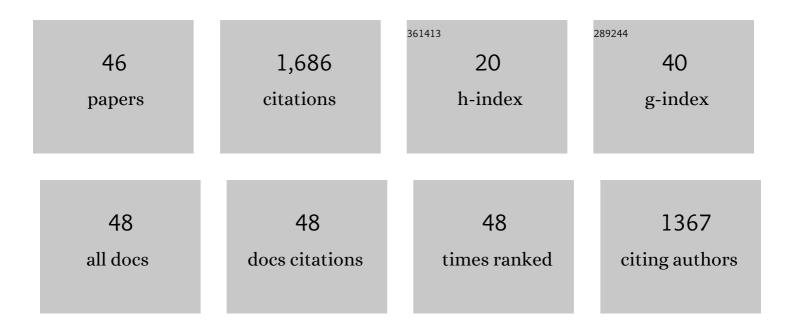
Tomoichiro Oka

List of Publications by Year in descending order

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Τομοιςμίρο Οκλ

#	Article	IF	CITATIONS
1	Atomic Structure of the Human Sapovirus Capsid Reveals a Unique Capsid Protein Conformation in Caliciviruses. Journal of Virology, 2022, 96, e0029822.	3.4	7
2	Sapoviruses detected from acute gastroenteritis outbreaks and hospitalized children in Taiwan. Journal of the Formosan Medical Association, 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. Japanese Journal of Infectious Diseases, 2021, , .	1.2	Ο
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. Journal of Biological Chemistry, 2021, 297, 101225.	3.4	2
5	Caliciviruses induce mRNA of tumor necrosis factor α via their protease activity. Virus Research, 2021, 306, 198595.	2.2	1
6	Human sapovirus propagation in human cell lines supplemented with bile acids. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 32078-32085.	7.1	22
7	Polymerase chain reaction primer sets for the detection of genetically diverse human sapoviruses. Archives of Virology, 2020, 165, 2335-2340.	2.1	9
8	First identification of Sapoviruses in wild boar. Virus Research, 2019, 271, 197680.	2.2	7
9	Complete genome sequencing and genetic characterization of porcine sapovirus genogroup (G) X and GXI: GVI, GVII, CX, and GXI sapoviruses share common genomic features and form a unique porcine SaV clade. Infection, Genetics and Evolution, 2019, 75, 103959.	2.3	5
10	Broadly reactive realâ€time reverse transcriptionâ€polymerase chain reaction assay for the detection of human sapovirus genotypes. Journal of Medical Virology, 2019, 91, 370-377.	5.0	11
11	First Complete Genome Sequences of Human Sapovirus Strains Classified as Gl.3, Gl.4, Gl.6, Gl.7, and Gll.7. Genome Announcements, 2018, 6, .	0.8	6
12	Attempts to grow human noroviruses, a sapovirus, and a bovine norovirus in vitro. PLoS ONE, 2018, 13, e0178157.	2.5	41
13	Genetic diversity and intergenogroup recombination events of sapoviruses detected from feces of pigs in Japan. Infection, Genetics and Evolution, 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. Virus Genes, 2017, 53, 848-855.	1.6	16
15	Genetic Characterization and Classification of Human and Animal Sapoviruses. PLoS ONE, 2016, 11, e0156373.	2.5	71
16	Epidemics of GI.2 sapovirus in gastroenteritis outbreaks during 2012â^'2013 in Osaka City, Japan. Journal of Medical Virology, 2016, 88, 1187-1193.	5.0	18
17	Mechanism of Cell Culture Adaptation of an Enteric Calicivirus, the Porcine Sapovirus Cowden Strain. Journal of Virology, 2016, 90, 1345-1358.	3.4	14
18	Antigenic Relationships among Porcine Epidemic Diarrhea Virus and Transmissible Gastroenteritis Virus Strains. Journal of Virology, 2015, 89, 3332-3342.	3.4	96

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19	Comprehensive Review of Human Sapoviruses. Clinical Microbiology Reviews, 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. Genome Announcements, 2015, 3, .	0.8	23
21	Genomic characterization of a US porcine kobuvirus strain. Archives of Microbiology, 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. Veterinary Microbiology, 2014, 173, 258-269.	1.9	150
23	Development of a novel single step reverse genetics system for feline calicivirus. Journal of Virological Methods, 2014, 207, 178-181.	2.1	19
24	First Complete Genome Sequences of Genogroup VI Porcine Sapoviruses. Genome Announcements, 2014, 2, .	0.8	1
25	Detection of Multiple Human Sapoviruses from Imported Frozen Individual Clams. Food and Environmental Virology, 2013, 5, 119-125.	3.4	12
26	First Complete Genome Sequence of a Genogroup II Genotype 18 Porcine Norovirus, Strain QW125. Genome Announcements, 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. Journal of Clinical Microbiology, 2013, 51, 2344-2353.	3.9	66
28	Complete Genome Sequence of the Feline Calicivirus 2280 Strain from the American Tissue Culture Collection. Genome Announcements, 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. Japanese Journal of Infectious Diseases, 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. Archives of Virology, 2012, 157, 1999-2003.	2.1	28
31	Human sapovirus classification based on complete capsid nucleotide sequences. Archives of Virology, 2012, 157, 349-352.	2.1	81
32	Comparative site-directed mutagenesis in the catalytic amino acid triad in calicivirus proteases. Microbiology and Immunology, 2011, 55, 108-114.	1.4	8
33	Bioluminescence technologies to detect calicivirus protease activity in cell-free system and in infected cells. Antiviral Research, 2011, 90, 9-16.	4.1	12
34	Molecular characterization of sapovirus detected in a gastroenteritis outbreak at a wedding hall. Journal of Medical Virology, 2010, 82, 720-726.	5.0	23
35	Detection of sapoviruses and noroviruses in an outbreak of gastroenteritis linked genetically to shellfish. Journal of Medical Virology, 2010, 82, 1247-1254.	5.0	55
36	Detection and Genetic Analysis of Human Sapoviruses in River Water in Japan. Applied and Environmental Microbiology, 2010, 76, 2461-2467.	3.1	47

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37	Structural and biological constraints on diversity of regions immediately upstream of cleavage sites in calicivirus precursor proteins. Virology, 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. Journal of Medical Virology, 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. Archives of Virology, 2009, 154, 689-693.	2.1	26
40	Selfâ€assembly of sapovirus recombinant virusâ€like particles from polyprotein in mammalian cells. Microbiology and Immunology, 2009, 53, 49-52.	1.4	7
41	Distinct genotype and antigenicity among genogroup II sapoviruses. Microbiology and Immunology, 2009, 53, 417-420.	1.4	11
42	Characterization of sapoviruses detected in gastroenteritis outbreaks and identification of asymptomatic adults with high viral load. Journal of Clinical Virology, 2009, 45, 67-71.	3.1	29
43	Highly Conserved Configuration of Catalytic Amino Acid Residues among Calicivirus-Encoded Proteases. Journal of Virology, 2007, 81, 6798-6806.	3.4	26
44	Detection of human sapovirus by real-time reverse transcription-polymerase chain reaction. Journal of Medical Virology, 2006, 78, 1347-1353.	5.0	228
45	Identification of the cleavage sites of sapovirus open reading frame 1 polyprotein. Journal of General Virology, 2006, 87, 3329-3338.	2.9	34
46	Proteolytic Processing of Sapovirus ORF1 Polyprotein. Journal of Virology, 2005, 79, 7283-7290.	3.4	54