

Mami Oba

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

731
citations

516215

16
h-index

610482

24
g-index

55
all docs

55
docs citations

55
times ranked

991
citing authors

#	ARTICLE	IF	CITATIONS
1	Validation of the usefulness of 26S rDNA D1/D2, internal transcribed spacer, and intergenic spacer 1 for molecular epidemiological analysis of <i>Macrorhabdus ornithogaster</i> . <i>Journal of Veterinary Medical Science</i> , 2022, 84, 244-250.	0.3	1
2	First isolation and genomic characterization of bovine parechovirus from faecal samples of cattle in Japan. <i>Journal of General Virology</i> , 2022, 103, .	1.3	4
3	Genomic diversity and intragenic recombination of species C rotaviruses. <i>Journal of General Virology</i> , 2022, 103, .	1.3	8
4	Metagenomic identification, sequencing, and genome analysis of porcine hepe-astroviruses (bastroviruses) in porcine feces in Japan. <i>Infection, Genetics and Evolution</i> , 2021, 88, 104664.	1.0	2
5	Novel herpesvirus discovered in walrus liver. <i>Virus Genes</i> , 2021, 57, 228-232.	0.7	0
6	Isolation and characterization of mammalian orthoreovirus type 3 from a fecal sample from a wild boar in Japan. <i>Archives of Virology</i> , 2021, 166, 1671-1680.	0.9	6
7	Natto extract, a Japanese fermented soybean food, directly inhibits viral infections including SARS-CoV-2 in vitro. <i>Biochemical and Biophysical Research Communications</i> , 2021, 570, 21-25.	1.0	19
8	African pygmy hedgehog adenovirus: Virus replication, virus-induced cytopathogenesis and activation of mitogen-activated protein kinase signaling pathways in infected MDCK cells. <i>Research in Veterinary Science</i> , 2021, 139, 152-158.	0.9	0
9	Complete genome sequencing and genetic analysis of a Japanese porcine torovirus strain detected in swine feces. <i>Archives of Virology</i> , 2020, 165, 471-477.	0.9	7
10	Multiple genotypes of enterovirus G carrying a papain-like cysteine protease (PL-CP) sequence circulating on two pig farms in Japan: first identification of enterovirus G10 carrying a PL-CP sequence. <i>Archives of Virology</i> , 2020, 165, 2909-2914.	0.9	3
11	ATeam technology for detecting early signs of viral cytopathic effect. <i>Journal of Veterinary Medical Science</i> , 2020, 82, 387-393.	0.3	2
12	Genetic diversity of enterovirus G detected in faecal samples of wild boars in Japan: identification of novel genotypes carrying a papain-like cysteine protease sequence. <i>Journal of General Virology</i> , 2020, 101, 840-852.	1.3	5
13	Detection of Viral Infection and Subsequent Apoptosis in Cells by Raman Scattering Microspectroscopy. , 2020, , .		0
14	First identification of Sapoviruses in wild boar. <i>Virus Research</i> , 2019, 271, 197680.	1.1	7
15	Complete genome sequencing and genetic characterization of porcine sapovirus genogroup (G) X and GXI: GVI, GVII, GX, and GXI sapoviruses share common genomic features and form a unique porcine SaV clade. <i>Infection, Genetics and Evolution</i> , 2019, 75, 103959.	1.0	5
16	A novel defective recombinant porcine enterovirus G virus carrying a porcine torovirus papain-like cysteine protease gene and a putative anti-apoptosis gene in place of viral structural protein genes. <i>Infection, Genetics and Evolution</i> , 2019, 75, 103975.	1.0	14
17	Phylogenetic analysis of novel posaviruses detected in feces of Japanese pigs with posaviruses and posaviruses of vertebrates and invertebrates. <i>Archives of Virology</i> , 2019, 164, 2147-2151.	0.9	8
18	Encephalomyocarditis virus is potentially derived from eastern bent-wing bats living in East Asian countries. <i>Virus Research</i> , 2019, 259, 62-67.	1.1	6

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19	Complete genomic analysis and molecular characterization of Japanese porcine sapeloviruses. <i>Virus Genes</i> , 2019, 55, 198-208.	0.7	9
20	A new comprehensive method for detection of livestock-related pathogenic viruses using a target enrichment system. <i>Biochemical and Biophysical Research Communications</i> , 2018, 495, 1871-1877.	1.0	7
21	Metagenomic identification and sequence analysis of a Teschovirus A-related virus in porcine feces in Japan, 2014–2016. <i>Infection, Genetics and Evolution</i> , 2018, 66, 210-216.	1.0	10
22	Dembo polymerase chain reaction technique for detection of bovine abortion, diarrhea, and respiratory disease complex infectious agents in potential vectors and reservoirs. <i>Journal of Veterinary Science</i> , 2018, 19, 350.	0.5	5
23	Whole genome analysis of a novel picornavirus related to the Enterovirus/Sapelovirus supergroup from porcine feces in Japan. <i>Virus Research</i> , 2018, 257, 68-73.	1.1	3
24	Genetic diversity and recombination of enterovirus G strains in Japanese pigs: High prevalence of strains carrying a papain-like cysteine protease sequence in the enterovirus G population. <i>PLoS ONE</i> , 2018, 13, e0190819.	1.1	30
25	Diversity in VP3, NSP3, and NSP4 of rotavirus B detected from Japanese cattle. <i>Infection, Genetics and Evolution</i> , 2017, 49, 97-103.	1.0	10
26	Whole genome analysis of porcine astroviruses detected in Japanese pigs reveals genetic diversity and possible intra-genotypic recombination. <i>Infection, Genetics and Evolution</i> , 2017, 50, 38-48.	1.0	30
27	Complete genome analysis of porcine kobuviruses from the feces of pigs in Japan. <i>Virus Genes</i> , 2017, 53, 593-602.	0.7	8
28	<i>Mycobacterium avium</i> subsp. <i>hominissuis</i> meningoencephalitis in a cat. <i>Veterinary Microbiology</i> , 2017, 204, 43-45.	0.8	7
29	Genetic diversity and intergenogroup recombination events of sapoviruses detected from feces of pigs in Japan. <i>Infection, Genetics and Evolution</i> , 2017, 55, 209-217.	1.0	20
30	Generation of a novel live rabies vaccine strain with a high level of safety by introducing attenuating mutations in the nucleoprotein and glycoprotein. <i>Vaccine</i> , 2017, 35, 5622-5628.	1.7	8
31	Molecular characteristics and prevalence of small ruminant lentiviruses in goats in Japan. <i>Archives of Virology</i> , 2017, 162, 3007-3015.	0.9	5
32	Identification of a novel bovine enterovirus possessing highly divergent amino acid sequences in capsid protein. <i>BMC Microbiology</i> , 2017, 17, 18.	1.3	17
33	Development of a one-run real-time PCR detection system for pathogens associated with bovine respiratory disease complex. <i>Journal of Veterinary Medical Science</i> , 2017, 79, 517-523.	0.3	70
34	Discovery of fur seal feces-associated circular DNA virus in swine feces in Japan. <i>Journal of Veterinary Medical Science</i> , 2017, 79, 1664-1666.	0.3	5
35	Involvement of the 3'™ Untranslated Region in Encapsidation of the Hepatitis C Virus. <i>PLoS Pathogens</i> , 2016, 12, e1005441.	2.1	21
36	Whole genome sequences of Japanese porcine species C rotaviruses reveal a high diversity of genotypes of individual genes and will contribute to a comprehensive, generally accepted classification system. <i>Infection, Genetics and Evolution</i> , 2016, 44, 106-113.	1.0	17

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37	Characterization and phylogenetic analysis of a novel picornavirus from swine feces in Japan. Archives of Virology, 2016, 161, 1685-1690.	0.9	9
38	Development of a novel detection system for microbes from bovine diarrhea by real-time PCR. Journal of Veterinary Medical Science, 2016, 78, 383-389.	0.3	26
39	Detection of novel kobu-like viruses in Japanese black cattle in Japan. Journal of Veterinary Medical Science, 2016, 78, 321-324.	0.3	12
40	A novel Bunyavirus from the soft tick, <i>Argas vespertilionis</i>, in Japan. Journal of Veterinary Medical Science, 2016, 78, 443-445.	0.3	26
41	Identification of further diversity among posaviruses. Archives of Virology, 2016, 161, 3541-3548.	0.9	12
42	Whole genome analysis of Japanese bovine toroviruses reveals natural recombination between porcine and bovine toroviruses. Infection, Genetics and Evolution, 2016, 38, 90-95.	1.0	13
43	H2 genotypes of G4P[6], G5P[7], and G9[23] porcine rotaviruses show super-short RNA electropherotypes. Veterinary Microbiology, 2015, 176, 250-256.	0.8	17
44	Full genome analysis of bovine astrovirus from fecal samples of cattle in Japan: identification of possible interspecies transmission of bovine astrovirus. Archives of Virology, 2015, 160, 2491-2501.	0.9	65
45	Isolation and characterization of a novel Rhabdovirus from a wild boar (<i>Sus scrofa</i>) in Japan. Veterinary Microbiology, 2015, 179, 197-203.	0.8	5
46	Detection of a novel herpesvirus from bats in the Philippines. Virus Genes, 2015, 51, 136-139.	0.7	19
47	Identification and complete genome analysis of a novel bovine picornavirus in Japan. Virus Research, 2015, 210, 205-212.	1.1	20
48	Detection of enterovirus genome sequence from diarrheal feces of goat. Virus Genes, 2014, 48, 550-552.	0.7	16
49	Identification of novel bovine group A rotavirus G15P[14] strain from epizootic diarrhea of adult cows by de novo sequencing using a next-generation sequencer. Veterinary Microbiology, 2014, 171, 66-73.	0.8	35
50	Detection of Bovine Group A Rotavirus Using Rapid Antigen Detection Kits, RT-PCR and Next-Generation DNA Sequencing. Journal of Veterinary Medical Science, 2013, 75, 1651-1655.	0.3	10
51	Novel DNA virus isolated from samples showing endothelial cell necrosis in the Japanese eel, <i>Anguilla japonica</i> . Virology, 2011, 412, 179-187.	1.1	45
52	A novel sapelovirus-like virus isolation from wild boar. Virus Genes, 2011, 43, 243-248.	0.7	21