

Tomoichiro Oka

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/107393/publications.pdf>

Version: 2024-02-01

46
papers

1,686
citations

361388

20
h-index

289230

40
g-index

48
all docs

48
docs citations

48
times ranked

1367
citing authors

#	ARTICLE	IF	CITATIONS
1	Atomic Structure of the Human Sapovirus Capsid Reveals a Unique Capsid Protein Conformation in Caliciviruses. <i>Journal of Virology</i> , 2022, 96, e0029822.	3.4	7
2	Sapoviruses detected from acute gastroenteritis outbreaks and hospitalized children in Taiwan. <i>Journal of the Formosan Medical Association</i> , 2021, 120, 1591-1601.	1.7	7
3	A human intestinal cell line suitable for the propagation of Type 1-6 human parechovirus with a clear cytopathic effect. <i>Japanese Journal of Infectious Diseases</i> , 2021, , .	1.2	0
4	The predicted stem-loop structure in the 3' end of the human norovirus antigenomic sequence is required for its genomic RNA synthesis by its RdRp. <i>Journal of Biological Chemistry</i> , 2021, 297, 101225.	3.4	2
5	Caliciviruses induce mRNA of tumor necrosis factor α via their protease activity. <i>Virus Research</i> , 2021, 306, 198595.	2.2	1
6	Human sapovirus propagation in human cell lines supplemented with bile acids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 32078-32085.	7.1	22
7	Polymerase chain reaction primer sets for the detection of genetically diverse human sapoviruses. <i>Archives of Virology</i> , 2020, 165, 2335-2340.	2.1	9
8	First identification of Sapoviruses in wild boar. <i>Virus Research</i> , 2019, 271, 197680.	2.2	7
9	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.	2.3	5
10	Broadly reactive real-time reverse transcription-polymerase chain reaction assay for the detection of human sapovirus genotypes. <i>Journal of Medical Virology</i> , 2019, 91, 370-377.	5.0	11
11	First Complete Genome Sequences of Human Sapovirus Strains Classified as GI.3, GI.4, GI.6, GI.7, and GII.7. <i>Genome Announcements</i> , 2018, 6, .	0.8	6
12	Attempts to grow human noroviruses, a sapovirus, and a bovine norovirus in vitro. <i>PLoS ONE</i> , 2018, 13, e0178157.	2.5	41
13	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.	2.3	20
14	First complete genome sequences of genogroup V, genotype 3 porcine sapoviruses: common 5' terminal genomic feature of sapoviruses. <i>Virus Genes</i> , 2017, 53, 848-855.	1.6	16
15	Genetic Characterization and Classification of Human and Animal Sapoviruses. <i>PLoS ONE</i> , 2016, 11, e0156373.	2.5	71
16	Epidemics of GI.2 sapovirus in gastroenteritis outbreaks during 2012~2013 in Osaka City, Japan. <i>Journal of Medical Virology</i> , 2016, 88, 1187-1193.	5.0	18
17	Mechanism of Cell Culture Adaptation of an Enteric Calicivirus, the Porcine Sapovirus Cowden Strain. <i>Journal of Virology</i> , 2016, 90, 1345-1358.	3.4	14
18	Antigenic Relationships among Porcine Epidemic Diarrhea Virus and Transmissible Gastroenteritis Virus Strains. <i>Journal of Virology</i> , 2015, 89, 3332-3342.	3.4	96

#	ARTICLE	IF	CITATIONS
19	Comprehensive Review of Human Sapoviruses. <i>Clinical Microbiology Reviews</i> , 2015, 28, 32-53.	13.6	271
20	Complete Genome Sequence of a Novel GV.2 Sapovirus Strain, NGY-1, Detected from a Suspected Foodborne Gastroenteritis Outbreak. <i>Genome Announcements</i> , 2015, 3, .	0.8	23
21	Genomic characterization of a US porcine kobuvirus strain. <i>Archives of Microbiology</i> , 2015, 197, 1033-1040.	2.2	7
22	Cell culture isolation and sequence analysis of genetically diverse US porcine epidemic diarrhea virus strains including a novel strain with a large deletion in the spike gene. <i>Veterinary Microbiology</i> , 2014, 173, 258-269.	1.9	150
23	Development of a novel single step reverse genetics system for feline calicivirus. <i>Journal of Virological Methods</i> , 2014, 207, 178-181.	2.1	19
24	First Complete Genome Sequences of Genogroup VI Porcine Sapoviruses. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
25	Detection of Multiple Human Sapoviruses from Imported Frozen Individual Clams. <i>Food and Environmental Virology</i> , 2013, 5, 119-125.	3.4	12
26	First Complete Genome Sequence of a Genogroup II Genotype 18 Porcine Norovirus, Strain QW125. <i>Genome Announcements</i> , 2013, 1, .	0.8	2
27	Prevalence of Porcine Noroviruses, Molecular Characterization of Emerging Porcine Sapoviruses from Finisher Swine in the United States, and Unified Classification Scheme for Sapoviruses. <i>Journal of Clinical Microbiology</i> , 2013, 51, 2344-2353.	3.9	66
28	Complete Genome Sequence of the Feline Calicivirus 2280 Strain from the American Tissue Culture Collection. <i>Genome Announcements</i> , 2013, 1, .	0.8	6
29	Phylogenetic Analysis of the Nonstructural and Structural Protein Encoding Region Sequences, Indicating Successive Appearance of Genomically Diverse Sapovirus Strains from Gastroenteritis Patients. <i>Japanese Journal of Infectious Diseases</i> , 2013, 66, 454-457.	1.2	19
30	A confirmation of sapovirus re-infection gastroenteritis cases with different genogroups and genetic shifts in the evolving sapovirus genotypes, 2002-2011. <i>Archives of Virology</i> , 2012, 157, 1999-2003.	2.1	28
31	Human sapovirus classification based on complete capsid nucleotide sequences. <i>Archives of Virology</i> , 2012, 157, 349-352.	2.1	81
32	Comparative site-directed mutagenesis in the catalytic amino acid triad in calicivirus proteases. <i>Microbiology and Immunology</i> , 2011, 55, 108-114.	1.4	8
33	Bioluminescence technologies to detect calicivirus protease activity in cell-free system and in infected cells. <i>Antiviral Research</i> , 2011, 90, 9-16.	4.1	12
34	Molecular characterization of sapovirus detected in a gastroenteritis outbreak at a wedding hall. <i>Journal of Medical Virology</i> , 2010, 82, 720-726.	5.0	23
35	Detection of sapoviruses and noroviruses in an outbreak of gastroenteritis linked genetically to shellfish. <i>Journal of Medical Virology</i> , 2010, 82, 1247-1254.	5.0	55
36	Detection and Genetic Analysis of Human Sapoviruses in River Water in Japan. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2461-2467.	3.1	47

#	ARTICLE	IF	CITATIONS
37	Structural and biological constraints on diversity of regions immediately upstream of cleavage sites in calicivirus precursor proteins. <i>Virology</i> , 2009, 394, 119-129.	2.4	20
38	Surveillance of pathogens in outpatients with gastroenteritis and characterization of sapovirus strains between 2002 and 2007 in Kumamoto Prefecture, Japan. <i>Journal of Medical Virology</i> , 2009, 81, 1117-1127.	5.0	67
39	Quantitative analysis of fecal sapovirus shedding: identification of nucleotide substitutions in the capsid protein during prolonged excretion. <i>Archives of Virology</i> , 2009, 154, 689-693.	2.1	26
40	Self-assembly of sapovirus recombinant virus-like particles from polyprotein in mammalian cells. <i>Microbiology and Immunology</i> , 2009, 53, 49-52.	1.4	7
41	Distinct genotype and antigenicity among genogroup II sapoviruses. <i>Microbiology and Immunology</i> , 2009, 53, 417-420.	1.4	11
42	Characterization of sapoviruses detected in gastroenteritis outbreaks and identification of asymptomatic adults with high viral load. <i>Journal of Clinical Virology</i> , 2009, 45, 67-71.	3.1	29
43	Highly Conserved Configuration of Catalytic Amino Acid Residues among Calicivirus-Encoded Proteases. <i>Journal of Virology</i> , 2007, 81, 6798-6806.	3.4	26
44	Detection of human sapovirus by real-time reverse transcription-polymerase chain reaction. <i>Journal of Medical Virology</i> , 2006, 78, 1347-1353.	5.0	228
45	Identification of the cleavage sites of sapovirus open reading frame 1 polyprotein. <i>Journal of General Virology</i> , 2006, 87, 3329-3338.	2.9	34
46	Proteolytic Processing of Sapovirus ORF1 Polyprotein. <i>Journal of Virology</i> , 2005, 79, 7283-7290.	3.4	54