

# Jelle Matthijnsens

## List of Publications by Year in descending order

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175  
papers

11,666  
citations

47004

47  
h-index

32838

100  
g-index

190  
all docs

190  
docs citations

190  
times ranked

6652  
citing authors

#	ARTICLE	IF	CITATIONS
1	Uniformity of rotavirus strain nomenclature proposed by the Rotavirus Classification Working Group (RCWG). <i>Archives of Virology</i> , 2011, 156, 1397-1413.	2.1	827
2	Full Genome-Based Classification of Rotaviruses Reveals a Common Origin between Human Wa-Like and Porcine Rotavirus Strains and Human DS-1-Like and Bovine Rotavirus Strains. <i>Journal of Virology</i> , 2008, 82, 3204-3219.	3.4	791
3	Recommendations for the classification of group A rotaviruses using all 11 genomic RNA segments. <i>Archives of Virology</i> , 2008, 153, 1621-1629.	2.1	642
4	Zoonotic aspects of rotaviruses. <i>Veterinary Microbiology</i> , 2010, 140, 246-255.	1.9	479
5	RotaC: A web-based tool for the complete genome classification of group A rotaviruses. <i>BMC Microbiology</i> , 2009, 9, 238.	3.3	365
6	VP6-sequence-based cutoff values as a criterion for rotavirus species demarcation. <i>Archives of Virology</i> , 2012, 157, 1177-1182.	2.1	344
7	Rotavirus disease and vaccination: impact on genotype diversity. <i>Future Microbiology</i> , 2009, 4, 1303-1316.	2.0	280
8	Modular approach to customise sample preparation procedures for viral metagenomics: a reproducible protocol for virome analysis. <i>Scientific Reports</i> , 2015, 5, 16532.	3.3	277
9	Evolutionary History and Global Spread of the Emerging G12 Human Rotaviruses. <i>Journal of Virology</i> , 2007, 81, 2382-2390.	3.4	276
10	Genotype constellation and evolution of group A rotaviruses infecting humans. <i>Current Opinion in Virology</i> , 2012, 2, 426-433.	5.4	255
11	Phylogenetic Analyses of Rotavirus Genotypes G9 and G12 Underscore Their Potential for Swift Global Spread. <i>Molecular Biology and Evolution</i> , 2010, 27, 2431-2436.	8.9	253
12	STAT2 signaling restricts viral dissemination but drives severe pneumonia in SARS-CoV-2 infected hamsters. <i>Nature Communications</i> , 2020, 11, 5838.	12.8	225
13	Full Genomic Analysis of Human Rotavirus Strain B4106 and Lapine Rotavirus Strain 30/96 Provides Evidence for Interspecies Transmission. <i>Journal of Virology</i> , 2006, 80, 3801-3810.	3.4	206
14	Rotavirus incidence and genotype distribution before and after national rotavirus vaccine introduction in Belgium. <i>Vaccine</i> , 2010, 28, 7507-7513.	3.8	206
15	Rotavirus genotypes co-circulating in Europe between 2006 and 2009 as determined by EuroRotaNet, a pan-European collaborative strain surveillance network. <i>Epidemiology and Infection</i> , 2011, 139, 895-909.	2.1	204
16	Are Human P[14] Rotavirus Strains the Result of Interspecies Transmissions from Sheep or Other Ungulates That Belong to the Mammalian Order <i>Artiodactyla</i> ?. <i>Journal of Virology</i> , 2009, 83, 2917-2929.	3.4	202
17	Review of group A rotavirus strains reported in swine and cattle. <i>Veterinary Microbiology</i> , 2013, 165, 190-199.	1.9	195
18	Evolutionary Dynamics of Human Rotaviruses: Balancing Reassortment with Preferred Genome Constellations. <i>PLoS Pathogens</i> , 2009, 5, e1000634.	4.7	178

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19	Prevalence of G2P[4] and G12P[6] Rotavirus, Bangladesh. <i>Emerging Infectious Diseases</i> , 2007, 13, 18-24.	4.3	161
20	Genetic Analyses Reveal Differences in the VP7 and VP4 Antigenic Epitopes between Human Rotaviruses Circulating in Belgium and Rotaviruses in Rotarix and RotaTeq. <i>Journal of Clinical Microbiology</i> , 2012, 50, 966-976.	3.9	160
21	A single-dose live-attenuated YF17D-vectored SARS-CoV-2 vaccine candidate. <i>Nature</i> , 2021, 590, 320-325.	27.8	148
22	Effectiveness of rotavirus vaccination in prevention of hospital admissions for rotavirus gastroenteritis among young children in Belgium: case-control study. <i>BMJ</i> , The, 2012, 345, e4752-e4752.	6.0	124
23	Characterization of a Novel P[25],G11 Human Group A Rotavirus. <i>Journal of Clinical Microbiology</i> , 2005, 43, 3208-3212.	3.9	121
24	Molecular and biological characterization of the 5 human-bovine rotavirus (WC3)-based reassortant strains of the pentavalent rotavirus vaccine, RotaTeq®. <i>Virology</i> , 2010, 403, 111-127.	2.4	114
25	A robust human norovirus replication model in zebrafish larvae. <i>PLoS Pathogens</i> , 2019, 15, e1008009.	4.7	112
26	G8 Rotavirus Strains Isolated in the Democratic Republic of Congo Belong to the DS-1-Like Genogroup. <i>Journal of Clinical Microbiology</i> , 2006, 44, 1801-1809.	3.9	109
27	Stable distinct core eukaryotic viromes in different mosquito species from Guadeloupe, using single mosquito viral metagenomics. <i>Microbiome</i> , 2019, 7, 121.	11.1	109
28	Multiple reassortment and interspecies transmission events contribute to the diversity of feline, canine and feline/canine-like human group A rotavirus strains. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1396-1406.	2.3	105
29	Rapid detection and high occurrence of porcine rotavirus A, B, and C by RT-qPCR in diagnostic samples. <i>Journal of Virological Methods</i> , 2014, 209, 30-34.	2.1	94
30	Cameroonian fruit bats harbor divergent viruses, including rotavirus H, bastroviruses, and picobirnaviruses using an alternative genetic code. <i>Virus Evolution</i> , 2018, 4, vey008.	4.9	90
31	Reassortment of Human Rotavirus Gene Segments into G11 Rotavirus Strains. <i>Emerging Infectious Diseases</i> , 2010, 16, 625-630.	4.3	84
32	Two out of the 11 genes of an unusual human G6P[6] rotavirus isolate are of bovine origin. <i>Journal of General Virology</i> , 2008, 89, 2630-2635.	2.9	81
33	Predominance of rotavirus G9 genotype in children hospitalized for rotavirus gastroenteritis in Belgium during 1999-2003. <i>Journal of Clinical Virology</i> , 2005, 33, 1-6.	3.1	80
34	Detection of substantial porcine group B rotavirus genetic diversity in the United States, resulting in a modified classification proposal for G genotypes. <i>Virology</i> , 2012, 433, 85-96.	2.4	74
35	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.	2.3	71
36	Identification, phylogenetic analysis and classification of porcine group C rotavirus VP7 sequences from the United States and Canada. <i>Virology</i> , 2013, 446, 189-198.	2.4	71

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37	Complete Genome Sequence of a Porcine Epidemic Diarrhea Virus from a Novel Outbreak in Belgium, January 2015. <i>Genome Announcements</i> , 2015, 3, .	0.8	70
38	Reassortment among bovine, porcine and human rotavirus strains results in G8P[7] and G6P[7] strains isolated from cattle in South Korea. <i>Veterinary Microbiology</i> , 2011, 152, 55-66.	1.9	64
39	Whole genome sequencing and phylogenetic analysis of a zoonotic human G8P[14] rotavirus strain. <i>Infection, Genetics and Evolution</i> , 2010, 10, 1140-1144.	2.3	63
40	Characterization of a Novel G3P[3] Rotavirus Isolated from a Lesser Horseshoe Bat: a Distant Relative of Feline/Canine Rotaviruses. <i>Journal of Virology</i> , 2013, 87, 12357-12366.	3.4	63
41	Simian Rotaviruses Possess Divergent Gene Constellations That Originated from Interspecies Transmission and Reassortment. <i>Journal of Virology</i> , 2010, 84, 2013-2026.	3.4	60
42	Zoonotic transmission of reassortant porcine G4P[6] rotaviruses in Hungarian pediatric patients identified sporadically over a 15year period. <i>Infection, Genetics and Evolution</i> , 2013, 19, 71-80.	2.3	60
43	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.	3.3	59
44	Gut Virome Analysis of Cameroonians Reveals High Diversity of Enteric Viruses, Including Potential Interspecies Transmitted Viruses. <i>MSphere</i> , 2019, 4, .	2.9	57
45	Complete molecular genome analyses of equine rotavirus A strains from different continents reveal several novel genotypes and a largely conserved genotype constellation. <i>Journal of General Virology</i> , 2012, 93, 866-875.	2.9	56
46	Group A rotavirus universal mass vaccination: how and to what extent will selective pressure influence prevalence of rotavirus genotypes?. <i>Expert Review of Vaccines</i> , 2012, 11, 1347-1354.	4.4	55
47	Full genome characterization of a porcine-like human G9P[6] rotavirus strain isolated from an infant in Belgium. <i>Infection, Genetics and Evolution</i> , 2012, 12, 1492-1500.	2.3	54
48	Higher proportion of G2P[4] rotaviruses in vaccinated hospitalized cases compared with unvaccinated hospitalized cases, despite high vaccine effectiveness against heterotypic G2P[4] rotaviruses. <i>Clinical Microbiology and Infection</i> , 2014, 20, O702-O710.	6.0	50
49	Widespread Rotavirus H in Commercially Raised Pigs, United States. <i>Emerging Infectious Diseases</i> , 2014, 20, 1203-1206.	4.3	48
50	Successional Stages in Infant Gut Microbiota Maturation. <i>MBio</i> , 2021, 12, e0185721.	4.1	48
51	A feline rotavirus G3P[9] carries traces of multiple reassortment events and resembles rare human G3P[9] rotaviruses. <i>Journal of General Virology</i> , 2011, 92, 1214-1221.	2.9	47
52	What is (not) known about the dynamics of the human gut virome in health and disease. <i>Current Opinion in Virology</i> , 2019, 37, 52-57.	5.4	47
53	Complete Genome Characterization of Recent and Ancient Belgian Pig Group A Rotaviruses and Assessment of Their Evolutionary Relationship with Human Rotaviruses. <i>Journal of Virology</i> , 2015, 89, 1043-1057.	3.4	46
54	Low eukaryotic viral richness is associated with faecal microbiota transplantation success in patients with UC. <i>Gut</i> , 2018, 67, 1558-1559.	12.1	46

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55	Genomic characterization of a novel group A lamb rotavirus isolated in Zaragoza, Spain. <i>Virus Genes</i> , 2008, 37, 250-265.	1.6	45
56	Evolution of DS-1-like human G2P[4] rotaviruses assessed by complete genome analyses. <i>Journal of General Virology</i> , 2014, 95, 91-109.	2.9	44
57	Novel highly divergent reassortant bat rotaviruses in Cameroon, without evidence of zoonosis. <i>Scientific Reports</i> , 2016, 6, 34209.	3.3	44
58	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.	6.5	44
59	Unusual Assortment of Segments in 2 Rare Human Rotavirus Genomes. <i>Emerging Infectious Diseases</i> , 2010, 16, 859-862.	4.3	43
60	Rotavirus Surveillance in Kisangani, the Democratic Republic of the Congo, Reveals a High Number of Unusual Genotypes and Gene Segments of Animal Origin in Non-Vaccinated Symptomatic Children. <i>PLoS ONE</i> , 2014, 9, e100953.	2.5	43
61	Genome-Wide Evolutionary Analyses of G1P[8] Strains Isolated Before and After Rotavirus Vaccine Introduction. <i>Genome Biology and Evolution</i> , 2015, 7, 2473-2483.	2.5	43
62	Genetic heterogeneity in human G6P[14] rotavirus strains detected in Hungary suggests independent zoonotic origin. <i>Journal of Infection</i> , 2009, 59, 213-215.	3.3	42
63	Highly diverse population of Picornaviridae and other members of the Picornavirales, in Cameroonian fruit bats. <i>BMC Genomics</i> , 2017, 18, 249.	2.8	42
64	Stability of the Virome in Lab- and Field-Collected <i>Aedes albopictus</i> Mosquitoes across Different Developmental Stages and Possible Core Viruses in the Publicly Available Virome Data of <i>Aedes</i> Mosquitoes. <i>MSystems</i> , 2020, 5, .	3.8	40
65	Global distribution of group A rotavirus strains in horses: A systematic review. <i>Vaccine</i> , 2013, 31, 5627-5633.	3.8	39
66	Full-length genomic analysis of porcine G9P[23] and G9P[7] rotavirus strains isolated from pigs with diarrhea in South Korea. <i>Infection, Genetics and Evolution</i> , 2012, 12, 1427-1435.	2.3	37
67	Equine G3P[3] rotavirus strain E3198 related to simian RRV and feline/canine-like rotaviruses based on complete genome analyses. <i>Veterinary Microbiology</i> , 2013, 161, 239-246.	1.9	37
68	Phylogenetic analyses of typical bovine rotavirus genotypes G6, G10, P[5] and P[11] circulating in Argentinean beef and dairy herds. <i>Infection, Genetics and Evolution</i> , 2013, 18, 18-30.	2.3	36
69	Did Large-Scale Vaccination Drive Changes in the Circulating Rotavirus Population in Belgium?. <i>Scientific Reports</i> , 2015, 5, 18585.	3.3	36
70	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.	7.1	36
71	Experimental feline enteric coronavirus infection reveals an aberrant infection pattern and shedding of mutants with impaired infectivity in enterocyte cultures. <i>Scientific Reports</i> , 2016, 6, 20022.	3.3	35
72	Typing of human rotaviruses: nucleotide mismatches between the VP7 gene and primer are associated with genotyping failure. <i>Virology Journal</i> , 2005, 2, 24.	3.4	34

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73	Genetic diversity in three bovine-like human G8P[14] and G10P[14] rotaviruses suggests independent interspecies transmission events. <i>Journal of General Virology</i> , 2015, 96, 1161-1168.	2.9	34
74	NetoVIR: Modular Approach to Customize Sample Preparation Procedures for Viral Metagenomics. <i>Methods in Molecular Biology</i> , 2018, 1838, 85-95.	0.9	33
75	Genetic Characterization of the Belgian Nephropathogenic Infectious Bronchitis Virus (NIBV) Reference Strain B1648. <i>Viruses</i> , 2015, 7, 4488-4506.	3.3	32
76	Presence and characterization of pig group A and C rotaviruses in feces of Belgian diarrheic suckling piglets. <i>Virus Research</i> , 2016, 213, 172-183.	2.2	32
77	Sequence and phylogenetic analyses of human rotavirus strains: Comparison of VP7 and VP8 <sup>^</sup> — antigenic epitopes between Tunisian and vaccine strains before national rotavirus vaccine introduction. <i>Infection, Genetics and Evolution</i> , 2013, 18, 132-144.	2.3	31
78	At Least Seven Distinct Rotavirus Genotype Constellations in Bats with Evidence of Reassortment and Zoonotic Transmissions. <i>MBio</i> , 2021, 12, .	4.1	31
79	Discovery and molecular characterization of a group A rotavirus strain detected in an Argentinean vicuña ( <i>Vicugna vicugna</i> ). <i>Veterinary Microbiology</i> , 2013, 161, 247-254.	1.9	30
80	Identification of an enterovirus recombinant with a torovirus-like gene insertion during a diarrhea outbreak in fattening pigs. <i>Virus Evolution</i> , 2017, 3, vex024.	4.9	30
81	Molecular characterization of human group A rotavirus genotypes circulating in Rawalpindi, Islamabad, Pakistan during 2015-2016. <i>PLoS ONE</i> , 2019, 14, e0220387.	2.5	30
82	Comparative analysis of pentavalent rotavirus vaccine strains and G8 rotaviruses identified during vaccine trial in Africa. <i>Scientific Reports</i> , 2015, 5, 14658.	3.3	30
83	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.	7.1	30
84	Human infection with a P[14], G3 lapine rotavirus. <i>Virology</i> , 2004, 325, 11-17.	2.4	29
85	The complete genome sequence of a G3P[10] Chinese bat rotavirus suggests multiple bat rotavirus inter-host species transmission events. <i>Infection, Genetics and Evolution</i> , 2014, 28, 1-4.	2.3	29
86	Fecal virome analysis of three carnivores reveals a novel nodavirus and multiple gemycircularviruses. <i>Virology Journal</i> , 2015, 12, 79.	3.4	29
87	Intestinal and extra-intestinal pathogenicity of a bovine reassortant rotavirus in calves and piglets. <i>Veterinary Microbiology</i> , 2011, 152, 291-303.	1.9	28
88	Epidemiology and phylogenetic analysis of VP7 and VP4 genes of rotaviruses circulating in Rawalpindi, Pakistan during 2010. <i>Infection, Genetics and Evolution</i> , 2013, 14, 161-168.	2.3	28
89	Porcine group a rotaviruses with heterogeneous VP7 and VP4 genotype combinations can be found together with enteric bacteria on Belgian swine farms. <i>Veterinary Microbiology</i> , 2014, 172, 23-34.	1.9	28
90	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.	1.9	28

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91	Group A Rotaviruses in Chinese Bats: Genetic Composition, Serology, and Evidence for Bat-to-Human Transmission and Reassortment. <i>Journal of Virology</i> , 2017, 91, .	3.4	28
92	In-season and out-of-season variation of rotavirus genotype distribution and age of infection across 12 European countries before the introduction of routine vaccination, 2007/08 to 2012/13. <i>Eurosurveillance</i> , 2016, 21, .	7.0	28
93	Molecular characterization of genotype G6 human rotavirus strains detected in Italy from 1986 to 2009. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1449-1455.	2.3	27
94	Rabbit colony infected with a bovine-like G6P[11] rotavirus strain. <i>Veterinary Microbiology</i> , 2013, 166, 154-164.	1.9	27
95	Emerging OP354-Like P[8] Rotaviruses Have Rapidly Dispersed from Asia to Other Continents. <i>Molecular Biology and Evolution</i> , 2015, 32, 2060-2071.	8.9	27
96	Loop model: Mechanism to explain partial gene duplications in segmented dsRNA viruses. <i>Biochemical and Biophysical Research Communications</i> , 2006, 340, 140-144.	2.1	26
97	Prevalence and genomic characterization of G2P[4] group A rotavirus strains during monovalent vaccine introduction in Brazil. <i>Infection, Genetics and Evolution</i> , 2014, 28, 486-494.	2.3	26
98	VP6 genetic diversity, reassortment, intragenic recombination and classification of rotavirus B in American and Japanese pigs. <i>Veterinary Microbiology</i> , 2014, 172, 359-366.	1.9	26
99	Distinct evolutionary origins of G12P[8] and G12P[9] group A rotavirus strains circulating in Brazil. <i>Infection, Genetics and Evolution</i> , 2014, 28, 385-388.	2.3	25
100	Characterization of a genetically heterogeneous porcine rotavirus C, and other viruses present in the fecal virome of a non-diarrheic Belgian piglet. <i>Infection, Genetics and Evolution</i> , 2016, 43, 135-145.	2.3	25
101	Genomic evolution, host-species barrier, reassortment and classification of rotaviruses. <i>Future Virology</i> , 2010, 5, 385-390.	1.8	24
102	Genetic diversity of the VP7, VP4 and VP6 genes of Korean porcine group C rotaviruses. <i>Veterinary Microbiology</i> , 2015, 176, 61-69.	1.9	24
103	Reassortment among picobirnaviruses found in wolves. <i>Archives of Virology</i> , 2016, 161, 2859-2862.	2.1	24
104	Novel genome sequences of cell-fusing agent virus allow comparison of virus phylogeny with the genetic structure of <i>Aedes aegypti</i> populations. <i>Virus Evolution</i> , 2020, 6, veaa018.	4.9	24
105	Chromatography Paper Strip Method for Collection, Transportation, and Storage of Rotavirus RNA in Stool Samples. <i>Journal of Clinical Microbiology</i> , 2004, 42, 1605-1608.	3.9	23
106	Complete genomic analysis of a Bangladeshi G1P[8] rotavirus strain detected in 2003 reveals a close evolutionary relationship with contemporary human Wa-like strains. <i>Infection, Genetics and Evolution</i> , 2010, 10, 746-754.	2.3	23
107	Epidemiology and genetic diversity of human astrovirus infection among hospitalized patients with acute diarrhea in Bangladesh from 2010 to 2012. <i>Journal of Clinical Virology</i> , 2013, 58, 612-618.	3.1	23
108	Complete genetic characterization of human G2P[6] and G3P[6] rotavirus strains. <i>Infection, Genetics and Evolution</i> , 2013, 13, 27-35.	2.3	23



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109	Genetic characterization of a rare bovine-like human VP4 mono-reassortant G6P[8] rotavirus strain detected from an infant in Bangladesh. <i>Infection, Genetics and Evolution</i> , 2013, 19, 120-126.	2.3	23
110	Metagenomics in Virology. , 2021, , 133-140.		23
111	Sustained Decline in Cases of Rotavirus Gastroenteritis Presenting to the Children's Hospital of Philadelphia in the New Rotavirus Vaccine Era. <i>Pediatric Infectious Disease Journal</i> , 2010, 29, 699-702.	2.0	22
112	The first caprine rotavirus detected in Argentina displays genomic features resembling virus strains infecting members of the Bovidae and Camelidae. <i>Veterinary Microbiology</i> , 2014, 171, 189-197.	1.9	22
113	A Previously Undescribed Highly Prevalent Phage Identified in a Danish Enteric Virome Catalog. <i>MSystems</i> , 2021, 6, e0038221.	3.8	22
114	Symptomatic and Subclinical Infection with Rotavirus P[8]G9, Rural Ecuador. <i>Emerging Infectious Diseases</i> , 2007, 13, 574-580.	4.3	21
115	Complete Genome Analysis of a Rabbit Rotavirus Causing Gastroenteritis in a Human Infant. <i>Viruses</i> , 2015, 7, 844-856.	3.3	21
116	Sequence analysis and evolution of group B rotaviruses. <i>Virus Research</i> , 2007, 125, 219-225.	2.2	20
117	Genetic diversity of G9P[8] rotavirus strains circulating in Italy in 2007 and 2010 as determined by whole genome sequencing. <i>Infection, Genetics and Evolution</i> , 2013, 16, 426-432.	2.3	20
118	Molecular detection of bovine Noroviruses in Argentinean dairy calves: Circulation of a tentative new genotype. <i>Infection, Genetics and Evolution</i> , 2016, 40, 144-150.	2.3	20
119	Canine rotavirus C strain detected in Hungary shows marked genotype diversity. <i>Journal of General Virology</i> , 2015, 96, 3059-3071.	2.9	20
120	Feline Origin of Rotavirus Strain, Tunisia, 2008. <i>Emerging Infectious Diseases</i> , 2013, 19, 630-634.	4.3	19
121	Establishment of <i>Culex modestus</i> in Belgium and a Glance into the Virome of Belgian Mosquito Species. <i>MSphere</i> , 2021, 6, .	2.9	19
122	Characterization of human rotaviruses circulating in Iraq in 2008: Atypical G8 and high prevalence of P[6] strains. <i>Infection, Genetics and Evolution</i> , 2013, 16, 212-217.	2.3	18
123	Human P[6] Rotaviruses From Sub-Saharan Africa and Southeast Asia Are Closely Related to Those of Human P[4] and P[8] Rotaviruses Circulating Worldwide. <i>Journal of Infectious Diseases</i> , 2016, 214, 1039-1049.	4.0	18
124	Different virulence of porcine and porcine-like bovine rotavirus strains with genetically nearly identical genomes in piglets and calves. <i>Veterinary Research</i> , 2013, 44, 88.	3.0	17
125	Novel intergenotype human norovirus recombinant GII.16/GII.3 in Bangladesh. <i>Infection, Genetics and Evolution</i> , 2013, 20, 325-329.	2.3	17
126	Cold case: The disappearance of Egypt bee virus, a fourth distinct master strain of deformed wing virus linked to honeybee mortality in 1970s Egypt. <i>Virology Journal</i> , 2022, 19, 12.	3.4	17



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127	Temporal changes of rotavirus strain distribution in a city in the northwest of China, 1996â€“2005. <i>International Journal of Infectious Diseases</i> , 2008, 12, e11-e17.	3.3	16
128	Molecular characterization of the NSP4 gene of human group A rotavirus strains circulating in Tunisia from 2006 to 2008. <i>Infection, Genetics and Evolution</i> , 2012, 12, 997-1004.	2.3	16
129	High incidence of reassortant G9P[4] rotavirus strain in Bangladesh: Fully heterotypic from vaccine strains. <i>Journal of Clinical Virology</i> , 2013, 58, 755-756.	3.1	16
130	Differences in lineage replacement dynamics of G1 and G2 rotavirus strains versus G9 strain over a period of 22 years in Bangladesh. <i>Infection, Genetics and Evolution</i> , 2014, 28, 214-222.	2.3	16
131	Molecular epidemiology of Korean porcine sapeloviruses. <i>Archives of Virology</i> , 2014, 159, 1175-1180.	2.1	16
132	Molecular characterization of equine rotaviruses isolated in Europe in 2013: Implications for vaccination. <i>Veterinary Microbiology</i> , 2015, 176, 179-185.	1.9	16
133	Metagenomic Approach with the NetoVIR Enrichment Protocol Reveals Virus Diversity within Ethiopian Honey Bees ( <i>Apis mellifera simensis</i> ). <i>Viruses</i> , 2020, 12, 1218.	3.3	16
134	Comparative analysis of the Rotarixâ„¢ vaccine strain and G1P[8] rotaviruses detected before and after vaccine introduction in Belgium. <i>PeerJ</i> , 2017, 5, e2733.	2.0	16
135	Complete genomic sequence analyses of the first group A giraffe rotavirus reveals close evolutionary relationship with rotaviruses infecting other members of the Artiodactyla. <i>Veterinary Microbiology</i> , 2014, 170, 151-156.	1.9	14
136	Use of Next-Generation Sequencing for Diagnosis of West Nile Virus Infection in Patient Returning to Belgium from Hungary. <i>Emerging Infectious Diseases</i> , 2018, 24, 2380-2382.	4.3	14
137	Emerging G9 rotavirus strains in the northwest of China. <i>Virus Research</i> , 2008, 137, 157-162.	2.2	13
138	Phylogenetic analysis of G1P[6] group A rotavirus strains detected in Northeast Brazilian children fully vaccinated with Rotarixâ„¢. <i>Infection, Genetics and Evolution</i> , 2013, 19, 395-402.	2.3	13
139	Pathogenicity of porcine G9P[23] and G9P[7] rotaviruses in piglets. <i>Veterinary Microbiology</i> , 2013, 166, 123-137.	1.9	13
140	Comparison of pathogenicities and nucleotide changes between porcine and bovine reassortant rotavirus strains possessing the same genotype constellation in piglets and calves. <i>Veterinary Microbiology</i> , 2014, 172, 51-62.	1.9	13
141	Complete genome analyses of the first porcine rotavirus group H identified from a South African pig does not provide evidence for recent interspecies transmission events. <i>Infection, Genetics and Evolution</i> , 2016, 38, 1-7.	2.3	13
142	Exploration of the virome of the European brown shrimp ( <i>Crangon crangon</i> ). <i>Journal of General Virology</i> , 2020, 101, 651-666.	2.9	13
143	Complete Genome Sequence of Equid Herpesvirus 3. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
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