

Hakdong Shin

List of Publications by Year in descending order

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57
papers

2,093
citations

236612

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3003
citing authors

#	ARTICLE	IF	CITATIONS
1	Bifidobacterium bifidum BGN4 and Bifidobacterium longum BORI promotes neuronal rejuvenation in aged mice. <i>Biochemical and Biophysical Research Communications</i> , 2022, 603, 41-48.	1.0	8
2	Complete genome sequence of <i>Salmonella enterica</i> strain K_SA184, multidrug resistance bacterium isolated from lamb (<i>Ovis aries</i>). <i>Journal of Animal Science and Technology</i> , 2021, 63, 194-197.	0.8	3
3	Complete genome sequence of <i>Escherichia coli</i> K_EC180, a bacterium producing shiga-like toxin isolated from swine feces. <i>Journal of Animal Science and Technology</i> , 2021, 63, 461-464.	0.8	1
4	Administration of <i>Bifidobacterium bifidum</i> BGN4 and <i>Bifidobacterium longum</i> BORI Improves Cognitive and Memory Function in the Mouse Model of Alzheimer's Disease. <i>Frontiers in Aging Neuroscience</i> , 2021, 13, 709091.	1.7	29
5	Evaluation of applicability of male-specific coliphage-based detection methods for microbial contamination tracking. <i>Journal of Microbiology and Biotechnology</i> , 2021, 31, .	0.9	0
6	Delayed Establishment of Gut Microbiota in Infants Delivered by Cesarean Section. <i>Frontiers in Microbiology</i> , 2020, 11, 2099.	1.5	53
7	Geranii Herba as a Potential Inhibitor of SARS-CoV-2 Main 3CLpro, Spike RBD, and Regulation of Unfolded Protein Response: An In Silico Approach. <i>Antibiotics</i> , 2020, 9, 863.	1.5	24
8	Maternal <i>H. pylori</i> is associated with differential fecal microbiota in infants born by vaginal delivery. <i>Scientific Reports</i> , 2020, 10, 7305.	1.6	2
9	Microbiota Analysis for the Optimization of <i>Campylobacter</i> Isolation From Chicken Carcasses Using Selective Media. <i>Frontiers in Microbiology</i> , 2019, 10, 1381.	1.5	14
10	Anti-methanogenic effect of rhubarb (<i>Rheum</i> spp.) – An in silico docking studies on methyl-coenzyme M reductase (MCR). <i>Saudi Journal of Biological Sciences</i> , 2019, 26, 1458-1462.	1.8	13
11	Differences in the fecal microbiota of neonates born at home or in the hospital. <i>Scientific Reports</i> , 2018, 8, 15660.	1.6	38
12	Chemical composition, antioxidant activity and antibacterial mechanism of action from <i>Marsilea minuta</i> leaf hexane: methanol extract. <i>Chemistry Central Journal</i> , 2018, 12, 105.	2.6	21
13	Bacterial DNA is present in the fetal intestine and overlaps with that in the placenta in mice. <i>PLoS ONE</i> , 2018, 13, e0197439.	1.1	44
14	Comparison of gizzard and intestinal microbiota of wild neotropical birds. <i>PLoS ONE</i> , 2018, 13, e0194857.	1.1	30
15	Modulation of Gut Microbiota of Overweight Mice by Agavins and Their Association with Body Weight Loss. <i>Nutrients</i> , 2017, 9, 821.	1.7	53
16	Delivery Mode and the Transition of Pioneering Gut-Microbiota Structure, Composition and Predicted Metabolic Function. <i>Genes</i> , 2017, 8, 364.	1.0	55
17	Modulation of Gut Microbiota of Overweight Mice by Agavins and Their Association with Body Weight Loss. <i>Nutrients</i> , 2017, 9, 821.	1.7	7
18	Characterization and Genomic Study of the Novel Bacteriophage HY01 Infecting Both <i>Escherichia coli</i> O157:H7 and <i>Shigella flexneri</i> : Potential as a Biocontrol Agent in Food. <i>PLoS ONE</i> , 2016, 11, e0168985.	1.1	59

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19	The Gestational Vaginal Microbiome and Spontaneous Preterm Birth among Nulliparous African American Women. <i>American Journal of Perinatology</i> , 2016, 33, 887-893.	0.6	47
20	Microbial Community Patterns Associated with Automated Teller Machine Keypads in New York City. <i>MSphere</i> , 2016, 1, .	1.3	28
21	Birth mode-dependent association between pre-pregnancy maternal weight status and the neonatal intestinal microbiome. <i>Scientific Reports</i> , 2016, 6, 23133.	1.6	120
22	Changes in the Eye Microbiota Associated with Contact Lens Wearing. <i>MBio</i> , 2016, 7, e00198.	1.8	170
23	A Novel Bacteriophage Targeting <i>Cronobacter sakazakii</i> Is a Potential Biocontrol Agent in Foods. <i>Applied and Environmental Microbiology</i> , 2016, 82, 192-201.	1.4	29
24	The first microbial environment of infants born by C-section: the operating room microbes. <i>Microbiome</i> , 2015, 3, 59.	4.9	110
25	Isolation and Genome Characterization of the Virulent <i>Staphylococcus aureus</i> Bacteriophage SA97. <i>Viruses</i> , 2015, 7, 5225-5242.	1.5	49
26	<i>Weissella jogaejeotgali</i> sp. nov., isolated from jogae jeotgal, a traditional Korean fermented seafood. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 4674-4681.	0.8	29
27	Comparative Genomic Analysis of <i>Staphylococcus aureus</i> FORC_001 and <i>S. aureus</i> MRSA252 Reveals the Characteristics of Antibiotic Resistance and Virulence Factors for Human Infection. <i>Journal of Microbiology and Biotechnology</i> , 2015, 25, 98-108.	0.9	11
28	Genomic Investigation of Lysogen Formation and Host Lysis Systems of the <i>Salmonella</i> Temperate Bacteriophage SPN9CC. <i>Applied and Environmental Microbiology</i> , 2014, 80, 374-384.	1.4	37
29	Complete genome sequence of marine bacterium <i>Pseudoalteromonas phenolica</i> bacteriophage TW1. <i>Archives of Virology</i> , 2014, 159, 159-162.	0.9	10
30	Draft genome sequence of <i>Xanthomonas axonopodis</i> pv. <i>glycines</i> 8ra possessing transcription activator-like effectors used for genetic engineering. <i>Journal of Biotechnology</i> , 2014, 179, 15-16.	1.9	5
31	Complete genome sequence of the <i>Pectobacterium carotovorum</i> subsp. <i>carotovorum</i> virulent bacteriophage PM1. <i>Archives of Virology</i> , 2014, 159, 2185-2187.	0.9	29
32	Characterization and comparative genomic analysis of bacteriophages infecting members of the <i>Bacillus cereus</i> group. <i>Archives of Virology</i> , 2014, 159, 871-884.	0.9	19
33	<i>Vibrio vulnificus</i> Bacteriophage SSP002 as a Possible Biocontrol Agent. <i>Applied and Environmental Microbiology</i> , 2014, 80, 515-524.	1.4	31
34	Characterization and genome analysis of the <i>Bacillus cereus</i> -infecting bacteriophages BPS10C and BPS13. <i>Archives of Virology</i> , 2014, 159, 2171-2175.	0.9	14
35	Exogenous Lytic Activity of SPN9CC Endolysin Against Gram-Negative Bacteria. <i>Journal of Microbiology and Biotechnology</i> , 2014, 24, 803-811.	0.9	75
36	Characterization and complete genome sequence of a virulent bacteriophage B4 infecting food-borne pathogenic <i>Bacillus cereus</i> . <i>Archives of Virology</i> , 2013, 158, 2101-2108.	0.9	31

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37	Complete genome sequence analysis of bacterial-flagellum-targeting bacteriophage chi. Archives of Virology, 2013, 158, 2179-2183.	0.9	18
38	Characterization and complete genome sequence analysis of Staphylococcus aureus bacteriophage SA12. Virus Genes, 2013, 47, 389-393.	0.7	14
39	Identification and Characterization of a Novel Flagellum-Dependent Salmonella-Infecting Bacteriophage, iEPS5. Applied and Environmental Microbiology, 2013, 79, 4829-4837.	1.4	68
40	Sequence Analysis of a Cryptic Plasmid pKW2124 from Weissella cibaria KLC140 and Construction of a Surface Display Vector. Journal of Microbiology and Biotechnology, 2013, 23, 545-554.	0.9	8
41	Complete Genome Sequence of Bacillus cereus Bacteriophage BCP78. Journal of Virology, 2012, 86, 637-638.	1.5	24
42	Complete Genome Sequence of the Hyperthermophilic Archaeon Thermococcus sp. Strain CL1, Isolated from a Paralvinella sp. Polychaete Worm Collected from a Hydrothermal Vent. Journal of Bacteriology, 2012, 194, 4769-4770.	1.0	12
43	Complete Genome Sequence of Pectobacterium carotovorum subsp. carotovorum Bacteriophage My1. Journal of Virology, 2012, 86, 11410-11411.	1.5	21
44	Complete Genome Sequence of Phytopathogenic Pectobacterium carotovorum subsp. carotovorum Bacteriophage PP1. Journal of Virology, 2012, 86, 8899-8900.	1.5	45
45	Complete Genome Sequence of Salmonella enterica Serovar Typhimurium Bacteriophage SPN1S. Journal of Virology, 2012, 86, 1284-1285.	1.5	11
46	Complete Genome Sequence of the Opportunistic Food-Borne Pathogen Cronobacter sakazakii ES15. Journal of Bacteriology, 2012, 194, 4438-4439.	1.0	14
47	Complete Genome Sequence of Cronobacter sakazakii Temperate Bacteriophage phiES15. Journal of Virology, 2012, 86, 7713-7714.	1.5	17
48	Complete Genome Sequence of the Hyperthermophilic Archaeon Pyrococcus sp. Strain ST04, Isolated from a Deep-Sea Hydrothermal Sulfide Chimney on the Juan de Fuca Ridge. Journal of Bacteriology, 2012, 194, 4434-4435.	1.0	16
49	Complete Genome Sequence of Cronobacter sakazakii Bacteriophage CR3. Journal of Virology, 2012, 86, 6367-6368.	1.5	13
50	Complete Genome Sequence of Salmonella enterica Serovar Typhimurium Bacteriophage SPN3UB. Journal of Virology, 2012, 86, 3404-3405.	1.5	11
51	Possible roles of LysR-type transcriptional regulator (LTTR) homolog as a global regulator in Cronobacter sakazakii ATCC 29544. International Journal of Medical Microbiology, 2012, 302, 270-275.	1.5	13
52	Characterization and Comparative Genomic Analysis of a Novel Bacteriophage, SFP10, Simultaneously Inhibiting both Salmonella enterica and Escherichia coli O157:H7. Applied and Environmental Microbiology, 2012, 78, 58-69.	1.4	142
53	Characterization of endolysin from a Salmonella Typhimurium-infecting bacteriophage SPN1S. Research in Microbiology, 2012, 163, 233-241.	1.0	62
54	Characterization of LysB4, an endolysin from the Bacillus cereus-infecting bacteriophage B4. BMC Microbiology, 2012, 12, 33.	1.3	90

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55	Receptor Diversity and Host Interaction of Bacteriophages Infecting Salmonella enterica Serovar Typhimurium. PLoS ONE, 2012, 7, e43392.	1.1	98
56	Prevalence of Bacillus cereus bacteriophages in fermented foods and characterization of phage JBP901. Research in Microbiology, 2011, 162, 791-797.	1.0	50
57	Complete Genome Sequence of Salmonella Bacteriophage SPN3US. Journal of Virology, 2011, 85, 13470-13471.	1.5	45