Frontiers in Immunology, 2020, 11, 596761.	2.2	45
47	SARS-CoV-2 Detection for Diagnosis Purposes in the Setting of a Molecular Biology Research Lab. Methods and Protocols, 2020, 3, 59.	0.9	11
48	BKTyper: Free Online Tool for Polyoma BK Virus VP1 and NCCR Typing. Viruses, 2020, 12, 837.	1.5	9
49	2020 taxonomic update for phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. Archives of Virology, 2020, 165, 3023-3072.	0.9	184
50	Common occurrence of Belerina virus, a novel paramyxovirus found in Belgian hedgehogs. Scientific Reports, 2020, 10, 19341.	1.6	17
51	Accounting for population structure reveals ambiguity in the Zaire Ebolavirus reservoir dynamics. PLoS Neglected Tropical Diseases, 2020, 14, e0008117.	1.3	8
52	Common Occurrence of Belerina Virus, a Novel Paramyxovirus Found in Belgian Hedgehogs. Proceedings (mdpi), 2020, 50, 40.	0.2	1
53	Detection of Known and Novel Viral Pathogens in Belgian Ixodes ricinus Ticks. Proceedings (mdpi), 2020, 50, .	0.2	0
54	Novel hepatitis B virus subgenotype A8 and quasi-subgenotype D12 in African–Belgian chronic carriers. International Journal of Infectious Diseases, 2020, 93, 98-101.	1.5	11

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55	Meeting report: Eleventh International Conference on Hantaviruses. Antiviral Research, 2020, 176, 104733.	1.9	8
56	First genomic characterization of a Belgian Enterovirus C104 using sequence-independent Nanopore sequencing. Infection, Genetics and Evolution, 2020, 81, 104267.	1.0	7
57	Honey-bee–associated prokaryotic viral communities reveal wide viral diversity and a profound metabolic coding potential. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10511-10519.	3.3	36
58	Laboratory information system requirements to manage the COVID-19 pandemic: A report from the Belgian national reference testing center. Journal of the American Medical Informatics Association: JAMIA, 2020, 27, 1293-1299.	2.2	22
59	Identifying the patterns and drivers of Puumala hantavirus enzootic dynamics using reservoir sampling. Virus Evolution, 2019, 5, vez009.	2.2	16
60	Hantaviridae: Current Classification and Future Perspectives. Viruses, 2019, 11, 788.	1.5	94
61	Classify viruses — the gain is worth the pain. Nature, 2019, 566, 318-320.	13.7	104
62	Taxonomy of the order Mononegavirales: second update 2018. Archives of Virology, 2019, 164, 1233-1244.	0.9	70
63	Taxonomy of the order Bunyavirales: second update 2018. Archives of Virology, 2019, 164, 927-941.	0.9	115
64	Gut Virome Analysis of Cameroonians Reveals High Diversity of Enteric Viruses, Including Potential Interspecies Transmitted Viruses. MSphere, 2019, 4, .	1.3	57
65	Complete Genome Sequence of a New Ebola Virus Strain Isolated during the 2017 Likati Outbreak in the Democratic Republic of the Congo. Microbiology Resource Announcements, 2019, 8, .	0.3	11
66	Taxonomy of the order Bunyavirales: update 2019. Archives of Virology, 2019, 164, 1949-1965.	0.9	285
67	Taxonomy of the order Mononegavirales: update 2019. Archives of Virology, 2019, 164, 1967-1980.	0.9	224
68	Human cytomegalovirus genomics and transcriptomics through the lens of next-generation sequencing: revision and future challenges. Virus Genes, 2019, 55, 138-164.	0.7	39
69	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. Systematic Biology, 2019, 68, 828-839.	2.7	11
70	Taxonomy of the family Arenaviridae and the order Bunyavirales: update 2018. Archives of Virology, 2018, 163, 2295-2310.	0.9	157
71	Taxonomy of the order Mononegavirales: update 2018. Archives of Virology, 2018, 163, 2283-2294.	0.9	153
72	Antibiotic Resistance Plasmids Cointegrated into a Megaplasmid Harboring the <i>bla</i> _{OXA-427} Carbapenemase Gene. Antimicrobial Agents and Chemotherapy, 2018, 62, .	1.4	20

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73	A Novel Hantavirus of the European Mole, Bruges Virus, Is Involved in Frequent Nova Virus Coinfections. Genome Biology and Evolution, 2018, 10, 45-55.	1.1	23
74	Low eukaryotic viral richness is associated with faecal microbiota transplantation success in patients with UC. Gut, 2018, 67, 1558-1559.	6.1	46
75	Acute hantavirus infection presenting as haemolytic-uraemic syndrome (HUS): the importance of early clinical diagnosis. European Journal of Clinical Microbiology and Infectious Diseases, 2018, 37, 135-140.	1.3	5
76	Host switching pathogens, infectious outbreaks and zoonosis: A Marie SkÅ,odowska-Curie innovative training network (HONOURs). Virus Research, 2018, 257, 120-124.	1.1	2
77	Discovery and genome characterization of three new Jeilongviruses, a lineage of paramyxoviruses characterized by their unique membrane proteins. BMC Genomics, 2018, 19, 617.	1.2	35
78	Nanopore sequencing as a revolutionary diagnostic tool for porcine viral enteric disease complexes identifies porcine kobuvirus as an important enteric virus. Scientific Reports, 2018, 8, 9830.	1.6	59
79	Expanding the Arterivirus Host Spectrum: Olivier's Shrew Virus 1, A Novel Arterivirus Discovered in African Giant Shrews. Scientific Reports, 2018, 8, 11171.	1.6	6
80	Cameroonian fruit bats harbor divergent viruses, including rotavirus H, bastroviruses, and picobirnaviruses using an alternative genetic code. Virus Evolution, 2018, 4, vey008.	2.2	90
81	Genomic characterization of Erethizon dorsatum papillomavirus 2, a new papillomavirus species marked by its exceptional genome size. Journal of General Virology, 2018, 99, 1699-1704.	1.3	5
82	Virus Hunting: Discovery of New Episomal Circular Viruses by Rolling Circle Techniques. Current Protocols in Microbiology, 2017, 44, 1E.12.1-1E.12.18.	6.5	3
83	Viral gut metagenomics of sympatric wild and domestic canids, and monitoring of viruses: Insights from an endangered wolf population. Ecology and Evolution, 2017, 7, 4135-4146.	0.8	28
84	Novel highly divergent sapoviruses detected by metagenomics analysis in straw-colored fruit bats in Cameroon. Emerging Microbes and Infections, 2017, 6, 1-7.	3.0	44
85	Highly diverse population of Picornaviridae and other members of the Picornavirales, in Cameroonian fruit bats. BMC Genomics, 2017, 18, 249.	1.2	42
86	Identification of a novel species of papillomavirus in giraffe lesions using nanopore sequencing. Veterinary Microbiology, 2017, 201, 26-31.	0.8	13
87	The Papillomavirus Episteme: a major update to the papillomavirus sequence database. Nucleic Acids Research, 2017, 45, D499-D506.	6.5	298
88	Grotenhout Virus, a Novel Nairovirus Found in Ixodes ricinus in Belgium. Genome Announcements, 2017, 5, .	0.8	19
89	Phylogenetic analysis of Puumala virus strains from Central Europe highlights the need for a full-genome perspective on hantavirus evolution. Virus Genes, 2017, 53, 913-917.	0.7	11
90	A lethal disease model for New World hantaviruses using immunosuppressed Syrian hamsters. PLoS Neglected Tropical Diseases, 2017, 11, e0006042.	1.3	13

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91	Comment on "A Cluster of Three Cases of <i> Hantavirus</i> Pulmonary Syndrome among Canadian Military Personnel― Canadian Journal of Infectious Diseases and Medical Microbiology, 2016, 2016, 1-3.	0.7	3
92	A single bat species in Cameroon harbors multiple highly divergent papillomaviruses in stool identified by metagenomics analysis. Virology Reports, 2016, 6, 74-80.	0.4	8
93	Analysis of Diagnostic Findings From the European Mobile Laboratory in Guéckédou, Guinea, March 2014 Through March 2015. Journal of Infectious Diseases, 2016, 214, S250-S257.	1.9	32
94	Spatioâ€ŧemporal analysis of Nova virus, a divergent hantavirus circulating in the European mole in Belgium. Molecular Ecology, 2016, 25, 5994-6008.	2.0	28
95	Novel highly divergent reassortant bat rotaviruses in Cameroon, without evidence of zoonosis. Scientific Reports, 2016, 6, 34209.	1.6	44
96	Glycoprotein-Specific Antibodies Produced by DNA Vaccination Protect Guinea Pigs from Lethal Argentine and Venezuelan Hemorrhagic Fever. Journal of Virology, 2016, 90, 3515-3529.	1.5	21
97	Modular approach to customise sample preparation procedures for viral metagenomics: a reproducible protocol for virome analysis. Scientific Reports, 2015, 5, 16532.	1.6	277
98	Temporal and spatial analysis of the 2014–2015 Ebola virus outbreak in West Africa. Nature, 2015, 524, 97-101.	13.7	272
99	High-Throughput Analysis of Human Cytomegalovirus Genome Diversity Highlights the Widespread Occurrence of Gene-Disrupting Mutations and Pervasive Recombination. Journal of Virology, 2015, 89, 7673-7695.	1.5	148
100	Complete Genome Sequence of Nova Virus, a Hantavirus Circulating in the European Mole in Belgium. Genome Announcements, 2015, 3, .	0.8	3
101	A rare case of HBV genotype fluctuation (shifting and reversion) after liver transplantation. Journal of Clinical Virology, 2015, 71, 93-97.	1.6	5
102	Epidemiological history and genomic characterization of non-D1 HBV strains identified in Iran. Journal of Clinical Virology, 2015, 63, 38-41.	1.6	7
103	A decade of norovirus genetic diversity in Belgium. Infection, Genetics and Evolution, 2015, 30, 37-44.	1.0	7
104	Genomic Diversity of Hepatitis B Virus Infection Associated With Fulminant Hepatitis B Development. Hepatitis Monthly, 2015, 15, e29477.	0.1	26
105	Genomic and Functional Characteristics of Human Cytomegalovirus Revealed by Next-Generation Sequencing. Viruses, 2014, 6, 1049-1072.	1.5	53
106	Complete Genome Sequence of Equid Herpesvirus 3. Genome Announcements, 2014, 2, .	0.8	12
107	Modelling seasonal and multi-annual variation in bank vole populations and nephropathia epidemica. Biosystems Engineering, 2014, 121, 25-37.	1.9	8
108	A Method Enabling High-Throughput Sequencing of Human Cytomegalovirus Complete Genomes from Clinical Isolates. PLoS ONE, 2014, 9, e95501.	1.1	23

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109	Another case of "European hantavirus pulmonary syndrome―with severe lung, prior to kidney, involvement, and diagnosed by viral inclusions in lung macrophages. European Journal of Clinical Microbiology and Infectious Diseases, 2013, 32, 1341-1345.	1.3	44
110	Complete Genome Sequence of a Papillomavirus Isolated from the European Mole. Genome Announcements, 2013, 1, .	0.8	1
111	Hepatitis C Virus NS5B Sequence-Based Genotyping Analysis of Patients From the Sharkia Governorate, Egypt. Hepatitis Monthly, 2013, 13, e12706.	0.1	15
112	Ecological Niche Modelling of Bank Voles in Western Europe. International Journal of Environmental Research and Public Health, 2013, 10, 499-514.	1.2	13
113	Satellite Derived Forest Phenology and Its Relation with Nephropathia Epidemica in Belgium. International Journal of Environmental Research and Public Health, 2010, 7, 2486-2500.	1.2	18
114	Beechnuts and outbreaks of nephropathia epidemica (NE): of mast, mice and men. Nephrology Dialysis Transplantation, 2010, 25, 1740-1746.	0.4	47
115	RotaC: A web-based tool for the complete genome classification of group A rotaviruses. BMC Microbiology, 2009, 9, 238.	1.3	365
116	A proposal for new criteria for the classification of hantaviruses, based on S and M segment protein sequences. Infection, Genetics and Evolution, 2009, 9, 813-820.	1.0	71
117	Recent approaches in hantavirus vaccine development. Expert Review of Vaccines, 2009, 8, 67-76.	2.0	59
118	Truncated Recombinant Puumala Virus Nucleocapsid Proteins Protect Mice Against Challengein Vivo. Viral Immunology, 2008, 21, 49-60.	0.6	18
119	Truncated Recombinant Dobrava Hantavirus Nucleocapsid Proteins Induce Strong, Long-Lasting Immune Responses in Mice. Intervirology, 2006, 49, 253-260.	1.2	20
120	Tumor Necrosis Factor-α Genetic Predisposing Factors Can Influence Clinical Severity in Nephropathia Epidemica. Viral Immunology, 2006, 19, 558-564.	0.6	33
121	Detection of Puumala Hantavirus Antibody with ELISA Using a Recombinant Truncated Nucleocapsid Protein Expressed in Escherichia coli. Viral Immunology, 2004, 17, 315-321.	0.6	10
122	Hantaviruses: Immunology, Treatment, and Prevention. Viral Immunology, 2004, 17, 481-497.	0.6	148
123	Poliovirus sampling by using sodium dodecyl sulfate/EDTA-pretreated chromatography paper strips. Biochemical and Biophysical Research Communications, 2004, 325, 711-715.	1.0	2
124	NetoVIR: a reproducible protocol for virome analysis. Protocol Exchange, 0, , .	0.3	8
125	Considerable escape of SARS-CoV-2 Omicron to antibody neutralization. Nature, 0, , .	13.7	88
126	Antiviral treatment with fluoxetine for rituximabâ€associated chronic echovirus 13 meningoencephalitis and myofasciitis. European Journal of Neurology, 0, , .	1.7	2