## Domonkos SvÃ;b

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2104828/publications.pdf

Version: 2024-02-01

20 papers 189

8 h-index 14 g-index

20 all docs

20 docs citations

times ranked

20

289 citing authors

#	Article	IF	CITATIONS
1	Identification and Characterization of T5-Like Bacteriophages Representing Two Novel Subgroups from Food Products. Frontiers in Microbiology, 2018, 9, 202.	1.5	39
2	Comparative analysis of the Shiga toxin converting bacteriophage first detected in Shigella sonnei. Infection, Genetics and Evolution, 2016, 37, 150-157.	1.0	31
3	Sequence Variability of P2-Like Prophage Genomes Carrying the Cytolethal Distending Toxin V Operon in Escherichia coli O157. Applied and Environmental Microbiology, 2013, 79, 4958-4964.	1.4	20
4	Comparative Genomic and Phylogenetic Analysis of a Shiga Toxin Producing Shigella sonnei (STSS) Strain. Frontiers in Cellular and Infection Microbiology, 2017, 7, 229.	1.8	18
5	Preferential ligation during TA-cloning of multitemplate PCR products — A factor causing bias in microbial community structure analysis. Journal of Microbiological Methods, 2011, 85, 131-136.	0.7	16
6	Identification and characterization of new broad host-range rV5-like coliphages C203 and P206 directed against enterobacteria. Infection, Genetics and Evolution, 2018, 64, 254-261.	1.0	14
7	A novel transducible chimeric phage from Escherichia coli O157:H7 Sakai strain encoding Stx1 production. Infection, Genetics and Evolution, 2015, 29, 42-47.	1.0	12
8	Cytolethal distending toxin A, B and C subunit proteins are necessary for the genotoxic effect of Escherichia coli CDT-V. Acta Veterinaria Hungarica, 2015, 63, 1-10.	0.2	8
9	Draft Genome Sequence of an Escherichia coli O157:H43 Strain Isolated from Cattle. Genome Announcements, 2013, $1$ , .	0.8	6
10	Complete genome sequence of C130_2, a novel myovirus infecting pathogenic Escherichia coli and Shigella strains. Archives of Virology, 2019, 164, 321-324.	0.9	5
11	Allelic types of long polar fimbriae in bovine and human Escherichia coli O157 strains. Acta Veterinaria Hungarica, 2012, 60, 1-15.	0.2	4
12	R18C is a new viable P2-like bacteriophage of rabbit origin infecting Citrobacter rodentium and Shigella sonnei strains. Archives of Virology, 2019, 164, 3157-3160.	0.9	4
13	Cytolethal distending toxin producing Escherichia coli O157:H43 strain T22 represents a novel evolutionary lineage within the O157 serogroup. Infection, Genetics and Evolution, 2016, 46, 110-117.	1.0	3
14	The long polar fimbriae operon and its flanking regions in bovineEscherichia coliO157:H43 and STEC O136:H12 strains. Pathogens and Disease, 2013, 68, 1-7.	0.8	2
15	Multiplex polymerase chain reaction typing scheme based on Escherichia coli O157:H7 Sakai prophage (Sp)-associated genes. International Journal of Infectious Diseases, 2022, 120, 68-76.	1.5	2
16	Complete Genome Sequences of Novel Bovine T4, rv5-Like, and Dhillonviruses Effective against Escherichia coli O157. Microbiology Resource Announcements, 2021, 10, .	0.3	1
17	Genome Analysis of a Historical Shigella dysenteriae Serotype $1$ Strain Carrying a Conserved Stx Prophage Region. Frontiers in Microbiology, 2020, $11$ , $614793$ .	1.5	1
18	Novel prophage-like sequences in Mycoplasma anserisalpingitidis. Infection, Genetics and Evolution, 2021, 92, 104886.	1.0	1

#	Article	IF	CITATIONS
19	Characterisation of new anti-O157 bacteriophages of bovine origin representing three genera. Archives of Microbiology, 2022, 204, 231.	1.0	1
20	Genomic Diversity, Virulence Gene, and Prophage Arrays of Bovine and Human Shiga Toxigenic and Enteropathogenic Escherichia coli Strains Isolated in Hungary. Frontiers in Microbiology, 0, 13, .	1.5	1