Szilvia L Farkas

List of Publications by Year
in descending order

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39
papers

1,436
citations

430874

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39
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39
docs citations

39
times ranked

2191
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic characterization of avian and neoavian orthoreoviruses detected in pheasants. Virus Research, 2021, 297, 198349.	2.2	3
2	Genomic sequence and phylogenetic analyses of two novel orthoreovirus strains isolated from Pekin ducks in 2014 in Germany. Virus Research, 2018, 257, 57-62.	2.2	17
3	Novel adenovirus detected in kowari (Dasyuroides byrnei) with pneumonia. Acta Microbiologica Et Immunologica Hungarica, 2017, 64, 81-90.	0.8	5
4	Isolation and complete genome characterization of novel reassortant orthoreovirus from common vole (Microtus arvalis). Virus Genes, 2017, 53, 307-311.	1.6	17
5	Whole genome sequencing of a rare rotavirus from archived stool sample demonstrates independent zoonotic origin of human G8P[14] strains in Hungary. Virus Research, 2017, 227, 96-103.	2.2	13
6	Detection and sequencing of West Nile virus RNA from human urine and serum samples during the 2014 seasonal period. Archives of Virology, 2016, 161, 1797-1806.	2.1	25
7	Whole genome characterization of a chelonian orthoreovirus strain identifies significant genetic diversity and may classify reptile orthoreoviruses into distinct species. Virus Research, 2016, 215, 94-98.	2.2	10
8	Taxonomy of the order Mononegavirales: update 2016. Archives of Virology, 2016, 161, 2351-2360.	2.1	407
9	Complete Genome Sequence of a Genotype G23P[37] Pheasant Rotavirus Strain Identified in Hungary. Genome Announcements, 2016, 4, .	0.8	6
10	Development of a consensus reverse transcription PCR assay for the specific detection of tortoise picornaviruses. Journal of Veterinary Diagnostic Investigation, 2016, 28, 309-314.	1.1	7
11	Phylogenetic analysis of a novel reassortant orthoreovirus strain detected in partridge (Perdix) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	2.2	13
12	Whole genome sequencing and phylogenetic characterization of brown bullhead (Ameiurus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 307 Evolution, 2016, 45, 402-407.	2.3	5
13	Lineage diversification, homo- and heterologous reassortment and recombination shape the evolution of chicken orthoreoviruses. Scientific Reports, 2016, 6, 36960.	3.3	23
14	Neuroinvasive influenza virus A(H5N8) in fattening ducks, Hungary, 2015. Infection, Genetics and Evolution, 2016, 43, 418-423.	2.3	15
15	Ubiquiter circovirus sequences raise challenges in laboratory diagnosis: The case of honey bee and bee mite, reptiles, and free living amoebae. Acta Microbiologica Et Immunologica Hungarica, 2015, 62, 57-73.	0.8	13
16	Genome Sequences of Three Turkey Orthoreovirus Strains Isolated in Hungary. Genome Announcements, 2015, 3, .	0.8	3
17	Sequencing and phylogenetic analysis identifies candidate members of a new picornavirus genus in terrestrial tortoise species. Archives of Virology, 2015, 160, 811-816.	2.1	18
18	Reassortant human group C rotaviruses in Hungary. Infection, Genetics and Evolution, 2015, 34, 410-414.	2.3	10

#	ARTICLE	IF	CITATIONS
19	Zoonotic transmission of rotavirus: surveillance and control. Expert Review of Anti-Infective Therapy, 2015, 13, 1337-1350.	4.4	95
20	Candidate New Rotavirus Species in Sheltered Dogs, Hungary. Emerging Infectious Diseases, 2015, 21, 660-663.	4.3	170
21	Coding-complete sequencing classifies parrot bornavirus 5 into a novel virus species. Archives of Virology, 2015, 160, 2763-2768.	2.1	6
22	Unique genomic organization of a novel Avipoxvirus detected in turkey (Meleagris gallopavo). Infection, Genetics and Evolution, 2015, 35, 221-229.	2.3	39
23	Complete genome analysis identifies TvÃrminne avian virus as a candidate new species within the genus Orthoreovirus. Journal of General Virology, 2014, 95, 898-904.	2.9	19
24	Full genome characterization of human Rotavirus A strains isolated in Cameroon, 2010â€"2011: Diverse combinations of the G and P genes and lack of reassortment of the backbone genes. Infection, Genetics and Evolution, 2014, 28, 537-560.	2.3	31
25	Whole-genome sequencing of a green bush viper reovirus reveals a shared evolutionary history between reptilian and unusual mammalian orthoreoviruses. Archives of Virology, 2014, 159, 153-158.	2.1	24
26	The complete genome sequence of a European goose reovirus strain. Archives of Virology, 2014, 159, 2165-2169.	2.1	10
27	The fecal virome of domesticated animals. VirusDisease, 2014, 25, 150-157.	2.0	11
28	Classification and characterization of a laboratory chicken rotavirus strain carrying G7P[35] neutralization antigens on the genotype 4 backbone gene configuration. Biologicals, 2014, 42, 299-304.	1.4	4
29	Detection of shared genes among Asian and European waterfowl reoviruses in the whole genome constellations. Infection, Genetics and Evolution, 2014, 28, 55-57.	2.3	16
30	Rotavirus strains in neglected animal species including lambs, goats and camelids. VirusDisease, 2014, 25, 215-222.	2.0	25
31	Detection and characterization of a divergent avian reovirus strain from a broiler chicken with central nervous system disease. Archives of Virology, 2013, 158, 2583-2588.	2.1	34
32	Integrated circoviral rep-like sequences in the genome of cyprinid fish. Virus Genes, 2013, 47, 374-377.	1.6	13
33	Novel mastadenovirus infection and clinical disease in a pygmy marmoset (Callithrix [Cebuella]) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.9	14
34	Novel NSP4 genotype in a camel G10P[15] rotavirus strain. Acta Microbiologica Et Immunologica Hungarica, 2012, 59, 411-421.	0.8	33
35	First detection and analysis of a fish circovirus. Journal of General Virology, 2011, 92, 1817-1821.	2.9	67
36	Adenovirus and mycoplasma infection in an ornate box turtle (Terrapene ornata ornata) in Hungary. Veterinary Microbiology, 2009, 138, 169-173.	1.9	48

#	Article	IF	Citations
37	Completion of the genome analysis of snake adenovirus type 1, a representative of the reptilian lineage within the novel genus Atadenovirus. Virus Research, 2008, 132, 132-139.	2.2	43
38	A parvovirus isolated from royal python (Python regius) is a member of the genus Dependovirus. Journal of General Virology, 2004, 85, 555-561.	2.9	62
39	Genomic and phylogenetic analyses of an adenovirus isolated from a corn snake (Elaphe guttata) imply a common origin with members of the proposed new genus Atadenovirus. Journal of General Virology, 2002, 83, 2403-2410.	2.9	62