

Jelle Matthijnsens

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#	Paper	IF	Citations
178	Uniformity of rotavirus strain nomenclature proposed by the Rotavirus Classification Working Group (RCWG). <i>Archives of Virology</i> , 2011 , 156, 1397-413	2.6	699
177	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, 3204-19	6.6	661
176	Recommendations for the classification of group A rotaviruses using all 11 genomic RNA segments. <i>Archives of Virology</i> , 2008 , 153, 1621-9	2.6	523
175	Zoonotic aspects of rotaviruses. <i>Veterinary Microbiology</i> , 2010 , 140, 246-55	3.3	411
174	RotaC: a web-based tool for the complete genome classification of group A rotaviruses. <i>BMC Microbiology</i> , 2009 , 9, 238	4.5	322
173	VP6-sequence-based cutoff values as a criterion for rotavirus species demarcation. <i>Archives of Virology</i> , 2012 , 157, 1177-82	2.6	292
172	Evolutionary history and global spread of the emerging g12 human rotaviruses. <i>Journal of Virology</i> , 2007 , 81, 2382-90	6.6	254
171	Rotavirus disease and vaccination: impact on genotype diversity. <i>Future Microbiology</i> , 2009 , 4, 1303-16	2.9	248
170	Genotype constellation and evolution of group A rotaviruses infecting humans. <i>Current Opinion in Virology</i> , 2012 , 2, 426-33	7.5	218
169	Phylogenetic analyses of rotavirus genotypes G9 and G12 underscore their potential for swift global spread. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2431-6	8.3	207
168	Are human P[14] rotavirus strains the result of interspecies transmissions from sheep or other ungulates that belong to the mammalian order Artiodactyla?. <i>Journal of Virology</i> , 2009 , 83, 2917-29	6.6	185
167	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	4.3	184
166	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, 3801-10	6.6	182
165	Modular approach to customise sample preparation procedures for viral metagenomics: a reproducible protocol for virome analysis. <i>Scientific Reports</i> , 2015 , 5, 16532	4.9	168
164	Rotavirus incidence and genotype distribution before and after national rotavirus vaccine introduction in Belgium. <i>Vaccine</i> , 2010 , 28, 7507-13	4.1	165
163	Evolutionary dynamics of human rotaviruses: balancing reassortment with preferred genome constellations. <i>PLoS Pathogens</i> , 2009 , 5, e1000634	7.6	153
162	Review of group A rotavirus strains reported in swine and cattle. <i>Veterinary Microbiology</i> , 2013 , 165, 190-9	3.3	150

161	Prevalence of G2P[4] and G12P[6] rotavirus, Bangladesh. <i>Emerging Infectious Diseases</i> , 2007 , 13, 18-24	10.2	141
160	STAT2 signaling restricts viral dissemination but drives severe pneumonia in SARS-CoV-2 infected hamsters. <i>Nature Communications</i> , 2020 , 11, 5838	17.4	122
159	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, 966-76	9.7	117
158	Effectiveness of rotavirus vaccination in prevention of hospital admissions for rotavirus gastroenteritis among young children in Belgium: case-control study. <i>BMJ, The</i> , 2012 , 345, e4752	5.9	112
157	Characterization of a novel P[25],G11 human group a rotavirus. <i>Journal of Clinical Microbiology</i> , 2005 , 43, 3208-12	9.7	112
156	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, 111-27	3.6	102
155	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, 1801-9	9.7	101
154	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, 1396-406	4.5	88
153	Reassortment of human rotavirus gene segments into G11 rotavirus strains. <i>Emerging Infectious Diseases</i> , 2010 , 16, 625-30	10.2	80
152	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	4.9	78
151	A single-dose live-attenuated YF17D-vectored SARS-CoV-2 vaccine candidate. <i>Nature</i> , 2021 , 590, 320-325	50.4	74
150	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	14.5	72
149	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, 813-20	4.5	65
148	Whole genome sequencing and phylogenetic analysis of a zoonotic human G8P[14] rotavirus strain. <i>Infection, Genetics and Evolution</i> , 2010 , 10, 1140-4	4.5	62
147	Complete genome sequence of a porcine epidemic diarrhea virus from a novel outbreak in Belgium, January 2015. <i>Genome Announcements</i> , 2015 , 3,		60
146	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	3.6	59
145	Cameroonian fruit bats harbor divergent viruses, including rotavirus H, bastroviruses, and picobirnaviruses using an alternative genetic code. <i>Virus Evolution</i> , 2018 , 4, vey008	3.7	58
144	A robust human norovirus replication model in zebrafish larvae. <i>PLoS Pathogens</i> , 2019 , 15, e1008009	7.6	57

143	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, 30-4	2.6	57
142	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	3.3	54
141	Simian rotaviruses possess divergent gene constellations that originated from interspecies transmission and reassortment. <i>Journal of Virology</i> , 2010 , 84, 2013-26	6.6	54
140	Identification, phylogenetic analysis and classification of porcine group C rotavirus VP7 sequences from the United States and Canada. <i>Virology</i> , 2013 , 446, 189-98	3.6	53
139	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, 1492-500	4.5	51
138	Zoonotic transmission of reassortant porcine G4P[6] rotaviruses in Hungarian pediatric patients identified sporadically over a 15 year period. <i>Infection, Genetics and Evolution</i> , 2013 , 19, 71-80	4.5	50
137	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, 12357-66	6.6	50
136	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, 1347-54	5.2	49
135	Stable distinct core eukaryotic viromes in different mosquito species from Guadeloupe, using single mosquito viral metagenomics. <i>Microbiome</i> , 2019 , 7, 121	16.6	48
134	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	4.9	48
133	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, O702-10	9.5	45
132	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, 10433-37	6.6	39
131	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	4.9	39
130	Unusual assortment of segments in 2 rare human rotavirus genomes. <i>Emerging Infectious Diseases</i> , 2010 , 16, 859-62	10.2	39
129	Genetic heterogeneity in human G6P[14] rotavirus strains detected in Hungary suggests independent zoonotic origin. <i>Journal of Infection</i> , 2009 , 59, 213-5	18.9	39
128	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	4.9	39
127	Genomic characterization of a novel group A lamb rotavirus isolated in Zaragoza, Spain. <i>Virus Genes</i> , 2008 , 37, 250-65	2.3	38
126	Evolution of DS-1-like human G2P[4] rotaviruses assessed by complete genome analyses. <i>Journal of General Virology</i> , 2014 , 95, 91-109	4.9	36

125	Gut Virome Analysis of Cameroonians Reveals High Diversity of Enteric Viruses, Including Potential Interspecies Transmitted Viruses. <i>MSphere</i> , 2019 , 4,	5	35
124	Widespread rotavirus H in commercially raised pigs, United States. <i>Emerging Infectious Diseases</i> , 2014 , 20, 1195-8	10.2	35
123	Genome-Wide Evolutionary Analyses of G1P[8] Strains Isolated Before and After Rotavirus Vaccine Introduction. <i>Genome Biology and Evolution</i> , 2015 , 7, 2473-83	3.9	34
122	Novel highly divergent reassortant bat rotaviruses in Cameroon, without evidence of zoonosis. <i>Scientific Reports</i> , 2016 , 6, 34209	4.9	34
121	Low eukaryotic viral richness is associated with faecal microbiota transplantation success in patients with UC. <i>Gut</i> , 2018 , 67, 1558-1559	19.2	33
120	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, 1427-35	4.5	33
119	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, 239-46	3.3	33
118	Highly diverse population of Picornaviridae and other members of the Picornavirales, in Cameroonian fruit bats. <i>BMC Genomics</i> , 2017 , 18, 249	4.5	32
117	Did Large-Scale Vaccination Drive Changes in the Circulating Rotavirus Population in Belgium?. <i>Scientific Reports</i> , 2015 , 5, 18585	4.9	31
116	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	7.5	30
115	Global distribution of group A rotavirus strains in horses: a systematic review. <i>Vaccine</i> , 2013 , 31, 5627-33	4.1	30
114	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	3.7	30
113	STAT2 signaling as double-edged sword restricting viral dissemination but driving severe pneumonia in SARS-CoV-2 infected hamsters		30
112	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	4.5	27
111	Genetic Characterization of the Belgian Nephropathogenic Infectious Bronchitis Virus (NIBV) Reference Strain B1648. <i>Viruses</i> , 2015 , 7, 4488-506	6.2	27
110	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, 161-8	4.5	27
109	Comparative analysis of pentavalent rotavirus vaccine strains and G8 rotaviruses identified during vaccine trial in Africa. <i>Scientific Reports</i> , 2015 , 5, 14658	4.9	27
108	Novel highly divergent sapoviruses detected by metagenomics analysis in straw-colored fruit bats in Cameroon. <i>Emerging Microbes and Infections</i> , 2017 , 6, e38	18.9	26

107	Sequence and phylogenetic analyses of human rotavirus strains: comparison of VP7 and VP8(*) antigenic epitopes between Tunisian and vaccine strains before national rotavirus vaccine introduction. <i>Infection, Genetics and Evolution</i> , 2013 , 18, 132-44	4.5	26
106	Typing of human rotaviruses: nucleotide mismatches between the VP7 gene and primer are associated with genotyping failure. <i>Virology Journal</i> , 2005 , 2, 24	6.1	26
105	Loop model: mechanism to explain partial gene duplications in segmented dsRNA viruses. <i>Biochemical and Biophysical Research Communications</i> , 2006 , 340, 140-4	3.4	26
104	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, 247-54	3.3	25
103	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	4.9	25
102	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	6.4	24
101	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	4.5	24
100	Fecal virome analysis of three carnivores reveals a novel nodavirus and multiple gemycircularviruses. <i>Virology Journal</i> , 2015 , 12, 79	6.1	24
99	Molecular characterization of genotype G6 human rotavirus strains detected in Italy from 1986 to 2009. <i>Infection, Genetics and Evolution</i> , 2011 , 11, 1449-55	4.5	24
98	Human infection with a P[14], G3 lapine rotavirus. <i>Virology</i> , 2004 , 325, 11-7	3.6	24
97	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	4.9	23
96	Genomic evolution, host-species barrier, reassortment and classification of rotaviruses. <i>Future Virology</i> , 2010 , 5, 385-390	2.4	23
95	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	2.8	22
94	Distinct evolutionary origins of G12P[8] and G12P[9] group A rotavirus strains circulating in Brazil. <i>Infection, Genetics and Evolution</i> , 2014 , 28, 385-8	4.5	22
93	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	3.3	22
92	Intestinal and extra-intestinal pathogenicity of a bovine reassortant rotavirus in calves and piglets. <i>Veterinary Microbiology</i> , 2011 , 152, 291-303	3.3	22
91	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, 746-54	4.5	22
90	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,	6.6	21

89	Reassortment among picobirnaviruses found in wolves. <i>Archives of Virology</i> , 2016 , 161, 2859-62	2.6	21
88	Molecular characterization of human group A rotavirus genotypes circulating in Rawalpindi, Islamabad, Pakistan during 2015-2016. <i>PLoS ONE</i> , 2019 , 14, e0220387	3.7	21
87	Rabbit colony infected with a bovine-like G6P[11] rotavirus strain. <i>Veterinary Microbiology</i> , 2013 , 166, 154-64	3.3	21
86	Complete genetic characterization of human G2P[6] and G3P[6] rotavirus strains. <i>Infection, Genetics and Evolution</i> , 2013 , 13, 27-35	4.5	21
85	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, 486-94	4.5	21
84	Symptomatic and subclinical infection with rotavirus P[8]G9, rural Ecuador. <i>Emerging Infectious Diseases</i> , 2007 , 13, 574-80	10.2	21
83	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, 612-8	14.5	20
82	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	3.7	20
81	Genetic diversity of the VP7, VP4 and VP6 genes of Korean porcine group C rotaviruses. <i>Veterinary Microbiology</i> , 2015 , 176, 61-9	3.3	20
80	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	3.4	20
79	Sequence analysis and evolution of group B rotaviruses. <i>Virus Research</i> , 2007 , 125, 219-25	6.4	20
78	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,	19.8	20
77	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	4.5	19
76	VP6 genetic diversity, reassortment, intragenic recombination and classification of rotavirus B in American and Japanese pigs. <i>Veterinary Microbiology</i> , 2014 , 172, 359-66	3.3	19
75	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, 426-32	4.5	19
74	Emerging OP354-Like P[8] Rotaviruses Have Rapidly Dispersed from Asia to Other Continents. <i>Molecular Biology and Evolution</i> , 2015 , 32, 2060-71	8.3	18
73	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, 120-6	4.5	18
72	Chromatography paper strip method for collection, transportation, and storage of rotavirus RNA in stool samples. <i>Journal of Clinical Microbiology</i> , 2004 , 42, 1605-8	9.7	18

71	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	11.5	16
70	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, 212-7	4.5	16
69	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, 189-97	3.3	16
68	Feline origin of rotavirus strain, Tunisia, 2008. <i>Emerging Infectious Diseases</i> , 2013 , 19, 630-4	10.2	16
67	Temporal changes of rotavirus strain distribution in a city in the northwest of China, 1996-2005. <i>International Journal of Infectious Diseases</i> , 2008 , 12, e11-7	10.5	16
66	Complete genome analysis of a rabbit rotavirus causing gastroenteritis in a human infant. <i>Viruses</i> , 2015 , 7, 844-56	6.2	15
65	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, 135-45	4.5	15
64	High incidence of reassortant G9P[4] rotavirus strain in Bangladesh: fully heterotypic from vaccine strains. <i>Journal of Clinical Virology</i> , 2013 , 58, 755-6	14.5	15
63	Novel intergenotype human norovirus recombinant GII.16/GII.3 in Bangladesh. <i>Infection, Genetics and Evolution</i> , 2013 , 20, 325-9	4.5	15
62	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	4.5	14
61	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	3.8	14
60	Molecular characterization of equine rotaviruses isolated in Europe in 2013: implications for vaccination. <i>Veterinary Microbiology</i> , 2015 , 176, 179-85	3.3	14
59	Canine rotavirus C strain detected in Hungary shows marked genotype diversity. <i>Journal of General Virology</i> , 2015 , 96, 3059-3071	4.9	14
58	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, 1039-49	7.0	14
57	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	3.3	13
56	Phylogenetic analysis of G1P[6] group A rotavirus strains detected in Northeast Brazilian children fully vaccinated with Rotarix. <i>Infection, Genetics and Evolution</i> , 2013 , 19, 395-402	4.5	13
55	At Least Seven Distinct Rotavirus Genotype Constellations in Bats with Evidence of Reassortment and Zoonotic Transmissions. <i>MBio</i> , 2021 , 12,	7.8	13
54	Novel genome sequences of cell-fusing agent virus allow comparison of virus phylogeny with the genetic structure of populations. <i>Virus Evolution</i> , 2020 , 6, veaa018	3.7	12

53	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, 151-6	3.3	12
52	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 Mosquitoes. <i>MSystems</i> , 2020 , 5,	7.6	12
51	NetoVIR: Modular Approach to Customize Sample Preparation Procedures for Viral Metagenomics. <i>Methods in Molecular Biology</i> , 2018 , 1838, 85-95	1.4	11
50	Molecular epidemiology of Korean porcine sapeloviruses. <i>Archives of Virology</i> , 2014 , 159, 1175-80	2.6	11
49	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, 214-22	4.5	11
48	Comparative analysis of the Rotarix vaccine strain and G1P[8] rotaviruses detected before and after vaccine introduction in Belgium. <i>PeerJ</i> , 2017 , 5, e2733	3.1	11
47	Molecular analysis of non structural rotavirus group A enterotoxin gene of bovine origin from India. <i>Infection, Genetics and Evolution</i> , 2014 , 25, 20-7	4.5	10
46	Emerging G9 rotavirus strains in the northwest of China. <i>Virus Research</i> , 2008 , 137, 157-62	6.4	10
45	Metagenomic Approach with the NetoVIR Enrichment Protocol Reveals Virus Diversity within Ethiopian Honey Bees (<i>Bombus terrestris</i>). <i>Viruses</i> , 2020 , 12,	6.2	9
44	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	4.5	9
43	Emergence of human G2P[4] rotaviruses containing animal derived gene segments in the post-vaccine era. <i>Scientific Reports</i> , 2016 , 6, 36841	4.9	8
42	Pathogenicity of porcine G9P[23] and G9P[7] rotaviruses in piglets. <i>Veterinary Microbiology</i> , 2013 , 166, 123-37	3.3	8
41	Distribution of rotavirus genotypes causing nosocomial and community-acquired acute gastroenteritis at the Children's Hospital of Philadelphia in the new rotavirus vaccine era. <i>Hum Vaccin</i> , 2011 , 7, 1118-23		8
40	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	10.2	8
39	G1P[8] Rotavirus in children with severe diarrhea in the post-vaccine introduction era in Brazil: Evidence of reassortments and structural modifications of the antigenic VP7 and VP4 regions. <i>Infection, Genetics and Evolution</i> , 2019 , 69, 255-266	4.5	7
38	Complete genome sequence of equid herpesvirus 3. <i>Genome Announcements</i> , 2014 , 2,		7
37	Exploration of the virome of the European brown shrimp (<i>Penaeus vannamei</i>). <i>Journal of General Virology</i> , 2020 , 101, 651-666	6.9	7
36	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		7

35	Successional Stages in Infant Gut Microbiota Maturation.. <i>MBio</i> , 2021 , e0185721	7.8	7
34	Genotypes of rotavirus strains circulating in Amman, Jordan, in 2006/07 and their significance for the potential effectiveness of future rotavirus vaccination. <i>Archives of Virology</i> , 2011 , 156, 1543-50	2.6	6
33	Frequent rearrangement may explain the structural heterogeneity in the 11th genome segment of lapine rotaviruses - short communication. <i>Acta Veterinaria Hungarica</i> , 2009 , 57, 453-61	1	6
32	A robust human norovirus replication model in zebrafish larvae		6
31	Metagenomics in Virology 2021 , 133-140		6
30	A decade of G3P[8] and G9P[8] rotaviruses in Brazil: epidemiology and evolutionary analyses. <i>Infection, Genetics and Evolution</i> , 2014 , 28, 389-97	4.5	5
29	Evidence of zoonotic transmission of VP6 and NSP4 genes into human species A rotaviruses isolated in Pakistan in 2010. <i>Archives of Virology</i> , 2019 , 164, 1781-1791	2.6	4
28	Hymenoptera associated eukaryotic virome lacks host specificity		4
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