

# Jelle Matthijnsens

## List of Publications by Year in descending order

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175  
papers

11,666  
citations

46918

47  
h-index

32761

100  
g-index

190  
all docs

190  
docs citations

190  
times ranked

6652  
citing authors

#	ARTICLE	IF	CITATIONS
1	A reassortant G3P[12] rotavirus A strain associated with severe enteritis in donkeys ( <i>Equus</i> ) Tj ETQq1 1 0.784314.rgBT /Overlock 10	0.9	4
2	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.	1.4	17
3	Molecular characterization of the gastrointestinal eukaryotic virome in elderly people in Belem, Para, Brazil. <i>Infection, Genetics and Evolution</i> , 2022, 99, 105241.	1.0	1
4	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
5	The Virome of Healthy Honey Bee Colonies: Ubiquitous Occurrence of Known and New Viruses in Bee Populations. <i>MSystems</i> , 2022, 7, e0007222.	1.7	7
6	Metagenomics in Virology. , 2021, , 133-140.		23
7	Molecular characterization of group A rotavirus strains detected in alpacas ( <i>Vicugna pacos</i> ) from Peru. <i>Journal of General Virology</i> , 2021, 102, .	1.3	2
8	ITNâ€”VIROINF: Understanding (Harmful) Virus-Host Interactions by Linking Virology and Bioinformatics. <i>Viruses</i> , 2021, 13, 766.	1.5	5
9	Establishment of <i>Culex modestus</i> in Belgium and a Glance into the Virome of Belgian Mosquito Species. <i>MSphere</i> , 2021, 6, .	1.3	19
10	Whole genome analysis of Aichivirus A, isolated from a child, suffering from gastroenteritis, in Pakistan. <i>Virus Research</i> , 2021, 299, 198437.	1.1	2
11	Assessing <i>In Vitro</i> Resistance Development in Enterovirus A71 in the Context of Combination Antiviral Treatment. <i>ACS Infectious Diseases</i> , 2021, 7, 2801-2806.	1.8	6
12	High Prevalence of Coinfecting Enteropathogens in Suspected Rotavirus Vaccine Breakthrough Cases. <i>Journal of Clinical Microbiology</i> , 2021, 59, e0123621.	1.8	9
13	At Least Seven Distinct Rotavirus Genotype Constellations in Bats with Evidence of Reassortment and Zoonotic Transmissions. <i>MBio</i> , 2021, 12, .	1.8	31
14	A single-dose live-attenuated YF17D-vectored SARS-CoV-2 vaccine candidate. <i>Nature</i> , 2021, 590, 320-325.	13.7	148
15	Discovery of a Novel Class of Norovirus Inhibitors with High Barrier of Resistance. <i>Pharmaceuticals</i> , 2021, 14, 1006.	1.7	0
16	A Previously Undescribed Highly Prevalent Phage Identified in a Danish Enteric Virome Catalog. <i>MSystems</i> , 2021, 6, e0038221.	1.7	22
17	Successional Stages in Infant Gut Microbiota Maturation. <i>MBio</i> , 2021, 12, e0185721.	1.8	48
18	Rotavirus NSP1 Contributes to Intestinal Viral Replication, Pathogenesis, and Transmission. <i>MBio</i> , 2021, 12, e0320821.	1.8	10

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19	Phylogenetic analysis of open reading frame of 11 gene segments of novel humanâ€bovine reassortant RVA G6P[1] strain in Pakistan. <i>Journal of Medical Virology</i> , 2020, 92, 3179-3186.	2.5	1
20	STAT2 signaling restricts viral dissemination but drives severe pneumonia in SARS-CoV-2 infected hamsters. <i>Nature Communications</i> , 2020, 11, 5838.	5.8	225
21	Best Practices for Successfully Writing and Publishing a Genome Announcement in <i>Microbiology Resource Announcements</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
22	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.	1.5	16
23	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.	2.2	24
24	Honey-beeâ€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
25	Exploration of the virome of the European brown shrimp ( <i>Crangon crangon</i> ). <i>Journal of General Virology</i> , 2020, 101, 651-666.	1.3	13
26	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, .	1.7	40
27	Molecular characterization of human group A rotavirus genotypes circulating in Rawalpindi, Islamabad, Pakistan during 2015-2016. <i>PLoS ONE</i> , 2019, 14, e0220387.	1.1	30
28	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.	2.6	47
29	Stable distinct core eukaryotic viromes in different mosquito species from Guadeloupe, using single mosquito viral metagenomics. <i>Microbiome</i> , 2019, 7, 121.	4.9	109
30	A robust human norovirus replication model in zebrafish larvae. <i>PLoS Pathogens</i> , 2019, 15, e1008009.	2.1	112
31	Gut Virome Analysis of Cameroonians Reveals High Diversity of Enteric Viruses, Including Potential Interspecies Transmitted Viruses. <i>MSphere</i> , 2019, 4, .	1.3	57
32	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.	0.9	5
33	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.	1.0	12
34	Whole Genome Analysis of Selected Human Group A Rotavirus Strains Revealed Evolution of DS-1-Like Single- and Double-Gene Reassortant Rotavirus Strains in Pakistan During 2015â€2016. <i>Frontiers in Microbiology</i> , 2019, 10, 2641.	1.5	8
35	The Role of the Virome in the Gut-Liver Axis. , 2019, , 121-131.		0
36	Complete coding sequence of a novel picorna-like virus in a blackbird infected with Usutu virus. <i>Archives of Virology</i> , 2018, 163, 1701-1703.	0.9	4

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37	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
38	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.	2.0	14
39	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
40	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
41	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
42	NetoVIR: Modular Approach to Customize Sample Preparation Procedures for Viral Metagenomics. <i>Methods in Molecular Biology</i> , 2018, 1838, 85-95.	0.4	33
43	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
44	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
45	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
46	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, .	1.5	28
47	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.	2.2	30
48	A18â€fRandom amplification with next-generation sequencing to cover HIV and HCV full-length genomes. <i>Virus Evolution</i> , 2017, 3, .	2.2	1
49	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.	0.9	16
50	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.	1.6	35
51	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
52	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.	1.9	18
53	Whole genomic characterization of Korean porcine G8P[7] reassortant rotaviruses. <i>Archives of Virology</i> , 2016, 161, 2835-2841.	0.9	1
54	Reassortment among picobirnaviruses found in wolves. <i>Archives of Virology</i> , 2016, 161, 2859-2862.	0.9	24

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55	Emergence of human G2P[4] rotaviruses containing animal derived gene segments in the post-vaccine era. <i>Scientific Reports</i> , 2016, 6, 36841.	1.6	11
56	Novel highly divergent reassortant bat rotaviruses in Cameroon, without evidence of zoonosis. <i>Scientific Reports</i> , 2016, 6, 34209.	1.6	44
57	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.	1.0	25
58	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.	1.0	20
59	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.	1.0	13
60	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.	1.1	32
61	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, .	3.9	28
62	Did Large-Scale Vaccination Drive Changes in the Circulating Rotavirus Population in Belgium?. <i>Scientific Reports</i> , 2015, 5, 18585.	1.6	36
63	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
64	Fecal virome analysis of three carnivores reveals a novel nodavirus and multiple gemycircularviruses. <i>Virology Journal</i> , 2015, 12, 79.	1.4	29
65	Genetic Characterization of the Belgian Nephropathogenic Infectious Bronchitis Virus (NIBV) Reference Strain B1648. <i>Viruses</i> , 2015, 7, 4488-4506.	1.5	32
66	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
67	Genetic diversity of the VP7, VP4 and VP6 genes of Korean porcine group C rotaviruses. <i>Veterinary Microbiology</i> , 2015, 176, 61-69.	0.8	24
68	Molecular characterization of equine rotaviruses isolated in Europe in 2013: Implications for vaccination. <i>Veterinary Microbiology</i> , 2015, 176, 179-185.	0.8	16
69	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.	1.3	34
70	Complete Genome Analysis of a Rabbit Rotavirus Causing Gastroenteritis in a Human Infant. <i>Viruses</i> , 2015, 7, 844-856.	1.5	21
71	Emerging OP354-Like P[8] Rotaviruses Have Rapidly Dispersed from Asia to Other Continents. <i>Molecular Biology and Evolution</i> , 2015, 32, 2060-2071.	3.5	27
72	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.	1.1	43

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73	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.	1.5	46
74	Comparative analysis of pentavalent rotavirus vaccine strains and G8 rotaviruses identified during vaccine trial in Africa. <i>Scientific Reports</i> , 2015, 5, 14658.	1.6	30
75	Canine rotavirus C strain detected in Hungary shows marked genotype diversity. <i>Journal of General Virology</i> , 2015, 96, 3059-3071.	1.3	20
76	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.	1.1	43
77	Widespread Rotavirus H in Commercially Raised Pigs, United States. <i>Emerging Infectious Diseases</i> , 2014, 20, 1203-1206.	2.0	48
78	Complete Genome Sequence of Equid Herpesvirus 3. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
79	Differences in lineage replacement dynamics of G1 and G2 rotavirus strains versus G9 strain over a period of 22years in Bangladesh. <i>Infection, Genetics and Evolution</i> , 2014, 28, 214-222.	1.0	16
80	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.	1.0	26
81	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.	0.8	22
82	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.	0.8	14
83	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.	2.8	50
84	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.	1.0	25
85	Molecular analysis of non structural rotavirus group A enterotoxin gene of bovine origin from India. <i>Infection, Genetics and Evolution</i> , 2014, 25, 20-27.	1.0	10
86	Evolution of DS-1-like human G2P[4] rotaviruses assessed by complete genome analyses. <i>Journal of General Virology</i> , 2014, 95, 91-109.	1.3	44
87	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.	1.0	29
88	Enteric viral infection in human and animal. <i>VirusDisease</i> , 2014, 25, 145-146.	1.0	3
89	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.	1.0	94
90	Molecular epidemiology of Korean porcine sapeloviruses. <i>Archives of Virology</i> , 2014, 159, 1175-1180.	0.9	16

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91	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.	0.8	28
92	Sequence and structural analyses of NSP4 proteins from human group A rotavirus strains detected in Tunisia. <i>Pathologie Et Biologie</i> , 2014, 62, 146-151.	2.2	3
93	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.	0.8	13
94	A decade of G3P[8] and G9P[8] rotaviruses in Brazil: Epidemiology and evolutionary analyses. <i>Infection, Genetics and Evolution</i> , 2014, 28, 389-397.	1.0	6
95	VP6 genetic diversity, reassortment, intragenic recombination and classification of rotavirus B in American and Japanese pigs. <i>Veterinary Microbiology</i> , 2014, 172, 359-366.	0.8	26
96	Review of group A rotavirus strains reported in swine and cattle. <i>Veterinary Microbiology</i> , 2013, 165, 190-199.	0.8	195
97	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.	1.0	18
98	Evaluation of a reverse line blot assay for genotyping common human rotaviruses. <i>Journal of Virological Methods</i> , 2013, 193, 597-602.	1.0	0
99	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.	1.6	16
100	Global distribution of group A rotavirus strains in horses: A systematic review. <i>Vaccine</i> , 2013, 31, 5627-5633.	1.7	39
101	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.	1.6	23
102	Phylogenetic analysis of G1P[6] group A rotavirus strains detected in Northeast Brazilian children fully vaccinated with Rotarix <sup>®</sup> . <i>Infection, Genetics and Evolution</i> , 2013, 19, 395-402.	1.0	13
103	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.	1.1	71
104	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.	1.1	17
105	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.	0.8	37
106	Discovery and molecular characterization of a group A rotavirus strain detected in an Argentinean vicuña (Vicugna vicugna). <i>Veterinary Microbiology</i> , 2013, 161, 247-254.	0.8	30
107	Novel intergenotype human norovirus recombinant GII.16/GII.3 in Bangladesh. <i>Infection, Genetics and Evolution</i> , 2013, 20, 325-329.	1.0	17
108	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.	1.0	60

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109	Rabbit colony infected with a bovine-like G6P[11] rotavirus strain. <i>Veterinary Microbiology</i> , 2013, 166, 154-164.	0.8	27
110	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.	1.0	36
111	Complete genetic characterization of human G2P[6] and G3P[6] rotavirus strains. <i>Infection, Genetics and Evolution</i> , 2013, 13, 27-35.	1.0	23
112	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.	1.0	23
113	Pathogenicity of porcine G9P[23] and G9P[7] rotaviruses in piglets. <i>Veterinary Microbiology</i> , 2013, 166, 123-137.	0.8	13
114	Sequence and phylogenetic analyses of human rotavirus strains: Comparison of VP7 and VP8 <sup>â</sup> – antigenic epitopes between Tunisian and vaccine strains before national rotavirus vaccine introduction. <i>Infection, Genetics and Evolution</i> , 2013, 18, 132-144.	1.0	31
115	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.	1.0	28
116	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.	1.0	20
117	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.	1.5	63
118	Feline Origin of Rotavirus Strain, Tunisia, 2008. <i>Emerging Infectious Diseases</i> , 2013, 19, 630-634.	2.0	19
119	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.	1.3	56
120	Genotype constellation and evolution of group A rotaviruses infecting humans. <i>Current Opinion in Virology</i> , 2012, 2, 426-433.	2.6	255
121	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.	1.8	160
122	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.	2.0	55
123	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.	1.1	74
124	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-e4752.	3.0	124
125	VP6-sequence-based cutoff values as a criterion for rotavirus species demarcation. <i>Archives of Virology</i> , 2012, 157, 1177-1182.	0.9	344
126	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.	1.0	16

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127	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.	1.0	54
128	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.	1.0	37
129	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.	0.8	64
130	Intestinal and extra-intestinal pathogenicity of a bovine reassortant rotavirus in calves and piglets. <i>Veterinary Microbiology</i> , 2011, 152, 291-303.	0.8	28
131	Uniformity of rotavirus strain nomenclature proposed by the Rotavirus Classification Working Group (RCWG). <i>Archives of Virology</i> , 2011, 156, 1397-1413.	0.9	827
132	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, 1543-1550.	0.9	7
133	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.	1.0	105
134	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.	1.0	27
135	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, 1118-1123.	2.4	10
136	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.	1.0	204
137	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.	1.3	47
138	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.	1.1	22
139	Zoonotic aspects of rotaviruses. <i>Veterinary Microbiology</i> , 2010, 140, 246-255.	0.8	479
140	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.	1.1	114
141	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.	1.0	23
142	Whole genome sequencing and phylogenetic analysis of a zoonotic human G8P[14] rotavirus strain. <i>Infection, Genetics and Evolution</i> , 2010, 10, 1140-1144.	1.0	63
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