

Kristin Bnyai

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

273
papers

9,656
citations

45
h-index

89
g-index

286
ext. papers

10,880
ext. citations

5.2
avg. IF

6.02
L-index

#	Paper	IF	Citations
273	Identification and detection of mutations potentially associated with decreased susceptibility to macrolides and lincomycin in <i>Mycoplasma anserisalpingitidis</i> isolates.. <i>Veterinary Microbiology</i> , 2022 , 266, 109362	3.3	1
272	A novel gyrovirus in a common pheasant (<i>Phasianus colchicus</i>) with poult enteritis and mortality syndrome.. <i>Archives of Virology</i> , 2022 , 167, 1349	2.6	0
271	An outbreak of neonatal enteritis in buffalo calves associated with astrovirus. <i>Journal of Veterinary Science</i> , 2021 , 22, e84	1.6	0
270	Multilocus sequence typing of the goose pathogen <i>Mycoplasma anserisalpingitidis</i> . <i>Veterinary Microbiology</i> , 2021 , 254, 108972	3.3	3
269	Recombination Events Shape the Genomic Evolution of Infectious Bronchitis Virus in Europe. <i>Viruses</i> , 2021 , 13,	6.2	2
268	Genomic characterization of avian and neoavian orthoreoviruses detected in pheasants. <i>Virus Research</i> , 2021 , 297, 198349	6.4	0
267	Genomic evolution of avian polyomaviruses with a focus on budgerigar fledgling disease virus. <i>Infection, Genetics and Evolution</i> , 2021 , 90, 104762	4.5	1
266	Genetic heterogeneity of canine bufaviruses. <i>Transboundary and Emerging Diseases</i> , 2021 , 68, 802-812	4.2	4
265	Phylogeny of Hungarian EBLV-1 strains using whole-genome sequence data. <i>Transboundary and Emerging Diseases</i> , 2021 , 68, 1323-1331	4.2	0
264	Genome sequencing of a novel variant of fowl adenovirus B reveals mosaicism in the pattern of homologous recombination events. <i>Archives of Virology</i> , 2021 , 166, 1477-1480	2.6	0
263	Genomic Diversity of CRESS DNA Viruses in the Eukaryotic Virome of Swine Feces. <i>Microorganisms</i> , 2021 , 9,	4.9	1
262	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> , 2021 , 69, 110-115	1	1
261	Genomic Epidemiology and Evolution of Duck Hepatitis A Virus. <i>Viruses</i> , 2021 , 13,	6.2	2
260	Viral gene expression profile of goose haemorrhagic polyomavirus in susceptible primary cells. <i>Avian Pathology</i> , 2021 , 50, 447-452	2.4	0
259	Molecular epidemiology and phylodynamics of goose haemorrhagic polyomavirus. <i>Transboundary and Emerging Diseases</i> , 2020 , 67, 2602-2608	4.2	4
258	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> , 2020 , 245, 108663	3.3	10
257	Occurrence and genetic diversity of CRESS DNA viruses in wild birds: a Hungarian study. <i>Scientific Reports</i> , 2020 , 10, 7036	4.9	5

256	The core genome multi-locus sequence typing of <i>Mycoplasma anserisalpingitidis</i> . <i>BMC Genomics</i> , 2020 , 21, 403	4.5	6
255	Isolation of <i>Mycoplasma anserisalpingitidis</i> from swan goose (<i>Anser cygnoides</i>) in China. <i>BMC Veterinary Research</i> , 2020 , 16, 178	2.7	10
254	Development of mismatch amplification mutation assay for the rapid differentiation of K vaccine strain from field isolates. <i>Avian Pathology</i> , 2020 , 49, 317-324	2.4	
253	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> , 2020 , 177, 3635-3645	8.6	29
252	Complete genome analysis confirms that the pygmy marmoset adenovirus is a variant of the skunk adenovirus 1 - Short communication. <i>Acta Veterinaria Hungarica</i> , 2020 , 68, 323-327	1	2
251	Coding-complete genome sequencing suggests that Newcastle disease virus challenge strain HertsB3 (IVMP) may represent a distinct genotype. <i>Archives of Virology</i> , 2020 , 165, 245-248	2.6	
250	Mutations potentially associated with decreased susceptibility to fluoroquinolones, macrolides and lincomycin in <i>Mycoplasma synoviae</i> . <i>Veterinary Microbiology</i> , 2020 , 248, 108818	3.3	5
249	Retraction: Novel Orthobunyavirus Causing Severe Kidney Disease in Broiler Chickens, Malaysia, 2014-2017. <i>Emerging Infectious Diseases</i> , 2020 , 26, 1964	10.2	
248	Animal Rotaviruses. <i>Livestock Diseases and Management</i> , 2020 , 163-202	0.5	
247	Metagenomics revealing new virus species in farm and pet animals and aquaculture 2020 , 29-73		0
246	Identification of astroviruses in bovine and buffalo calves with enteritis. <i>Research in Veterinary Science</i> , 2020 , 131, 59-68	2.5	4
245	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> , 2020 , 7, 606661	3.1	1
244	Advances in Diagnostic Approaches for Viral Etiologies of Diarrhea: From the Lab to the Field. <i>Frontiers in Microbiology</i> , 2019 , 10, 1957	5.7	21
243	Molecular detection of canine bufaviruses in wild canids. <i>Archives of Virology</i> , 2019 , 164, 2315-2320	2.6	5
242	Novel Orthobunyavirus Causing Severe Kidney Disease in Broiler Chickens, Malaysia, 2014-2017. <i>Emerging Infectious Diseases</i> , 2019 , 25, 1110-1117	10.2	5
241	Vaccine-associated rabies in red fox, Hungary. <i>Vaccine</i> , 2019 , 37, 3535-3538	4.1	2
240	Development of Molecular Methods for Rapid Differentiation of <i>Mycoplasma gallisepticum</i> Vaccine Strains from Field Isolates. <i>Journal of Clinical Microbiology</i> , 2019 , 57,	9.7	6
239	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> , 2019 , 75, 103991	4.5	5

238	Coding-complete sequence of a vaccine-derived recombinant porcine reproductive and respiratory syndrome virus strain isolated in Hungary. <i>Archives of Virology</i> , 2019 , 164, 2605-2608	2.6	7
237	Phylogenetic Analysis of Lednice. <i>Microorganisms</i> , 2019 , 7,	4.9	1
236	Complete Genome Sequences of Three (sp. 1220) Strains. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	5
235	A Simple Method for Sample Preparation to Facilitate Efficient Whole-Genome Sequencing of African Swine Fever Virus. <i>Viruses</i> , 2019 , 11,	6.2	18
234	Identification of a novel parvovirus in domestic cats. <i>Veterinary Microbiology</i> , 2019 , 228, 246-251	3.3	19
233	Methylation Status of the Adeno-Associated Virus Type 2 (AAV2). <i>Viruses</i> , 2019 , 11,	6.2	8
232	First report and genetic characterization of porcine astroviruses of lineage 4 and 2 in diarrhoeic pigs in India. <i>Transboundary and Emerging Diseases</i> , 2019 , 66, 47-53	4.2	11
231	Tick-Borne Flaviviruses, with a Focus on Powassan Virus. <i>Clinical Microbiology Reviews</i> , 2019 , 32,	34	33
230	Molecular characterization of unusual bovine rotavirus A strains having high genetic relatedness with human rotavirus: evidence for zoonothropotic transmission. <i>Zoonoses and Public Health</i> , 2018 , 65, 431-442	2.9	13
229	Characterization of the genomic sequence of a novel CRESS DNA virus identified in Eurasian jay (<i>Garrulus glandarius</i>). <i>Archives of Virology</i> , 2018 , 163, 285-289	2.6	5
228	Molecular evolutionary analysis of type-1 human astroviruses identifies putative sites under selection pressure on the capsid protein. <i>Infection, Genetics and Evolution</i> , 2018 , 58, 199-208	4.5	4
227	Resurgence of rabies in Hungary during 2013-2014: An attempt to track the origin of identified strains. <i>Transboundary and Emerging Diseases</i> , 2018 , 65, e14-e24	4.2	4
226	Novel Parvovirus Related to Primate Bufaviruses in Dogs. <i>Emerging Infectious Diseases</i> , 2018 , 24, 1061-1068	16.2	22
225	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> , 2018 , 222, 85-90	3.3	13
224	Complete Genome Sequences of <i>Mycoplasma anatis</i> , <i>M. anseris</i> , and <i>M. cloacale</i> Type Strains. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1.3	4
223	Study of Karolinska Institutet and Washington University polyomaviruses in tonsil, adenoid, throat swab and middle ear fluid samples. <i>Future Microbiology</i> , 2018 , 13, 1719-1730	2.9	6
222	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> , 2018 , 226, 41-49	3.3	5
221	Analysis of structure-function relationship in porcine rotavirus A enterotoxin gene. <i>Journal of Veterinary Science</i> , 2018 , 19, 35-43	1.6	3

220	Genomic sequence and phylogenetic analyses of two novel orthoreovirus strains isolated from Pekin ducks in 2014 in Germany. <i>Virus Research</i> , 2018 , 257, 57-62	6.4	12
219	Molecular epidemiology and characterization of picobirnaviruses in small ruminant populations in India. <i>Infection, Genetics and Evolution</i> , 2018 , 63, 39-42	4.5	12
218	Viral gastroenteritis. <i>Lancet, The</i> , 2018 , 392, 175-186	4.0	152
217	Novel G9 rotavirus strains co-circulate in children and pigs, Taiwan. <i>Scientific Reports</i> , 2017 , 7, 40731	4.9	21
216	Genome analysis of canine astroviruses reveals genetic heterogeneity and suggests possible inter-species transmission. <i>Virus Research</i> , 2017 , 232, 162-170	6.4	19
215	Seroprevalence for 2117-like vesiviruses in Italian household dogs. <i>Veterinary Microbiology</i> , 2017 , 201, 14-17	3.3	4
214	Putative vaccine breakthrough event associated with heterotypic rotavirus infection in newborn calves, Turkey, 2015. <i>Veterinary Microbiology</i> , 2017 , 201, 7-13	3.3	12
213	Identification of a novel canine norovirus. <i>Infection, Genetics and Evolution</i> , 2017 , 52, 75-81	4.5	14
212	Mutations Associated with Decreased Susceptibility to Seven Antimicrobial Families in Field and Laboratory-Derived Mycoplasma bovis Strains. <i>Antimicrobial Agents and Chemotherapy</i> , 2017 , 61,	5.9	36
211	Candidate new rotavirus species in Schreiber's bats, Serbia. <i>Infection, Genetics and Evolution</i> , 2017 , 48, 19-26	4.5	127
210	Molecular traces of a putative novel insect flavivirus from Anopheles hyrcanus mosquito species in Hungary. <i>Acta Virologica</i> , 2017 , 61, 127-129	2.2	1
209	Genome sequence of a mallard duck origin cyclovirus, DuACyV-1. <i>Archives of Virology</i> , 2017 , 162, 3925-3929	2.2	4
208	Unexpected detection of porcine rotavirus C strains carrying human origin VP6 gene. <i>Veterinary Quarterly</i> , 2017 , 37, 252-261	8	16
207	Novel adenovirus detected in kowari (<i>Dasyuroides byrnei</i>) with pneumonia. <i>Acta Microbiologica Et Immunologica Hungarica</i> , 2017 , 64, 81-90	1.8	4
206	Isolation and complete genome characterization of novel reassortant orthoreovirus from common vole (<i>Microtus arvalis</i>). <i>Virus Genes</i> , 2017 , 53, 307-311	2.3	12
205	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> , 2017 , 227, 96-103	6.4	10
204	Sequence analysis of Schmallenberg virus genomes detected in Hungary. <i>Acta Microbiologica Et Immunologica Hungarica</i> , 2017 , 64, 373-384	1.8	7
203	Norovirus GII.17 as Major Epidemic Strain in Italy, Winter 2015-16. <i>Emerging Infectious Diseases</i> , 2017 , 23, 1206-1208	10.2	10

202	Avian Group D Rotaviruses: Structure, Epidemiology, Diagnosis, and Perspectives on Future Research Challenges. <i>Pathogens</i> , 2017 , 6,	4.5	7
201	Multilocus Sequencing of Biotype Ovis Strains. <i>BioMed Research International</i> , 2017 , 2017, 1762162	3	2
200	Genome sequence of a cluster A13 mycobacteriophage detected in Mycobacterium phlei over a half century ago. <i>Archives of Virology</i> , 2016 , 161, 209-12	2.6	2
199	Role for migratory wild birds in the global spread of avian influenza H5N8. <i>Science</i> , 2016 , 354, 213-217	33.3	252
198	Lineage diversification, homo- and heterologous reassortment and recombination shape the evolution of chicken orthoreoviruses. <i>Scientific Reports</i> , 2016 , 6, 36960	4.9	16
197	Genetic Characterization of Providence Virus Isolated from Bat Guano in Hungary. <i>Genome Announcements</i> , 2016 , 4,		5
196	Neuroinvasive influenza virus A(H5N8) in fattening ducks, Hungary, 2015. <i>Infection, Genetics and Evolution</i> , 2016 , 43, 418-23	4.5	12
195	Detection and molecular characterization of sapoviruses in dogs. <i>Infection, Genetics and Evolution</i> , 2016 , 38, 8-12	4.5	7
194	Whole genome sequencing reveals genetic heterogeneity of G3P[8] rotaviruses circulating in Italy. <i>Infection, Genetics and Evolution</i> , 2016 , 40, 253-261	4.5	14
193	Analysis of the full genome of human group C rotaviruses reveals lineage diversification and reassortment. <i>Journal of General Virology</i> , 2016 , 97, 1888-1898	4.9	2
192	Complete Genome Sequence of a Variant Pyrrhula pyrrhula polyomavirus 1 Strain Isolated from White-Headed Munia (Lonchura maja). <i>Genome Announcements</i> , 2016 , 4,		6
191	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> , 2016 , 8,	6.2	6
190	Molecular Epidemiology and Evolution of Rotaviruses 2016 , 279-299		1
189	Peptide-Recombinant VP6 Protein Based Enzyme Immunoassay for the Detection of Group A Rotaviruses in Multiple Host Species. <i>PLoS ONE</i> , 2016 , 11, e0159027	3.7	8
188	Complete genome analysis of contemporary G12P[8] rotaviruses reveals heterogeneity within Wa-like genomic constellation. <i>Infection, Genetics and Evolution</i> , 2016 , 44, 85-93	4.5	3
187	Equine-like G3 rotavirus in Hungary, 2015 - Is it a novel intergenogroup reassortant pandemic strain?. <i>Acta Microbiologica Et Immunologica Hungarica</i> , 2016 , 63, 243-55	1.8	45
186	Molecular genetic investigations on Balantidium ctenopharyngodoni Chen, 1955, a parasite of the grass carp (Ctenopharyngodon idella). <i>Acta Veterinaria Hungarica</i> , 2016 , 64, 213-21	1	2
185	Introduction and prolonged circulation of G12 rotaviruses in Sicily. <i>Epidemiology and Infection</i> , 2016 , 144, 1943-50	4.3	5

184	Multispecies reassortant bovine rotavirus strain carries a novel simian G3-like VP7 genotype. <i>Infection, Genetics and Evolution</i> , 2016 , 41, 63-72	4.5	12
183	Detection and sequencing of West Nile virus RNA from human urine and serum samples during the 2014 seasonal period. <i>Archives of Virology</i> , 2016 , 161, 1797-806	2.6	16
182	Whole genome characterization of a chelonian orthoreovirus strain identifies significant genetic diversity and may classify reptile orthoreoviruses into distinct species. <i>Virus Research</i> , 2016 , 215, 94-8	6.4	9
181	Taxonomy of the order Mononegavirales: update 2016. <i>Archives of Virology</i> , 2016 , 161, 2351-60	2.6	324
180	First molecular identification of <i>Dirofilaria</i> spp. (Onchocercidae) in mosquitoes from Serbia. <i>Parasitology Research</i> , 2016 , 115, 3257-60	2.4	11
179	Temporal variation in the distribution of type-1 human astrovirus lineages in a settled population over 14 years. <i>Archives of Virology</i> , 2016 , 161, 1633-7	2.6	8
178	Complete Genome Sequence of a Genotype G23P[37] Pheasant Rotavirus Strain Identified in Hungary. <i>Genome Announcements</i> , 2016 , 4,		3
177	Development of a consensus reverse transcription PCR assay for the specific detection of tortoise picornaviruses. <i>Journal of Veterinary Diagnostic Investigation</i> , 2016 , 28, 309-14	1.5	5
176	Sequencing and molecular modeling identifies candidate members of Caliciviridae family in bats. <i>Infection, Genetics and Evolution</i> , 2016 , 41, 227-232	4.5	12
175	Phylogenetic analysis of a novel reassortant orthoreovirus strain detected in partridge (<i>Perdix perdix</i>). <i>Virus Research</i> , 2016 , 215, 99-103	6.4	7
174	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> , 2016 , 45, 402-407	4.5	1
173	Genomic characterization of West Nile virus strains derived from mosquito samples obtained during 2013 Serbian outbreak. <i>Journal of Vector Borne Diseases</i> , 2016 , 53, 379-383	0.7	2
172	Sequencing and phylogenetic analysis identifies candidate members of a new picornavirus genus in terrestrial tortoise species. <i>Archives of Virology</i> , 2015 , 160, 811-6	2.6	16
171	Sequence and phylogenetic analysis identifies a putative novel gyrovirus 3 genotype in ferret feces. <i>Virus Genes</i> , 2015 , 50, 137-41	2.3	17
170	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> , 2015 , 35, 34-7	4.5	7
169	Reassortant human group C rotaviruses in Hungary. <i>Infection, Genetics and Evolution</i> , 2015 , 34, 410-4	4.5	8
168	Analysis of codon usage pattern evolution in avian rotaviruses and their preferred host. <i>Infection, Genetics and Evolution</i> , 2015 , 34, 17-25	4.5	17
167	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> , 2015 , 50, 310-5	2.3	9

166	Genetic heterogeneity and recombination in type-3 human astroviruses. <i>Infection, Genetics and Evolution</i> , 2015 , 32, 156-60	4.5	20
165	Emergence of multireassortant bluetongue virus serotype 4 in Hungary. <i>Infection, Genetics and Evolution</i> , 2015 , 33, 6-10	4.5	10
164	Zoonotic transmission of rotavirus: surveillance and control. <i>Expert Review of Anti-Infective Therapy</i> , 2015 , 13, 1337-50	5.5	66
163	First isolation and characterization of Brucella microti from wild boar. <i>BMC Veterinary Research</i> , 2015 , 11, 147	2.7	20
162	Candidate new rotavirus species in sheltered dogs, Hungary. <i>Emerging Infectious Diseases</i> , 2015 , 21, 660-30.2	30.2	149
161	Serologic survey of orthopoxvirus infection among rodents in Hungary. <i>Vector-Borne and Zoonotic Diseases</i> , 2015 , 15, 317-22	2.4	10
160	Coding-complete sequencing classifies parrot bornavirus 5 into a novel virus species. <i>Archives of Virology</i> , 2015 , 160, 2763-8	2.6	6
159	Unique genomic organization of a novel Avipoxvirus detected in turkey (Meleagris gallopavo). <i>Infection, Genetics and Evolution</i> , 2015 , 35, 221-9	4.5	29
158	Genetic characterization of a novel picornavirus detected in Miniopterus schreibersii bats. <i>Journal of General Virology</i> , 2015 , 96, 815-821	4.9	20
157	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> , 2015 , 160, 417-22 ^{2,6}	2.6	7
156	Ubiquitous 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> , 2015 , 62, 57-73	1.8	9
155	Genome Sequences of Three Turkey Orthoreovirus Strains Isolated in Hungary. <i>Genome Announcements</i> , 2015 , 3,		2
154	Detection and Full-Length Genome Characterization of Novel Canine Vesiviruses. <i>Emerging Infectious Diseases</i> , 2015 , 21, 1433-6	10.2	16
153	Epidemiological dynamics of norovirus GII.4 variant New Orleans 2009. <i>Journal of General Virology</i> , 2015 , 96, 2919-2927	4.9	6
152	Genetic diversity and recombination within bufaviruses: Detection of a novel strain in Hungarian bats. <i>Infection, Genetics and Evolution</i> , 2015 , 33, 288-92	4.5	31
151	Circulation of Dirofilaria repens, Setaria tundra, and Onchocercidae species in Hungary during the period 2011-2013. <i>Veterinary Parasitology</i> , 2015 , 214, 108-13	2.8	27
150	Draft Genome Sequence of a Highly Virulent Rabbit Staphylococcus aureus Strain. <i>Genome Announcements</i> , 2015 , 3,		2
149	Identification of a Bovine Enteric Calicivirus, Kékklareli Virus, Distantly Related to Neboviruses, in Calves with Enteritis in Turkey. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 3614-7	9.7	15

148	Novel bocaparvoviruses in rabbits. <i>Veterinary Journal</i> , 2015 , 206, 131-5	2.5	18
147	Antibodies for strain 2117-like vesiviruses (caliciviruses) in humans. <i>Virus Research</i> , 2015 , 210, 279-82	6.4	5
146	Full genome sequence analysis of a wild, non-MLV-related type 2 Hungarian PRRSV variant isolated in Europe. <i>Virus Research</i> , 2015 , 200, 1-8	6.4	10
145	Canine rotavirus C strain detected in Hungary shows marked genotype diversity. <i>Journal of General Virology</i> , 2015 , 96, 3059-3071	4.9	14
144	The complete genome sequence of a European goose reovirus strain. <i>Archives of Virology</i> , 2014 , 159, 2165-9	2.6	7
143	The fecal virome of domesticated animals. <i>VirusDisease</i> , 2014 , 25, 150-7	3.4	8
142	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
141	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
140	Putative novel lineage of West Nile virus in <i>Uranotaenia unguiculata</i> mosquito, Hungary. <i>VirusDisease</i> , 2014 , 25, 500-3	3.4	15
139	Classification and characterization of a laboratory chicken rotavirus strain carrying G7P[35] neutralization antigens on the genotype 4 backbone gene configuration. <i>Biologicals</i> , 2014 , 42, 299-304	1.8	2
138	Monitoring of West Nile virus in mosquitoes between 2011-2012 in Hungary. <i>Vector-Borne and Zoonotic Diseases</i> , 2014 , 14, 648-55	2.4	13
137	Detection of shared genes among Asian and European waterfowl reoviruses in the whole genome constellations. <i>Infection, Genetics and Evolution</i> , 2014 , 28, 55-7	4.5	10
136	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> , 2014 , 14, 847-56	25.5	146
135	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> , 2014 , 28, 446-61	4.5	131
134	Molecular epidemiology of human G2P[4] rotaviruses in Taiwan, 2004-2011. <i>Infection, Genetics and Evolution</i> , 2014 , 28, 530-6	4.5	9
133	Rotavirus strains in neglected animal species including lambs, goats and camelids. <i>VirusDisease</i> , 2014 , 25, 215-22	3.4	18
132	Genome sequencing identifies genetic and antigenic divergence of porcine picobirnaviruses. <i>Journal of General Virology</i> , 2014 , 95, 2233-2239	4.9	17
131	Whole genome sequence of a goose haemorrhagic polyomavirus detected in Hungary. <i>Acta Microbiologica Et Immunologica Hungarica</i> , 2014 , 61, 221-7	1.8	6

130	Epidemiology, phylogeny, and evolution of emerging enteric Picobirnaviruses of animal origin and their relationship to human strains. <i>BioMed Research International</i> , 2014 , 2014, 780752	3	47
129	Novel European lineages of bat astroviruses identified in Hungary. <i>Acta Virologica</i> , 2014 , 58, 95-8	2.2	12
128	649 Distribution of rotavirus strains and strain-specific effectiveness following vaccine introduction: a global review and meta-analysis. <i>Open Forum Infectious Diseases</i> , 2014 , 1, S35-S35	1	78
127	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> , 2014 , 159, 3185-96	2.6	25
126	Serosurvey of pathogenic hantaviruses among forestry workers in Hungary. <i>International Journal of Occupational Medicine and Environmental Health</i> , 2014 , 27, 766-73	1.5	5
125	Complete genome analysis identifies Tvāminne avian virus as a candidate new species within the genus Orthoreovirus. <i>Journal of General Virology</i> , 2014 , 95, 898-904	4.9	17
124	Molecular survey of RNA viruses in Hungarian bats: discovering novel astroviruses, coronaviruses, and caliciviruses. <i>Vector-Borne and Zoonotic Diseases</i> , 2014 , 14, 846-55	2.4	45
123	MLB1 astrovirus in children with gastroenteritis, Italy. <i>Emerging Infectious Diseases</i> , 2014 , 20, 169-70	10.2	13
122	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> , 2014 , 14, 621-4	2.4	7
121	Tembusu-like flavivirus (Perak virus) as the cause of neurological disease outbreaks in young Pekin ducks. <i>Avian Pathology</i> , 2014 , 43, 552-60	2.4	62
120	Molecular detection and characterization of human gyroviruses identified in the ferret fecal virome. <i>Archives of Virology</i> , 2014 , 159, 3401-6	2.6	25
119	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> , 2014 , 28, 537-60	4.5	24
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