

# Hakdong Shin

## List of Publications by Year in descending order

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57  
papers

2,093  
citations

236833

25  
h-index

254106

43  
g-index

59  
all docs

59  
docs citations

59  
times ranked

3003  
citing authors

#	ARTICLE	IF	CITATIONS
1	Changes in the Eye Microbiota Associated with Contact Lens Wearing. <i>MBio</i> , 2016, 7, e00198.	1.8	170
2	Characterization and Comparative Genomic Analysis of a Novel Bacteriophage, SFP10, Simultaneously Inhibiting both <i>Salmonella enterica</i> and <i>Escherichia coli</i> O157:H7. <i>Applied and Environmental Microbiology</i> , 2012, 78, 58-69.	1.4	142
3	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
4	The first microbial environment of infants born by C-section: the operating room microbes. <i>Microbiome</i> , 2015, 3, 59.	4.9	110
5	Receptor Diversity and Host Interaction of Bacteriophages Infecting <i>Salmonella enterica</i> Serovar Typhimurium. <i>PLoS ONE</i> , 2012, 7, e43392.	1.1	98
6	Characterization of LysB4, an endolysin from the <i>Bacillus cereus</i> -infecting bacteriophage B4. <i>BMC Microbiology</i> , 2012, 12, 33.	1.3	90
7	Exogenous Lytic Activity of SPN9CC Endolysin Against Gram-Negative Bacteria. <i>Journal of Microbiology and Biotechnology</i> , 2014, 24, 803-811.	0.9	75
8	Identification and Characterization of a Novel Flagellum-Dependent <i>Salmonella</i> -Infecting Bacteriophage, iEPS5. <i>Applied and Environmental Microbiology</i> , 2013, 79, 4829-4837.	1.4	68
9	Characterization of endolysin from a <i>Salmonella</i> Typhimurium-infecting bacteriophage SPN1S. <i>Research in Microbiology</i> , 2012, 163, 233-241.	1.0	62
10	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
11	Delivery Mode and the Transition of Pioneering Gut-Microbiota Structure, Composition and Predicted Metabolic Function. <i>Genes</i> , 2017, 8, 364.	1.0	55
12	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
13	Delayed Establishment of Gut Microbiota in Infants Delivered by Cesarean Section. <i>Frontiers in Microbiology</i> , 2020, 11, 2099.	1.5	53
14	Prevalence of <i>Bacillus cereus</i> bacteriophages in fermented foods and characterization of phage JBP901. <i>Research in Microbiology</i> , 2011, 162, 791-797.	1.0	50
15	Isolation and Genome Characterization of the Virulent <i>Staphylococcus aureus</i> Bacteriophage SA97. <i>Viruses</i> , 2015, 7, 5225-5242.	1.5	49
16	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
17	Complete Genome Sequence of <i>Salmonella</i> Bacteriophage SPN3US. <i>Journal of Virology</i> , 2011, 85, 13470-13471.	1.5	45
18	Complete Genome Sequence of Phytopathogenic <i>Pectobacterium carotovorum</i> subsp. <i>carotovorum</i> Bacteriophage PP1. <i>Journal of Virology</i> , 2012, 86, 8899-8900.	1.5	45

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19	Bacterial DNA is present in the fetal intestine and overlaps with that in the placenta in mice. PLoS ONE, 2018, 13, e0197439.	1.1	44
20	Differences in the fecal microbiota of neonates born at home or in the hospital. Scientific Reports, 2018, 8, 15660.	1.6	38
21	Genomic Investigation of Lysogen Formation and Host Lysis Systems of the Salmonella Temperate Bacteriophage SPN9CC. Applied and Environmental Microbiology, 2014, 80, 374-384.	1.4	37
22	Characterization and complete genome sequence of a virulent bacteriophage B4 infecting food-borne pathogenic Bacillus cereus. Archives of Virology, 2013, 158, 2101-2108.	0.9	31
23	Vibrio vulnificus Bacteriophage SSP002 as a Possible Biocontrol Agent. Applied and Environmental Microbiology, 2014, 80, 515-524.	1.4	31
24	Comparison of gizzard and intestinal microbiota of wild neotropical birds. PLoS ONE, 2018, 13, e0194857.	1.1	30
25	Complete genome sequence of the Pectobacterium carotovorum subsp. carotovorum virulent bacteriophage PM1. Archives of Virology, 2014, 159, 2185-2187.	0.9	29
26	A Novel Bacteriophage Targeting Cronobacter sakazakii Is a Potential Biocontrol Agent in Foods. Applied and Environmental Microbiology, 2016, 82, 192-201.	1.4	29
27	Administration of Bifidobacterium bifidum BGN4 and Bifidobacterium longum BORI Improves Cognitive and Memory Function in the Mouse Model of Alzheimer's Disease. Frontiers in Aging Neuroscience, 2021, 13, 709091.	1.7	29
28	Weissella jogaejeotgali sp. nov., isolated from jogae jeotgal, a traditional Korean fermented seafood. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 4674-4681.	0.8	29
29	Microbial Community Patterns Associated with Automated Teller Machine Keypads in New York City. MSphere, 2016, 1, .	1.3	28
30	Complete Genome Sequence of Bacillus cereus Bacteriophage BCP78. Journal of Virology, 2012, 86, 637-638.	1.5	24
31	Geranii Herba as a Potential Inhibitor of SARS-CoV-2 Main 3CLpro, Spike RBD, and Regulation of Unfolded Protein Response: An In Silico Approach. Antibiotics, 2020, 9, 863.	1.5	24
32	Complete Genome Sequence of Pectobacterium carotovorum subsp. carotovorum Bacteriophage My1. Journal of Virology, 2012, 86, 11410-11411.	1.5	21
33	Chemical composition, antioxidant activity and antibacterial mechanism of action from Marsilea minuta leaf hexane: methanol extract. Chemistry Central Journal, 2018, 12, 105.	2.6	21
34	Characterization and comparative genomic analysis of bacteriophages infecting members of the Bacillus cereus group. Archives of Virology, 2014, 159, 871-884.	0.9	19
35	Complete genome sequence analysis of bacterial-flagellum-targeting bacteriophage chi. Archives of Virology, 2013, 158, 2179-2183.	0.9	18
36	Complete Genome Sequence of Cronobacter sakazakii Temperate Bacteriophage phiES15. Journal of Virology, 2012, 86, 7713-7714.	1.5	17

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37	Complete Genome Sequence of the Hyperthermophilic Archaeon <i>Pyrococcus</i> sp. Strain ST04, Isolated from a Deep-Sea Hydrothermal Sulfide Chimney on the Juan de Fuca Ridge. <i>Journal of Bacteriology</i> , 2012, 194, 4434-4435.	1.0	16
38	Complete Genome Sequence of the Opportunistic Food-Borne Pathogen <i>Cronobacter sakazakii</i> ES15. <i>Journal of Bacteriology</i> , 2012, 194, 4438-4439.	1.0	14
39	Characterization and complete genome sequence analysis of <i>Staphylococcus aureus</i> bacteriophage SA12. <i>Virus Genes</i> , 2013, 47, 389-393.	0.7	14
40	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
41	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
42	Complete Genome Sequence of <i>Cronobacter sakazakii</i> Bacteriophage CR3. <i>Journal of Virology</i> , 2012, 86, 6367-6368.	1.5	13
43	Possible roles of LysR-type transcriptional regulator (LTTR) homolog as a global regulator in <i>Cronobacter sakazakii</i> ATCC 29544. <i>International Journal of Medical Microbiology</i> , 2012, 302, 270-275.	1.5	13
44	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
45	Complete Genome Sequence of the Hyperthermophilic Archaeon <i>Thermococcus</i> sp. Strain CL1, Isolated from a <i>Paralvinella</i> sp. Polychaete Worm Collected from a Hydrothermal Vent. <i>Journal of Bacteriology</i> , 2012, 194, 4769-4770.	1.0	12
46	Complete Genome Sequence of <i>Salmonella enterica</i> Serovar Typhimurium Bacteriophage SPN1S. <i>Journal of Virology</i> , 2012, 86, 1284-1285.	1.5	11
47	Complete Genome Sequence of <i>Salmonella enterica</i> Serovar Typhimurium Bacteriophage SPN3UB. <i>Journal of Virology</i> , 2012, 86, 3404-3405.	1.5	11
48	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
49	Complete genome sequence of marine bacterium <i>Pseudoalteromonas phenolica</i> bacteriophage TW1. <i>Archives of Virology</i> , 2014, 159, 159-162.	0.9	10
50	Sequence Analysis of a Cryptic Plasmid pKW2124 from <i>Weissella cibaria</i> KLC140 and Construction of a Surface Display Vector. <i>Journal of Microbiology and Biotechnology</i> , 2013, 23, 545-554.	0.9	8
51	<i>Bifidobacterium bifidum</i> BGN4 and <i>Bifidobacterium longum</i> BORI promotes neuronal rejuvenation in aged mice. <i>Biochemical and Biophysical Research Communications</i> , 2022, 603, 41-48.	1.0	8
52	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
53	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
54	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

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55	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
56	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
57	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