

# Kristin Bnyai

## List of Publications by Citations

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273  
papers

9,656  
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45  
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89  
g-index

286  
ext. papers

10,880  
ext. citations

5.2  
avg. IF

6.02  
L-index

#	Paper	IF	Citations
273	Uniformity of rotavirus strain nomenclature proposed by the Rotavirus Classification Working Group (RCWG). <i>Archives of Virology</i> , <b>2011</b> , 156, 1397-413	2.6	699
272	Recommendations for the classification of group A rotaviruses using all 11 genomic RNA segments. <i>Archives of Virology</i> , <b>2008</b> , 153, 1621-9	2.6	523
271	Serotype diversity and reassortment between human and animal rotavirus strains: implications for rotavirus vaccine programs. <i>Journal of Infectious Diseases</i> , <b>2005</b> , 192 Suppl 1, S146-59	7	470
270	Zoonotic aspects of rotaviruses. <i>Veterinary Microbiology</i> , <b>2010</b> , 140, 246-55	3.3	411
269	Taxonomy of the order Mononegavirales: update 2016. <i>Archives of Virology</i> , <b>2016</b> , 161, 2351-60	2.6	324
268	Systematic review of regional and temporal trends in global rotavirus strain diversity in the pre rotavirus vaccine era: insights for understanding the impact of rotavirus vaccination programs. <i>Vaccine</i> , <b>2012</b> , 30 Suppl 1, A122-30	4.1	305
267	Role for migratory wild birds in the global spread of avian influenza H5N8. <i>Science</i> , <b>2016</b> , 354, 213-217	33.3	252
266	Rotavirus disease and vaccination: impact on genotype diversity. <i>Future Microbiology</i> , <b>2009</b> , 4, 1303-16	2.9	248
265	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> , <b>2009</b> , 83, 2917-29	6.6	185
264	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> , <b>2011</b> , 139, 895-909	4.3	184
263	Viral gastroenteritis. <i>Lancet, The</i> , <b>2018</b> , 392, 175-186	40	152
262	Review of group A rotavirus strains reported in swine and cattle. <i>Veterinary Microbiology</i> , <b>2013</b> , 165, 190-9	3.3	150
261	Candidate new rotavirus species in sheltered dogs, Hungary. <i>Emerging Infectious Diseases</i> , <b>2015</b> , 21, 660-30.2	30.2	149
260	Distribution of rotavirus strains and strain-specific effectiveness of the rotavirus vaccine after its introduction: a systematic review and meta-analysis. <i>Lancet Infectious Diseases, The</i> , <b>2014</b> , 14, 847-56	25.5	146
259	Review of global rotavirus strain prevalence data from six years post vaccine licensure surveillance: is there evidence of strain selection from vaccine pressure?. <i>Infection, Genetics and Evolution</i> , <b>2014</b> , 28, 446-61	4.5	131
258	Candidate new rotavirus species in Schreiber's bats, Serbia. <i>Infection, Genetics and Evolution</i> , <b>2017</b> , 48, 19-26	4.5	127
257	Detection and molecular characterization of a canine norovirus. <i>Emerging Infectious Diseases</i> , <b>2008</b> , 14, 1306-8	10.2	117

256	Relationships among porcine and human P[6] rotaviruses: evidence that the different human P[6] lineages have originated from multiple interspecies transmission events. <i>Virology</i> , <b>2006</b> , 344, 509-19	3.6	108
255	Identification of a novel VP4 genotype carried by a serotype G5 porcine rotavirus strain. <i>Virology</i> , <b>2006</b> , 346, 301-11	3.6	104
254	Rotavirus surveillance in Europe, 2005-2008: web-enabled reporting and real-time analysis of genotyping and epidemiological data. <i>Journal of Infectious Diseases</i> , <b>2009</b> , 200 Suppl 1, S215-21	7	94
253	Molecular analysis of the VP7 gene of pheasant rotaviruses identifies a new genotype, designated G23. <i>Archives of Virology</i> , <b>2009</b> , 154, 1365-9	2.6	92
252	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> , <b>2011</b> , 11, 1396-406	4.5	88
251	Diversity and zoonotic potential of rotaviruses in swine and cattle across Europe. <i>Veterinary Microbiology</i> , <b>2012</b> , 156, 238-45	3.3	87
250	Norovirus in captive lion cub ( <i>Panthera leo</i> ). <i>Emerging Infectious Diseases</i> , <b>2007</b> , 13, 1071-3	10.2	83
249	649 Distribution of rotavirus strains and strain-specific effectiveness following vaccine introduction: a global review and meta-analysis. <i>Open Forum Infectious Diseases</i> , <b>2014</b> , 1, S35-S35	1	78
248	Reassortant group A rotavirus from straw-colored fruit bat ( <i>Eidolon helvum</i> ). <i>Emerging Infectious Diseases</i> , <b>2010</b> , 16, 1844-52	10.2	76
247	Genetic heterogeneity and recombination in canine noroviruses. <i>Journal of Virology</i> , <b>2009</b> , 83, 11391-6	6.6	70
246	Sequence heterogeneity among human picobirnaviruses detected in a gastroenteritis outbreak. <i>Archives of Virology</i> , <b>2003</b> , 148, 2281-91	2.6	70
245	Genetic diversity and zoonotic potential of human rotavirus strains, 2003-2006, Hungary. <i>Journal of Medical Virology</i> , <b>2009</b> , 81, 362-70	19.7	68
244	Zoonotic transmission of rotavirus: surveillance and control. <i>Expert Review of Anti-Infective Therapy</i> , <b>2015</b> , 13, 1337-50	5.5	66
243	Identification of group A porcine rotavirus strains bearing a novel VP4 (P) Genotype in Italian swine herds. <i>Journal of Clinical Microbiology</i> , <b>2007</b> , 45, 577-80	9.7	66
242	Tembusu-like flavivirus (Perak virus) as the cause of neurological disease outbreaks in young Pekin ducks. <i>Avian Pathology</i> , <b>2014</b> , 43, 552-60	2.4	62
241	Whole genome sequencing and phylogenetic analysis of a zoonotic human G8P[14] rotavirus strain. <i>Infection, Genetics and Evolution</i> , <b>2010</b> , 10, 1140-4	4.5	62
240	Sequence analysis of the VP7 and VP4 genes identifies a novel VP7 gene allele of porcine rotaviruses, sharing a common evolutionary origin with human G2 rotaviruses. <i>Virology</i> , <b>2005</b> , 337, 111-23	3.6	60
239	Genogroup I picobirnaviruses in pigs: evidence for genetic diversity and relatedness to human strains. <i>Journal of General Virology</i> , <b>2008</b> , 89, 534-539	4.9	58

238	G and P types of circulating rotavirus strains in the United States during 1996-2005: nine years of prevaccine data. <i>Journal of Infectious Diseases</i> , <b>2009</b> , 200 Suppl 1, S99-S105	7	55
237	Genotyping canine distemper virus (CDV) by a hemi-nested multiplex PCR provides a rapid approach for investigation of CDV outbreaks. <i>Veterinary Microbiology</i> , <b>2007</b> , 122, 32-42	3.3	53
236	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> , <b>2013</b> , 19, 71-80	4.5	50
235	Novel human rotavirus genotype G5P[7] from child with diarrhea, Cameroon. <i>Emerging Infectious Diseases</i> , <b>2009</b> , 15, 83-6	10.2	50
234	Reovirus identified as cause of disease in young geese. <i>Avian Pathology</i> , <b>2003</b> , 32, 129-38	2.4	50
233	Prevalence of group C rotaviruses in weaning and post-weaning pigs with enteritis. <i>Veterinary Microbiology</i> , <b>2007</b> , 123, 26-33	3.3	49
232	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> , <b>2012</b> , 93, 866-875	4.9	48
231	Epidemiology, phylogeny, and evolution of emerging enteric Picobirnaviruses of animal origin and their relationship to human strains. <i>BioMed Research International</i> , <b>2014</b> , 2014, 780752	3	47
230	Genetic variability among serotype G6 human rotaviruses: identification of a novel lineage isolated in Hungary. <i>Journal of Medical Virology</i> , <b>2003</b> , 71, 124-34	19.7	47
229	Picobirnavirus infections: viral persistence and zoonotic potential. <i>Reviews in Medical Virology</i> , <b>2012</b> , 22, 245-56	11.7	46
228	Molecular survey of RNA viruses in Hungarian bats: discovering novel astroviruses, coronaviruses, and caliciviruses. <i>Vector-Borne and Zoonotic Diseases</i> , <b>2014</b> , 14, 846-55	2.4	45
227	Equine-like G3 rotavirus in Hungary, 2015 - Is it a novel intergenogroup reassortant pandemic strain?. <i>Acta Microbiologica Et Immunologica Hungarica</i> , <b>2016</b> , 63, 243-55	1.8	45
226	Identification of a porcine calicivirus related genetically to human sapoviruses. <i>Journal of Clinical Microbiology</i> , <b>2008</b> , 46, 1907-13	9.7	44
225	Emergence of serotype G12 rotaviruses, Hungary. <i>Emerging Infectious Diseases</i> , <b>2007</b> , 13, 916-9	10.2	43
224	Eight-year survey of human rotavirus strains demonstrates circulation of unusual G and P types in Hungary. <i>Journal of Clinical Microbiology</i> , <b>2004</b> , 42, 393-7	9.7	43
223	Molecular characterization of a rare, human-porcine reassortant rotavirus strain, G11P[6], from Ecuador. <i>Archives of Virology</i> , <b>2009</b> , 154, 1823-9	2.6	42
222	Genetic heterogeneity of porcine enteric caliciviruses identified from diarrhoeic piglets. <i>Virus Genes</i> , <b>2008</b> , 36, 365-73	2.3	40
221	Unusual assortment of segments in 2 rare human rotavirus genomes. <i>Emerging Infectious Diseases</i> , <b>2010</b> , 16, 859-62	10.2	39

220	Genetic heterogeneity in human G6P[14] rotavirus strains detected in Hungary suggests independent zoonotic origin. <i>Journal of Infection</i> , <b>2009</b> , 59, 213-5	18.9	39
219	A feline rotavirus G3P[9] carries traces of multiple reassortment events and resembles rare human G3P[9] rotaviruses. <i>Journal of General Virology</i> , <b>2011</b> , 92, 1214-1221	4.9	39
218	Lights and shades on an historical vaccine canine distemper virus, the Rockborn strain. <i>Vaccine</i> , <b>2011</b> , 29, 1222-7	4.1	38
217	The genomic constellation of a novel avian orthoreovirus strain associated with runting-stunting syndrome in broilers. <i>Virus Genes</i> , <b>2011</b> , 42, 82-9	2.3	38
216	Genomic characterization of a novel group A lamb rotavirus isolated in Zaragoza, Spain. <i>Virus Genes</i> , <b>2008</b> , 37, 250-65	2.3	38
215	Sequencing and phylogenetic analysis of human genotype P[6] rotavirus strains detected in Hungary provides evidence for genetic heterogeneity within the P[6] VP4 gene. <i>Journal of Clinical Microbiology</i> , <b>2004</b> , 42, 4338-43	9.7	37
214	Mutations Associated with Decreased Susceptibility to Seven Antimicrobial Families in Field and Laboratory-Derived Mycoplasma bovis Strains. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2017</b> , 61,	5.9	36
213	Evolution of DS-1-like human G2P[4] rotaviruses assessed by complete genome analyses. <i>Journal of General Virology</i> , <b>2014</b> , 95, 91-109	4.9	36
212	Detection and characterization of canine astroviruses. <i>Journal of General Virology</i> , <b>2011</b> , 92, 1880-1887	4.9	36
211	Genetic heterogeneity in the VP7 of group C rotaviruses. <i>Virology</i> , <b>2007</b> , 367, 358-66	3.6	36
210	Dominating prevalence of P[8],G1 and P[8],G9 rotavirus strains among children admitted to hospital between 2000 and 2003 in Budapest, Hungary. <i>Journal of Medical Virology</i> , <b>2005</b> , 76, 414-23	19.7	36
209	Astroviruses in rabbits. <i>Emerging Infectious Diseases</i> , <b>2011</b> , 17, 2287-93	10.2	34
208	Enteric disease in dogs naturally infected by a novel canine astrovirus. <i>Journal of Clinical Microbiology</i> , <b>2012</b> , 50, 1066-9	9.7	34
207	One year survey of human rotavirus strains suggests the emergence of genotype G12 in Cameroon. <i>Journal of Medical Virology</i> , <b>2013</b> , 85, 1485-90	19.7	33
206	Tick-Borne Flaviviruses, with a Focus on Powassan Virus. <i>Clinical Microbiology Reviews</i> , <b>2019</b> , 32,	34	33
205	Detection and quantification of group C rotaviruses in communal sewage. <i>Applied and Environmental Microbiology</i> , <b>2008</b> , 74, 3394-9	4.8	32
204	Genetic diversity and recombination within bufaviruses: Detection of a novel strain in Hungarian bats. <i>Infection, Genetics and Evolution</i> , <b>2015</b> , 33, 288-92	4.5	31
203	Novel NSP4 genotype in a camel G10P[15] rotavirus strain. <i>Acta Microbiologica Et Immunologica Hungarica</i> , <b>2012</b> , 59, 411-21	1.8	31

202	Global distribution of group A rotavirus strains in horses: a systematic review. <i>Vaccine</i> , <b>2013</b> , 31, 5627-334.1	30
201	Sequencing and phylogenetic analysis of the coding region of six common rotavirus strains: evidence for intragenogroup reassortment among co-circulating G1P[8] and G2P[4] strains from the United States. <i>Journal of Medical Virology</i> , <b>2011</b> , 83, 532-9	19.7 30
200	Zoonotic bovine rotavirus strain in a diarrhetic child, Nicaragua. <i>Journal of Clinical Virology</i> , <b>2009</b> , 46, 391-34.5	30
199	Unique genomic organization of a novel Avipoxvirus detected in turkey (Meleagris gallopavo). <i>Infection, Genetics and Evolution</i> , <b>2015</b> , 35, 221-9	4.5 29
198	Putative novel genotype of avian hepatitis E virus, Hungary, 2010. <i>Emerging Infectious Diseases</i> , <b>2012</b> , 18, 1365-8	10.2 29
197	Genome sequence based molecular epidemiology of unusual US Rotavirus A G9 strains isolated from Omaha, USA between 1997 and 2000. <i>Infection, Genetics and Evolution</i> , <b>2011</b> , 11, 522-7	4.5 29
196	Prevalence and molecular characterization of human group C rotaviruses in Hungary. <i>Journal of Clinical Virology</i> , <b>2006</b> , 37, 317-22	14.5 29
195	Detection of human rotavirus serotype G6 in Hungary. <i>Epidemiology and Infection</i> , <b>2003</b> , 130, 107-12	4.3 29
194	Repositioning PARP inhibitors for SARS-CoV-2 infection(COVID-19); a new multi-pronged therapy for acute respiratory distress syndrome?. <i>British Journal of Pharmacology</i> , <b>2020</b> , 177, 3635-3645	8.6 29
193	Genetic heterogeneity and recombination in human type 2 astroviruses. <i>Journal of Clinical Microbiology</i> , <b>2012</b> , 50, 3760-4	9.7 28
192	Circulation of <i>Dirofilaria repens</i> , <i>Setaria tundra</i> , and <i>Onchocercidae</i> species in Hungary during the period 2011-2013. <i>Veterinary Parasitology</i> , <b>2015</b> , 214, 108-13	2.8 27
191	Diverse origin of P[19] rotaviruses in children with acute diarrhea in Taiwan: Detection of novel lineages of the G3, G5, and G9 VP7 genes. <i>Journal of Medical Virology</i> , <b>2011</b> , 83, 1279-87	19.7 27
190	Genomic characterization of human rotavirus G10 strains from the African Rotavirus Network: relationship to animal rotaviruses. <i>Infection, Genetics and Evolution</i> , <b>2011</b> , 11, 237-41	4.5 27
189	Human astroviruses in raw sewage samples in Hungary. <i>Journal of Applied Microbiology</i> , <b>2006</b> , 101, 1123-27	27
188	Lineage diversification and recombination in type-4 human astroviruses. <i>Infection, Genetics and Evolution</i> , <b>2013</b> , 20, 330-5	4.5 26
187	Analysis of the ORF2 of human astroviruses reveals lineage diversification, recombination and rearrangement and provides the basis for a novel sub-classification system. <i>Archives of Virology</i> , <b>2014</b> , 159, 3185-96	2.6 25
186	Molecular detection and characterization of human gyroviruses identified in the ferret fecal virome. <i>Archives of Virology</i> , <b>2014</b> , 159, 3401-6	2.6 25
185	Genogroup I picobirnavirus in diarrhoeic foals: can the horse serve as a natural reservoir for human infection?. <i>Veterinary Research</i> , <b>2011</b> , 42, 52	3.8 25

184	Detection of a porcine-like rotavirus in a child with enteritis in Italy. <i>Journal of Clinical Microbiology</i> , <b>2008</b> , 46, 3501-7	9.7	25
183	Detection and characterization of a divergent avian reovirus strain from a broiler chicken with central nervous system disease. <i>Archives of Virology</i> , <b>2013</b> , 158, 2583-8	2.6	24
182	Full genome characterization of human Rotavirus A strains isolated in Cameroon, 2010-2011: diverse combinations of the G and P genes and lack of reassortment of the backbone genes. <i>Infection, Genetics and Evolution</i> , <b>2014</b> , 28, 537-60	4.5	24
181	Molecular characterization of genotype G6 human rotavirus strains detected in Italy from 1986 to 2009. <i>Infection, Genetics and Evolution</i> , <b>2011</b> , 11, 1449-55	4.5	24
180	Novel Parvovirus Related to Primate Bufaviruses in Dogs. <i>Emerging Infectious Diseases</i> , <b>2018</b> , 24, 1061-1068	10.6	22
179	Detection of novel porcine bocaviruses in fecal samples of asymptomatic pigs in Cameroon. <i>Infection, Genetics and Evolution</i> , <b>2013</b> , 17, 277-82	4.5	22
178	Trends in the epidemiology of human G1P[8] rotaviruses: a hungarian study. <i>Journal of Infectious Diseases</i> , <b>2009</b> , 200 Suppl 1, S222-7	7	22
177	One-year survey of astrovirus infection in children with gastroenteritis in a large hospital in Hungary: occurrence and genetic analysis of astroviruses. <i>Journal of Medical Virology</i> , <b>2004</b> , 74, 71-7	19.7	22
176	Novel G9 rotavirus strains co-circulate in children and pigs, Taiwan. <i>Scientific Reports</i> , <b>2017</b> , 7, 40731	4.9	21
175	Advances in Diagnostic Approaches for Viral Etiologies of Diarrhea: From the Lab to the Field. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 1957	5.7	21
174	Whole-genome sequencing of a green bush viper reovirus reveals a shared evolutionary history between reptilian and unusual mammalian orthoreoviruses. <i>Archives of Virology</i> , <b>2014</b> , 159, 153-8	2.6	21
173	Identification of porcine rotavirus-like genotype P[6] strains in Taiwanese children. <i>Journal of Medical Microbiology</i> , <b>2012</b> , 61, 990-997	3.2	21
172	Detection of rare reassortant G5P[6] rotavirus, Bulgaria. <i>Infection, Genetics and Evolution</i> , <b>2012</b> , 12, 1676-84	4.8	21
171	Molecular epidemiology of human P[8],G9 rotaviruses in Hungary between 1998 and 2001. <i>Journal of Medical Microbiology</i> , <b>2004</b> , 53, 791-801	3.2	21
170	Genetic heterogeneity and recombination in type-3 human astroviruses. <i>Infection, Genetics and Evolution</i> , <b>2015</b> , 32, 156-60	4.5	20
169	First isolation and characterization of Brucella microti from wild boar. <i>BMC Veterinary Research</i> , <b>2015</b> , 11, 147	2.7	20
168	Genetic characterization of a novel picornavirus detected in <i>Miniopterus schreibersii</i> bats. <i>Journal of General Virology</i> , <b>2015</b> , 96, 815-821	4.9	20
167	Genome analysis of canine astroviruses reveals genetic heterogeneity and suggests possible inter-species transmission. <i>Virus Research</i> , <b>2017</b> , 232, 162-170	6.4	19



166	Large-scale whole genome sequencing identifies country-wide spread of an emerging G9P[8] rotavirus strain in Hungary, 2012. <i>Infection, Genetics and Evolution</i> , <b>2014</b> , 28, 495-512	4.5	19
165	Surveillance of human rotaviruses in 2007-2011, Hungary: exploring the genetic relatedness between vaccine and field strains. <i>Journal of Clinical Virology</i> , <b>2012</b> , 55, 140-6	14.5	19
164	West Nile virus surveillance in mosquitoes, April to October 2013, Vojvodina province, Serbia: implications for the 2014 season. <i>Eurosurveillance</i> , <b>2014</b> , 19, 20779	19.8	19
163	Identification of a novel parvovirus in domestic cats. <i>Veterinary Microbiology</i> , <b>2019</b> , 228, 246-251	3.3	19
162	Rotavirus strains in neglected animal species including lambs, goats and camelids. <i>VirusDisease</i> , <b>2014</b> , 25, 215-22	3.4	18
161	Novel bocaparvoviruses in rabbits. <i>Veterinary Journal</i> , <b>2015</b> , 206, 131-5	2.5	18
160	Analysis of early strains of the norovirus pandemic variant GII.4 Sydney 2012 identifies mutations in adaptive sites of the capsid protein. <i>Virology</i> , <b>2014</b> , 450-451, 355-8	3.6	18
159	Detection of newly described astrovirus MLB1 in stool samples from children. <i>Emerging Infectious Diseases</i> , <b>2010</b> , 16, 169; author reply 169-70	10.2	18
158	Simian genogroup I picobirnaviruses: prevalence, genetic diversity, and zoonotic potential. <i>Journal of Clinical Microbiology</i> , <b>2012</b> , 50, 2779-82	9.7	18
157	A Simple Method for Sample Preparation to Facilitate Efficient Whole-Genome Sequencing of African Swine Fever Virus. <i>Viruses</i> , <b>2019</b> , 11,	6.2	18
156	Sequence and phylogenetic analysis identifies a putative novel gyrovirus 3 genotype in ferret feces. <i>Virus Genes</i> , <b>2015</b> , 50, 137-41	2.3	17
155	Analysis of codon usage pattern evolution in avian rotaviruses and their preferred host. <i>Infection, Genetics and Evolution</i> , <b>2015</b> , 34, 17-25	4.5	17
154	Genome sequencing identifies genetic and antigenic divergence of porcine picobirnaviruses. <i>Journal of General Virology</i> , <b>2014</b> , 95, 2233-2239	4.9	17
153	Complete genome analysis identifies TvËminne avian virus as a candidate new species within the genus Orthoreovirus. <i>Journal of General Virology</i> , <b>2014</b> , 95, 898-904	4.9	17
152	Mixed infection by Feline astrovirus and Feline panleukopenia virus in a domestic cat with gastroenteritis and panleukopenia. <i>Journal of Veterinary Diagnostic Investigation</i> , <b>2011</b> , 23, 581-4	1.5	17
151	Sequencing and phylogenetic analysis identifies candidate members of a new picornavirus genus in terrestrial tortoise species. <i>Archives of Virology</i> , <b>2015</b> , 160, 811-6	2.6	16
150	Lineage diversification, homo- and heterologous reassortment and recombination shape the evolution of chicken orthoreoviruses. <i>Scientific Reports</i> , <b>2016</b> , 6, 36960	4.9	16
149	Human G9P[8] rotavirus strains circulating in Cameroon, 1999-2000: Genetic relationships with other G9 strains and detection of a new G9 subtype. <i>Infection, Genetics and Evolution</i> , <b>2013</b> , 18, 315-24	4.5	16



148	Unexpected detection of porcine rotavirus C strains carrying human origin VP6 gene. <i>Veterinary Quarterly</i> , <b>2017</b> , 37, 252-261	8	16
147	Detection and Full-Length Genome Characterization of Novel Canine Vesiviruses. <i>Emerging Infectious Diseases</i> , <b>2015</b> , 21, 1433-6	10.2	16
146	Detection and molecular characterization of porcine picobirnavirus in feces of domestic pigs from kolkata, India. <i>Indian Journal of Virology: an Official Organ of Indian Virological Society</i> , <b>2012</b> , 23, 387-91		16
145	Detection and sequencing of West Nile virus RNA from human urine and serum samples during the 2014 seasonal period. <i>Archives of Virology</i> , <b>2016</b> , 161, 1797-806	2.6	16
144	Putative novel lineage of West Nile virus in <i>Uranotaenia unguiculata</i> mosquito, Hungary. <i>VirusDisease</i> , <b>2014</b> , 25, 500-3	3.4	15
143	Identification of a Bovine Enteric Calicivirus, K�klareli Virus, Distantly Related to Neboviruses, in Calves with Enteritis in Turkey. <i>Journal of Clinical Microbiology</i> , <b>2015</b> , 53, 3614-7	9.7	15
142	Human infection with novel G3P[25] rotavirus strain in Taiwan. <i>Clinical Microbiology and Infection</i> , <b>2011</b> , 17, 1570-3	9.5	15
141	Identification of the novel lapine rotavirus genotype P[22] from an outbreak of enteritis in a Hungarian rabbitry. <i>Virus Research</i> , <b>2005</b> , 113, 73-80	6.4	15
140	The goose reovirus genome segment encoding the minor outer capsid protein, sigma1/sigmaC, is bicistronic and shares structural similarities with its counterpart in Muscovy duck reovirus. <i>Virus Genes</i> , <b>2005</b> , 31, 285-91	2.3	15
139	Epidemiology of rotavirus diarrhea in children under 5 years in Northern Cameroon. <i>Pan African Medical Journal</i> , <b>2012</b> , 11, 73	1.2	15
138	Identification of a novel canine norovirus. <i>Infection, Genetics and Evolution</i> , <b>2017</b> , 52, 75-81	4.5	14
137	Whole genome sequencing reveals genetic heterogeneity of G3P[8] rotaviruses circulating in Italy. <i>Infection, Genetics and Evolution</i> , <b>2016</b> , 40, 253-261	4.5	14
136	Monitoring of group A rotaviruses in wild-living birds in Hungary. <i>Avian Diseases</i> , <b>2011</b> , 55, 123-7	1.6	14
135	Human astrovirus infection associated with childhood intussusception. <i>Pediatrics International</i> , <b>2007</b> , 49, 103-5	1.2	14
134	Canine rotavirus C strain detected in Hungary shows marked genotype diversity. <i>Journal of General Virology</i> , <b>2015</b> , 96, 3059-3071	4.9	14
133	Molecular characterization of unusual bovine rotavirus A strains having high genetic relatedness with human rotavirus: evidence for zoonothroponotic transmission. <i>Zoonoses and Public Health</i> , <b>2018</b> , 65, 431-442	2.9	13
132	Genotyping <i>Mycoplasma hyopneumoniae</i> isolates based on multi-locus sequence typing, multiple-locus variable-number tandem repeat analysis and analysing gene p146. <i>Veterinary Microbiology</i> , <b>2018</b> , 222, 85-90	3.3	13
131	Monitoring of West Nile virus in mosquitoes between 2011-2012 in Hungary. <i>Vector-Borne and Zoonotic Diseases</i> , <b>2014</b> , 14, 648-55	2.4	13

130	MLB1 astrovirus in children with gastroenteritis, Italy. <i>Emerging Infectious Diseases</i> , <b>2014</b> , 20, 169-70	10.2	13
129	Serologic evidence of Crimean-Congo hemorrhagic fever virus infection in Hungary. <i>Vector-Borne and Zoonotic Diseases</i> , <b>2013</b> , 13, 270-2	2.4	13
128	Searching for HAdV-52, the putative gastroenteritis-associated human adenovirus serotype in Southern Hungary. <i>New Microbiologica</i> , <b>2009</b> , 32, 185-8	1.1	13
127	Putative vaccine breakthrough event associated with heterotypic rotavirus infection in newborn calves, Turkey, 2015. <i>Veterinary Microbiology</i> , <b>2017</b> , 201, 7-13	3.3	12
126	Neuroinvasive influenza virus A(H5N8) in fattening ducks, Hungary, 2015. <i>Infection, Genetics and Evolution</i> , <b>2016</b> , 43, 418-23	4.5	12
125	Isolation and complete genome characterization of novel reassortant orthoreovirus from common vole ( <i>Microtus arvalis</i> ). <i>Virus Genes</i> , <b>2017</b> , 53, 307-311	2.3	12
124	Novel European lineages of bat astroviruses identified in Hungary. <i>Acta Virologica</i> , <b>2014</b> , 58, 95-8	2.2	12
123	Identification of a G8P[14] Rotavirus Isolate Obtained from a Taiwanese Child: Evidence for a Relationship with Bovine Rotaviruses. <i>Japanese Journal of Infectious Diseases</i> , <b>2012</b> , 65, 455-457	2.7	12
122	Multispecies reassortant bovine rotavirus strain carries a novel simian G3-like VP7 genotype. <i>Infection, Genetics and Evolution</i> , <b>2016</b> , 41, 63-72	4.5	12
121	Sequencing and molecular modeling identifies candidate members of Caliciviridae family in bats. <i>Infection, Genetics and Evolution</i> , <b>2016</b> , 41, 227-232	4.5	12
120	Genomic sequence and phylogenetic analyses of two novel orthoreovirus strains isolated from Pekin ducks in 2014 in Germany. <i>Virus Research</i> , <b>2018</b> , 257, 57-62	6.4	12
119	Molecular epidemiology and characterization of picobirnaviruses in small ruminant populations in India. <i>Infection, Genetics and Evolution</i> , <b>2018</b> , 63, 39-42	4.5	12
118	Integrated circoviral rep-like sequences in the genome of cyprinid fish. <i>Virus Genes</i> , <b>2013</b> , 47, 374-7	2.3	11
117	Molecular detection of novel adenoviruses in fecal specimens of captive monkeys with diarrhea in China. <i>Veterinary Microbiology</i> , <b>2010</b> , 142, 416-9	3.3	11
116	First molecular identification of <i>Dirofilaria</i> spp. (Onchocercidae) in mosquitoes from Serbia. <i>Parasitology Research</i> , <b>2016</b> , 115, 3257-60	2.4	11
115	First report and genetic characterization of porcine astroviruses of lineage 4 and 2 in diarrhoeic pigs in India. <i>Transboundary and Emerging Diseases</i> , <b>2019</b> , 66, 47-53	4.2	11
114	Emergence of multireassortant bluetongue virus serotype 4 in Hungary. <i>Infection, Genetics and Evolution</i> , <b>2015</b> , 33, 6-10	4.5	10
113	Serologic survey of orthopoxvirus infection among rodents in Hungary. <i>Vector-Borne and Zoonotic Diseases</i> , <b>2015</b> , 15, 317-22	2.4	10

112	Occurrence and spread of a reassortant very virulent genotype of infectious bursal disease virus with altered VP2 amino acid profile and pathogenicity in some European countries. <i>Veterinary Microbiology</i> , <b>2020</b> , 245, 108663	3.3	10
111	Isolation of <i>Mycoplasma anserisalpinitidis</i> from swan goose ( <i>Anser cygnoides</i> ) in China. <i>BMC Veterinary Research</i> , <b>2020</b> , 16, 178	2.7	10
110	Molecular analysis of non structural rotavirus group A enterotoxin gene of bovine origin from India. <i>Infection, Genetics and Evolution</i> , <b>2014</b> , 25, 20-7	4.5	10
109	Detection of shared genes among Asian and European waterfowl reoviruses in the whole genome constellations. <i>Infection, Genetics and Evolution</i> , <b>2014</b> , 28, 55-7	4.5	10
108	Whole genome sequencing of a rare rotavirus from archived stool sample demonstrates independent zoonotic origin of human G8P[14] strains in Hungary. <i>Virus Research</i> , <b>2017</b> , 227, 96-103	6.4	10
107	Norovirus GII.17 as Major Epidemic Strain in Italy, Winter 2015-16. <i>Emerging Infectious Diseases</i> , <b>2017</b> , 23, 1206-1208	10.2	10
106	Full genome sequence analysis of a wild, non-MLV-related type 2 Hungarian PRRSV variant isolated in Europe. <i>Virus Research</i> , <b>2015</b> , 200, 1-8	6.4	10
105	Frequency of norovirus in stool samples from hospitalized children due to acute gastroenteritis in Anatolia, Turkey, 2006-2007. <i>Scandinavian Journal of Infectious Diseases</i> , <b>2009</b> , 41, 685-8		10
104	Full-genome sequencing of a Hungarian canine G3P[3] Rotavirus A strain reveals high genetic relatedness with a historic Italian human strain. <i>Virus Genes</i> , <b>2015</b> , 50, 310-5	2.3	9
103	Molecular epidemiology of human G2P[4] rotaviruses in Taiwan, 2004-2011. <i>Infection, Genetics and Evolution</i> , <b>2014</b> , 28, 530-6	4.5	9
102	Identification of tick-borne encephalitis virus in ticks collected in southeastern Hungary. <i>Ticks and Tick-borne Diseases</i> , <b>2013</b> , 4, 427-31	3.6	9
101	Ubiquiter circovirus sequences raise challenges in laboratory diagnosis: the case of honey bee and bee mite, reptiles, and free living amoebae. <i>Acta Microbiologica Et Immunologica Hungarica</i> , <b>2015</b> , 62, 57-73	1.8	9
100	Putative canine origin of rotavirus strain detected in a child with diarrhea, Taiwan. <i>Vector-Borne and Zoonotic Diseases</i> , <b>2012</b> , 12, 170-3	2.4	9
99	Detection of Dobrava-Belgrade hantavirus using recombinant-nucleocapsid-based enzyme-linked immunosorbent assay and SYBR Green-based real-time reverse transcriptase-polymerase chain reaction. <i>Archives of Virology</i> , <b>2011</b> , 156, 1655-60	2.6	9
98	Severe gastroenteritis associated with G3P[9] rotavirus in Taiwan. <i>Infection</i> , <b>2011</b> , 39, 271-5	5.8	9
97	Assignment of the group A rotavirus NSP4 gene into genotypes using a hemi-nested multiplex PCR assay: a rapid and reproducible assay for strain surveillance studies. <i>Journal of Medical Microbiology</i> , <b>2009</b> , 58, 303-311	3.2	9
96	First detection of P[6],G9 rotaviruses in Hungary--an imported strain from India?. <i>Journal of Travel Medicine</i> , <b>2009</b> , 16, 141-3	12.9	9
95	Genome sequence of a monoreassortant H1N1 swine influenza virus isolated from a pig in Hungary. <i>Journal of Virology</i> , <b>2012</b> , 86, 13133	6.6	9

94	Whole genome characterization of a chelonian orthoreovirus strain identifies significant genetic diversity and may classify reptile orthoreoviruses into distinct species. <i>Virus Research</i> , <b>2016</b> , 215, 94-8	6.4	9
93	Reassortant human group C rotaviruses in Hungary. <i>Infection, Genetics and Evolution</i> , <b>2015</b> , 34, 410-4	4.5	8
92	The fecal virome of domesticated animals. <i>VirusDisease</i> , <b>2014</b> , 25, 150-7	3.4	8
91	Peptide-Recombinant VP6 Protein Based Enzyme Immunoassay for the Detection of Group A Rotaviruses in Multiple Host Species. <i>PLoS ONE</i> , <b>2016</b> , 11, e0159027	3.7	8
90	Temporal variation in the distribution of type-1 human astrovirus lineages in a settled population over 147years. <i>Archives of Virology</i> , <b>2016</b> , 161, 1633-7	2.6	8
89	Methylation Status of the Adeno-Associated Virus Type 2 (AAV2). <i>Viruses</i> , <b>2019</b> , 11,	6.2	8
88	Identification of a multi-reassortant G12P[9] rotavirus with novel VP1, VP2, VP3 and NSP2 genotypes in a child with acute gastroenteritis. <i>Infection, Genetics and Evolution</i> , <b>2015</b> , 35, 34-7	4.5	7
87	Full-length genome sequence analysis of a Hungarian porcine reproductive and respiratory syndrome virus isolated from a pig with severe respiratory disease. <i>Archives of Virology</i> , <b>2015</b> , 160, 417-22 <sup>6</sup>	2.6	7
86	Detection and molecular characterization of sapoviruses in dogs. <i>Infection, Genetics and Evolution</i> , <b>2016</b> , 38, 8-12	4.5	7
85	Coding-complete sequence of a vaccine-derived recombinant porcine reproductive and respiratory syndrome virus strain isolated in Hungary. <i>Archives of Virology</i> , <b>2019</b> , 164, 2605-2608	2.6	7
84	The complete genome sequence of a European goose reovirus strain. <i>Archives of Virology</i> , <b>2014</b> , 159, 2165-9	2.6	7
83	Sequence analysis of Schmallerberg virus genomes detected in Hungary. <i>Acta Microbiologica Et Immunologica Hungarica</i> , <b>2017</b> , 64, 373-384	1.8	7
82	Avian Group D Rotaviruses: Structure, Epidemiology, Diagnosis, and Perspectives on Future Research Challenges. <i>Pathogens</i> , <b>2017</b> , 6,	4.5	7
81	Molecular detection and phylogenetic analysis of tick-borne encephalitis virus in rodents captured in the transdanubian region of Hungary. <i>Vector-Borne and Zoonotic Diseases</i> , <b>2014</b> , 14, 621-4	2.4	7
80	Adenovirus gastroenteritis in Hungary, 2003-2006. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , <b>2009</b> , 28, 997-9	5.3	7
79	The Clinical Burden of Rotavirus Disease. <i>Pediatric Infectious Disease Journal</i> , <b>2008</b> , 27, S33-S41	3.4	7
78	Phylogenetic analysis of a novel reassortant orthoreovirus strain detected in partridge ( <i>Perdix perdix</i> ). <i>Virus Research</i> , <b>2016</b> , 215, 99-103	6.4	7
77	Development of Molecular Methods for Rapid Differentiation of <i>Mycoplasma gallisepticum</i> Vaccine Strains from Field Isolates. <i>Journal of Clinical Microbiology</i> , <b>2019</b> , 57,	9.7	6

76	Coding-complete sequencing classifies parrot bornavirus 5 into a novel virus species. <i>Archives of Virology</i> , <b>2015</b> , 160, 2763-8	2.6	6
75	The core genome multi-locus sequence typing of <i>Mycoplasma anserisalpingitidis</i> . <i>BMC Genomics</i> , <b>2020</b> , 21, 403	4.5	6
74	Whole genome sequence of a goose haemorrhagic polyomavirus detected in Hungary. <i>Acta Microbiologica Et Immunologica Hungarica</i> , <b>2014</b> , 61, 221-7	1.8	6
73	Epidemiological dynamics of norovirus GII.4 variant New Orleans 2009. <i>Journal of General Virology</i> , <b>2015</b> , 96, 2919-2927	4.9	6
72	Frequent rearrangement may explain the structural heterogeneity in the 11th genome segment of lapine rotaviruses - short communication. <i>Acta Veterinaria Hungarica</i> , <b>2009</b> , 57, 453-61	1	6
71	Complete Genome Sequence of a Variant Pyrrhula pyrrhula polyomavirus 1 Strain Isolated from White-Headed Munia ( <i>Lonchura maja</i> ). <i>Genome Announcements</i> , <b>2016</b> , 4,		6
70	In Vitro and in Vivo Evaluation of Mutations in the NS Region of Lineage 2 West Nile Virus Associated with Neuroinvasiveness in a Mammalian Model. <i>Viruses</i> , <b>2016</b> , 8,	6.2	6
69	Study of Karolinska Institutet and Washington University polyomaviruses in tonsil, adenoid, throat swab and middle ear fluid samples. <i>Future Microbiology</i> , <b>2018</b> , 13, 1719-1730	2.9	6
68	Molecular detection of canine bufaviruses in wild canids. <i>Archives of Virology</i> , <b>2019</b> , 164, 2315-2320	2.6	5
67	Novel Orthobunyavirus Causing Severe Kidney Disease in Broiler Chickens, Malaysia, 2014-2017. <i>Emerging Infectious Diseases</i> , <b>2019</b> , 25, 1110-1117	10.2	5
66	Occurrence and genetic diversity of CRESS DNA viruses in wild birds: a Hungarian study. <i>Scientific Reports</i> , <b>2020</b> , 10, 7036	4.9	5
65	Characterization of the genomic sequence of a novel CRESS DNA virus identified in Eurasian jay ( <i>Garrulus glandarius</i> ). <i>Archives of Virology</i> , <b>2018</b> , 163, 285-289	2.6	5
64	Genetic Characterization of Providence Virus Isolated from Bat Guano in Hungary. <i>Genome Announcements</i> , <b>2016</b> , 4,		5
63	Analysis of GII.P7 and GII.6 noroviruses circulating in Italy during 2011-2016 reveals a replacement of lineages and complex recombination history. <i>Infection, Genetics and Evolution</i> , <b>2019</b> , 75, 103991	4.5	5
62	Antibodies for strain 2117-like vesiviruses (caliciviruses) in humans. <i>Virus Research</i> , <b>2015</b> , 210, 279-82	6.4	5
61	Serosurvey of pathogenic hantaviruses among forestry workers in Hungary. <i>International Journal of Occupational Medicine and Environmental Health</i> , <b>2014</b> , 27, 766-73	1.5	5
60	Identification of hantavirus infection by Western blot assay and TaqMan PCR in patients hospitalized with acute kidney injury. <i>Diagnostic Microbiology and Infectious Disease</i> , <b>2014</b> , 79, 166-70	2.9	5
59	Shared G12 VP7 gene among human and bovine rotaviruses detected in Cameroonian villages. <i>Acta Microbiologica Et Immunologica Hungarica</i> , <b>2013</b> , 60, 21-8	1.8	5

58	Complete Genome Sequences of Three ( sp. 1220) Strains. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	5
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54	Introduction and prolonged circulation of G12 rotaviruses in Sicily. <i>Epidemiology and Infection</i> , <b>2016</b> , 144, 1943-50	4.3	5
53	Development of a consensus reverse transcription PCR assay for the specific detection of tortoise picornaviruses. <i>Journal of Veterinary Diagnostic Investigation</i> , <b>2016</b> , 28, 309-14	1.5	5
52	Genotyping <i>Mycoplasma synoviae</i> : Development of a multi-locus variable number of tandem-repeats analysis and comparison with current molecular typing methods. <i>Veterinary Microbiology</i> , <b>2018</b> , 226, 41-49	3.3	5
51	Seroprevalence for 2117-like vesiviruses in Italian household dogs. <i>Veterinary Microbiology</i> , <b>2017</b> , 201, 14-17	3.3	4
50	Molecular epidemiology and phylodynamics of goose haemorrhagic polyomavirus. <i>Transboundary and Emerging Diseases</i> , <b>2020</b> , 67, 2602-2608	4.2	4
49	Molecular evolutionary analysis of type-1 human astroviruses identifies putative sites under selection pressure on the capsid protein. <i>Infection, Genetics and Evolution</i> , <b>2018</b> , 58, 199-208	4.5	4
48	Resurgence of rabies in Hungary during 2013-2014: An attempt to track the origin of identified strains. <i>Transboundary and Emerging Diseases</i> , <b>2018</b> , 65, e14-e24	4.2	4
47	Molecular characterization of Dobrava and Kurkino genotypes of Dobrava-Belgrade hantavirus detected in Hungary and Northern Croatia. <i>Virus Genes</i> , <b>2013</b> , 47, 546-9	2.3	4
46	Genome sequence of a mallard duck origin cyclovirus, DuACyV-1. <i>Archives of Virology</i> , <b>2017</b> , 162, 3925-3929	2.2	4
45	Novel adenovirus detected in kowari ( <i>Dasyuroides byrnei</i> ) with pneumonia. <i>Acta Microbiologica Et Immunologica Hungarica</i> , <b>2017</b> , 64, 81-90	1.8	4
44	Identification of astroviruses in bovine and buffalo calves with enteritis. <i>Research in Veterinary Science</i> , <b>2020</b> , 131, 59-68	2.5	4
43	Genetic heterogeneity of canine bufaviruses. <i>Transboundary and Emerging Diseases</i> , <b>2021</b> , 68, 802-812	4.2	4
42	Complete Genome Sequences of <i>Mycoplasma anatis</i> , <i>M. anseris</i> , and <i>M. cloacale</i> Type Strains. <i>Microbiology Resource Announcements</i> , <b>2018</b> , 7,	1.3	4
41	Comparison of clinical characteristics between astrovirus and rotavirus infections diagnosed in 1997 to 2002 in Hungary. <i>Acta Paediatrica, International Journal of Paediatrics</i> , <b>2005</b> , 94, 667-671	3.1	3



40	Multilocus sequence typing of the goose pathogen <i>Mycoplasma anserisalpingtonis</i> . <i>Veterinary Microbiology</i> , <b>2021</b> , 254, 108972	3.3	3
39	Complete genome analysis of contemporary G12P[8] rotaviruses reveals heterogeneity within Wa-like genomic constellation. <i>Infection, Genetics and Evolution</i> , <b>2016</b> , 44, 85-93	4.5	3
38	Complete Genome Sequence of a Genotype G23P[37] Pheasant Rotavirus Strain Identified in Hungary. <i>Genome Announcements</i> , <b>2016</b> , 4,		3
37	Analysis of structure-function relationship in porcine rotavirus A enterotoxin gene. <i>Journal of Veterinary Science</i> , <b>2018</b> , 19, 35-43	1.6	3
36	Genome sequence of a cluster A13 mycobacteriophage detected in <i>Mycobacterium phlei</i> over a half century ago. <i>Archives of Virology</i> , <b>2016</b> , 161, 209-12	2.6	2
35	Vaccine-associated rabies in red fox, Hungary. <i>Vaccine</i> , <b>2019</b> , 37, 3535-3538	4.1	2
34	Classification and characterization of a laboratory chicken rotavirus strain carrying G7P[35] neutralization antigens on the genotype 4 backbone gene configuration. <i>Biologicals</i> , <b>2014</b> , 42, 299-304	1.8	2
33	Emergence and characterisation of pandemic H1N1 influenza viruses in Hungarian swine herds. <i>Acta Veterinaria Hungarica</i> , <b>2013</b> , 61, 125-34	1	2
32	Multilocus Sequencing of Biotype Ovis Strains. <i>BioMed Research International</i> , <b>2017</b> , 2017, 1762162	3	2
31	Genome Sequences of Three Turkey Orthoreovirus Strains Isolated in Hungary. <i>Genome Announcements</i> , <b>2015</b> , 3,		2
30	Draft Genome Sequence of a Highly Virulent Rabbit <i>Staphylococcus aureus</i> Strain. <i>Genome Announcements</i> , <b>2015</b> , 3,		2
29	Comparison of clinical characteristics between astrovirus and rotavirus infections diagnosed in 1997 to 2002 in Hungary. <i>Acta Paediatrica, International Journal of Paediatrics</i> , <b>2005</b> , 94, 667-71	3.1	2
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27	Analysis of the full genome of human group C rotaviruses reveals lineage diversification and reassortment. <i>Journal of General Virology</i> , <b>2016</b> , 97, 1888-1898	4.9	2
26	Recombination Events Shape the Genomic Evolution of Infectious Bronchitis Virus in Europe. <i>Viruses</i> , <b>2021</b> , 13,	6.2	2
25	Molecular genetic investigations on <i>Balantidium ctenopharyngodoni</i> Chen, 1955, a parasite of the grass carp ( <i>Ctenopharyngodon idella</i> ). <i>Acta Veterinaria Hungarica</i> , <b>2016</b> , 64, 213-21	1	2
24	Genomic Epidemiology and Evolution of Duck Hepatitis A Virus. <i>Viruses</i> , <b>2021</b> , 13,	6.2	2
23	Genomic characterization of West Nile virus strains derived from mosquito samples obtained during 2013 Serbian outbreak. <i>Journal of Vector Borne Diseases</i> , <b>2016</b> , 53, 379-383	0.7	2



22	Molecular traces of a putative novel insect flavivirus from <i>Anopheles hyrcanus</i> mosquito species in Hungary. <i>Acta Virologica</i> , <b>2017</b> , 61, 127-129	2.2	1
21	Phylogenetic Analysis of Lednice. <i>Microorganisms</i> , <b>2019</b> , 7,	4.9	1
20	Identification and detection of mutations potentially associated with decreased susceptibility to macrolides and lincomycin in <i>Mycoplasma anserisalpingitidis</i> isolates.. <i>Veterinary Microbiology</i> , <b>2022</b> , 266, 109362	3.3	1
19	Genomic evolution of avian polyomaviruses with a focus on budgerigar fledgling disease virus. <i>Infection, Genetics and Evolution</i> , <b>2021</b> , 90, 104762	4.5	1
18	Molecular Epidemiology and Evolution of Rotaviruses <b>2016</b> , 279-299		1
17	Whole genome sequencing and phylogenetic characterization of brown bullhead ( <i>Ameiurus nebulosus</i> ) origin ranavirus strains from independent disease outbreaks. <i>Infection, Genetics and Evolution</i> , <b>2016</b> , 45, 402-407	4.5	1
16	Genomic Analysis of an Indian G8P[1] Caprine Rotavirus-A Strain Revealing Artiodactyl and DS-1-Like Human Multispecies Reassortment. <i>Frontiers in Veterinary Science</i> , <b>2020</b> , 7, 606661	3.1	1
15	Genomic Diversity of CRESS DNA Viruses in the Eukaryotic Virome of Swine Feces. <i>Microorganisms</i> , <b>2021</b> , 9,	4.9	1
14	Development of a molecular biological assay for the detection of markers related to decreased susceptibility to macrolides and lincomycin in <i>Mycoplasma hyorhinis</i> . <i>Acta Veterinaria Hungarica</i> , <b>2021</b> , 69, 110-115	1	1
13	Molecular characterization of rotaviruses in mid-western Turkey, 2006-2007. <i>Open Medicine (Poland)</i> , <b>2010</b> , 5, 640-645	2.2	0
12	An outbreak of neonatal enteritis in buffalo calves associated with astrovirus. <i>Journal of Veterinary Science</i> , <b>2021</b> , 22, e84	1.6	0
11	Genomic characterization of avian and neoavian orthoreoviruses detected in pheasants. <i>Virus Research</i> , <b>2021</b> , 297, 198349	6.4	0
10	Metagenomics revealing new virus species in farm and pet animals and aquaculture <b>2020</b> , 29-73		0
9	Phylogeny of Hungarian EBLV-1 strains using whole-genome sequence data. <i>Transboundary and Emerging Diseases</i> , <b>2021</b> , 68, 1323-1331	4.2	0
8	Genome sequencing of a novel variant of fowl adenovirus B reveals mosaicism in the pattern of homologous recombination events. <i>Archives of Virology</i> , <b>2021</b> , 166, 1477-1480	2.6	0
7	Viral gene expression profile of goose haemorrhagic polyomavirus in susceptible primary cells. <i>Avian Pathology</i> , <b>2021</b> , 50, 447-452	2.4	0
6	A novel gyrovirus in a common pheasant ( <i>Phasianus colchicus</i> ) with poult enteritis and mortality syndrome.. <i>Archives of Virology</i> , <b>2022</b> , 167, 1349	2.6	0
5	Development of mismatch amplification mutation assay for the rapid differentiation of K vaccine strain from field isolates. <i>Avian Pathology</i> , <b>2020</b> , 49, 317-324	2.4	

4	Screening adenoviruses in stool samples: evaluation of a genus-specific monoclonal antibody based enzyme immunoassay. <i>Acta Microbiologica Et Immunologica Hungarica</i> , <b>2003</b> , 50, 23-32	1.8
3	Coding-complete genome sequencing suggests that Newcastle disease virus challenge strain HertsB3 (IVMP) may represent a distinct genotype. <i>Archives of Virology</i> , <b>2020</b> , 165, 245-248	2.6
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1	Animal Rotaviruses. <i>Livestock Diseases and Management</i> , <b>2020</b> , 163-202	0.5