

# Ju-Hoon Lee

## List of Publications by Year in descending order

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Version: 2024-02-01

80  
papers

2,878  
citations

257450

24  
h-index

189892

50  
g-index

81  
all docs

81  
docs citations

81  
times ranked

3604  
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular interaction between methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) and chicken breast reveals enhancement of pathogenesis and toxicity for food-borne outbreak. <i>Food Microbiology</i> , 2021, 93, 103602.	4.2	15
2	Characterization of bacteriophage VVP001 and its application for the inhibition of <i>Vibrio vulnificus</i> causing seafood-borne diseases. <i>Food Microbiology</i> , 2021, 94, 103630.	4.2	25
3	Development of an endolysin enzyme and its cell wall-binding domain protein and their applications for biocontrol and rapid detection of <i>Clostridium perfringens</i> in food. <i>Food Chemistry</i> , 2021, 345, 128562.	8.2	22
4	Complete genome sequence of <i>Lactococcus lactis</i> strain K_LL005, a xylose-utilizing bacterium isolated from grasshopper ( <i>Oxya chinensis sinuosa</i> ). <i>Journal of Animal Science and Technology</i> , 2021, 63, 191-193.	2.5	1
5	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.	2.5	3
6	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.	2.5	1
7	Fresh Crab Plays an Important Role as a Nutrient Reservoir for the Rapid Propagation of <i>Vibrio vulnificus</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 645860.	3.5	1
8	<i>Anaerococcus faecalis</i> sp. nov., Isolated from Swine Faeces. <i>Current Microbiology</i> , 2021, 78, 2589-2594.	2.2	1
9	<i>Peptoniphilus faecalis</i> sp. nov., isolated from swine faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	10
10	Description of <i>Anaerostipes faecalis</i> sp. nov., a new segmented filamentous bacterium isolated from swine faeces. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1867-1875.	1.7	7
11	<i>Phocaeicola faecicola</i> sp. nov., isolated from porcine faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	7
12	<i>Anaerosporebacter faecicola</i> sp. nov. isolated from faeces of Korean cow. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	5
13	<i>Faecalicatena faecalis</i> sp. nov., a moderately alkaliphilic bacterial strain isolated from swine faeces. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 2091-2099.	1.7	1
14	Evaluating the Prevalence of Foodborne Pathogens in Livestock Using Metagenomics Approach. <i>Journal of Microbiology and Biotechnology</i> , 2021, 31, 1701-1708.	2.1	11
15	Cancer-protective effect of a synbiotic combination between <i>Lactobacillus gasseri</i> 505 and a <i>Cudrania tricuspidata</i> leaf extract on colitis-associated colorectal cancer. <i>Gut Microbes</i> , 2020, 12, 1785803.	9.8	85
16	Effects of Probiotics on the Symptoms and Surgical Outcomes after Anterior Resection of Colon Cancer (POSTCARE): A Randomized, Double-Blind, Placebo-Controlled Trial. <i>Journal of Clinical Medicine</i> , 2020, 9, 2181.	2.4	26
17	Microbiome Study of Initial Gut Microbiota from Newborn Infants to Children Reveals that Diet Determines Its Compositional Development. <i>Journal of Microbiology and Biotechnology</i> , 2020, 30, 1067-1071.	2.1	14
18	Mutation of a <i>Staphylococcus aureus</i> temperate bacteriophage to a virulent one and evaluation of its application. <i>Food Microbiology</i> , 2019, 82, 523-532.	4.2	23

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19	Intestinal Microbial Dysbiosis in Beagles Naturally Infected with Canine Parvovirus. Journal of Microbiology and Biotechnology, 2019, 29, 1391-1400.	2.1	15
20	Role of Probiotics in Human Gut Microbiome-Associated Diseases. Journal of Microbiology and Biotechnology, 2019, 29, 1335-1340.	2.1	221
21	Peribacillus faecalis sp. nov., a moderately halophilic bacterium isolated from the faeces of a cow. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	1.7	9
22	Detection of Bacillus Cereus Using Bioluminescence Assay with Cell Wall-binding Domain Conjugated Magnetic Nanoparticles. Biochip Journal, 2018, 12, 287-293.	4.9	21
23	Oral consumption of cinnamon enhances the expression of immunity and lipid absorption genes in the small intestinal epithelium and alters the gut microbiota in normal mice. Journal of Functional Foods, 2018, 49, 96-104.	3.4	3
24	Potential Survival and Pathogenesis of a Novel Strain, Vibrio parahaemolyticus FORC_022, Isolated From a Soy Sauce Marinated Crab by Genome and Transcriptome Analyses. Frontiers in Microbiology, 2018, 9, 1504.	3.5	5
25	Lelliottia jeotgali sp. nov., isolated from a traditional Korean fermented clam. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1725-1731.	1.7	27
26	Metagenomic Approach to Identifying Foodborne Pathogens on Chinese Cabbage. Journal of Microbiology and Biotechnology, 2018, 28, 227-235.	2.1	32
27	Analysis of Microbiota in Bellflower Root, Platycodon grandiflorum, Obtained from South Korea. Journal of Microbiology and Biotechnology, 2018, 28, 551-560.	2.1	2
28	Isolation and Characterization of Bifidobacterium longum subsp. longum BCBL-583 for Probiotic Applications in Fermented Foods. Journal of Microbiology and Biotechnology, 2018, 28, 1846-1849.	2.1	1
29	The complete genome sequence of Cronobacter sakazakii ATCC 29544T, a food-borne pathogen, isolated from a child's throat. Gut Pathogens, 2017, 9, 2.	3.4	12
30	Characterization and genome analysis of novel bacteriophages infecting the opportunistic human pathogens Klebsiella oxytoca and K. pneumoniae. Archives of Virology, 2017, 162, 1129-1139.	2.1	18
31	Genomic Insights of Weissella jogaejeotgali FOL01T Reveals Its Food Fermentation Ability and Human Gut Adaptive Potential for Probiotic Applications in Food Industries. Journal of Microbiology and Biotechnology, 2017, 27, 943-946.	2.1	6
32	Deciphering Diversity Indices for a Better Understanding of Microbial Communities. Journal of Microbiology and Biotechnology, 2017, 27, 2089-2093.	2.1	578
33	Isolation and Characterization of a Novel Broad-host-range Bacteriophage Infecting Salmonella enterica subsp. enterica for Biocontrol and Rapid Detection. Journal of Microbiology and Biotechnology, 2017, 27, 2151-2155.	2.1	14
34	Biocontrol and Rapid Detection of Food-Borne Pathogens Using Bacteriophages and Endolysins. Frontiers in Microbiology, 2016, 7, 474.	3.5	99
35	Characterization and Genomic Study of the Novel Bacteriophage HY01 Infecting Both Escherichia coli O157:H7 and Shigella flexneri: Potential as a Biocontrol Agent in Food. PLoS ONE, 2016, 11, e0168985.	2.5	59
36	Complete genome sequence of Vibrio parahaemolyticus strain FORC_008, a foodborne pathogen from a flounder fish in South Korea. Pathogens and Disease, 2016, 74, ftw044.	2.0	5

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37	Complete genome sequence of <i>Vibrio parahaemolyticus</i> FORC_023 isolated from raw fish storage water. <i>Pathogens and Disease</i> , 2016, 74, ftw032.	2.0	4
38	Complete genome sequence of <i>Vibrio vulnificus</i> FORC_017 isolated from a patient with a hemorrhagic rash after consuming raw dotted gizzard shad. <i>Gut Pathogens</i> , 2016, 8, 22.	3.4	14
39	Morphological features and lipopolysaccharide attachment of coliphages specific to <i>Escherichia coli</i> O157:H7 and to a broad range of <i>E. coli</i> hosts. <i>Applied Biological Chemistry</i> , 2016, 59, 109-116.	1.9	5
40	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.	3.1	29
41	Genome Sequence of <i>Bacillus cereus</i> FORC_021, a Food-Borne Pathogen Isolated from a Knife at a Sashimi Restaurant. <i>Journal of Microbiology and Biotechnology</i> , 2016, 26, 2030-2035.	2.1	3
42	Complete genome sequence of <i>Bacillus cereus</i> FORC_005, a food-borne pathogen from the soy sauce braised fish-cake with quail-egg. <i>Standards in Genomic Sciences</i> , 2015, 10, 97.	1.5	7
43	Isolation and Genome Characterization of the Virulent <i>Staphylococcus aureus</i> Bacteriophage SA97. <i>Viruses</i> , 2015, 7, 5225-5242.	3.3	49
44	Characterization of a minimal pKW2124 replicon from <i>Weissella cibaria</i> KLC140 and its application for the construction of the <i>Weissella</i> expression vector pKUCm1. <i>Frontiers in Microbiology</i> , 2015, 6, 35.	3.5	1
45	<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.	1.7	29
46	Characterization of a Novel Fibrinolytic Enzyme, BsfA, from <i>Bacillus subtilis</i> ZA400 in Kimchi Reveals Its Pertinence to Thrombosis Treatment. <i>Journal of Microbiology and Biotechnology</i> , 2015, 25, 2090-2099.	2.1	16
47	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.	3.1	37
48	Complete genome sequence of marine bacterium <i>Pseudoalteromonas phenolica</i> bacteriophage TW1. <i>Archives of Virology</i> , 2014, 159, 159-162.	2.1	10
49	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.	3.8	5
50	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.	2.1	29
51	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.	2.1	19
52	Molecular cloning and expression of amylosucrase from highly radiation-resistant <i>Deinococcus radiopugnans</i> . <i>Food Science and Biotechnology</i> , 2014, 23, 2007-2012.	2.6	19
53	<i>Vibrio vulnificus</i> Bacteriophage SSP002 as a Possible Biocontrol Agent. <i>Applied and Environmental Microbiology</i> , 2014, 80, 515-524.	3.1	31
54	Characterization and genome analysis of the <i>Bacillus cereus</i> -infecting bacteriophages BPS10C and BPS13. <i>Archives of Virology</i> , 2014, 159, 2171-2175.	2.1	14

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55	Complete genome sequence of hyperthermophilic archaeon <i>Thermococcus</i> sp. ES1. <i>Journal of Biotechnology</i> , 2014, 174, 14-15.	3.8	7
56	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.	2.1	31
57	Complete genome sequence analysis of bacterial-flagellum-targeting bacteriophage chi. <i>Archives of Virology</i> , 2013, 158, 2179-2183.	2.1	18
58	Characterization and complete genome sequence analysis of <i>Staphylococcus aureus</i> bacteriophage SA12. <i>Virus Genes</i> , 2013, 47, 389-393.	1.6	14
59	Identification and Characterization of a Novel Flagellum-Dependent <i>Salmonella</i> -Infecting Bacteriophage, iEPS5. <i>Applied and Environmental Microbiology</i> , 2013, 79, 4829-4837.	3.1	68
60	Use of a Novel <i>Escherichia coli</i> - <i>Leuconostoc</i> Shuttle Vector for Metabolic Engineering of <i>Leuconostoc citreum</i> To Overproduce $\gamma$ -Lactate. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1428-1435.	3.1	11
61	Complete Genome Sequence of <i>Bacillus cereus</i> Bacteriophage BCP78. <i>Journal of Virology</i> , 2012, 86, 637-638.	3.4	24
62	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.	2.2	12
63	Complete Genome Sequence of <i>Pectobacterium carotovorum</i> subsp. <i>carotovorum</i> Bacteriophage My1. <i>Journal of Virology</i> , 2012, 86, 11410-11411.	3.4	21
64	Complete Genome Sequence of Phytopathogenic <i>Pectobacterium carotovorum</i> subsp. <i>carotovorum</i> Bacteriophage PP1. <i>Journal of Virology</i> , 2012, 86, 8899-8900.	3.4	45
65	Complete Genome Sequence of <i>Salmonella enterica</i> Serovar Typhimurium Bacteriophage SPN1S. <i>Journal of Virology</i> , 2012, 86, 1284-1285.	3.4	11
66	Complete Genome Sequence of the Opportunistic Food-Borne Pathogen <i>Cronobacter sakazakii</i> ES15. <i>Journal of Bacteriology</i> , 2012, 194, 4438-4439.	2.2	14
67	Complete Genome Sequence of <i>Cronobacter sakazakii</i> Temperate Bacteriophage phiES15. <i>Journal of Virology</i> , 2012, 86, 7713-7714.	3.4	17
68	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.	2.2	16
69	Complete Genome Sequence of <i>Cronobacter sakazakii</i> Bacteriophage CR3. <i>Journal of Virology</i> , 2012, 86, 6367-6368.	3.4	13
70	Complete Genome Sequence of <i>Salmonella enterica</i> Serovar Typhimurium Bacteriophage SPN3UB. <i>Journal of Virology</i> , 2012, 86, 3404-3405.	3.4	11
71	A suggested new bacteriophage genus: <i>Viunalikevirus</i> . <i>Archives of Virology</i> , 2012, 157, 2035-2046.	2.1	77
72	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.	3.1	142

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73	Receptor Diversity and Host Interaction of Bacteriophages Infecting <i>Salmonella enterica</i> Serovar Typhimurium. <i>PLoS ONE</i> , 2012, 7, e43392.	2.5	98
74	Complete Genome Sequence of <i>Salmonella</i> Bacteriophage SPN3US. <i>Journal of Virology</i> , 2011, 85, 13470-13471.	3.4	45
75	Transcription Analysis of a Lantibiotic Gene Cluster from <i>Bifidobacterium longum</i> DJO10A. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5879-5887.	3.1	41
76	Genomic Insights into <i>Bifidobacteria</i> . <i>Microbiology and Molecular Biology Reviews</i> , 2010, 74, 378-416.	6.6	237
77	Comparative Sequence Analysis of Plasmids from <i>Lactobacillus delbrueckii</i> and Construction of a Shuttle Cloning Vector. <i>Applied and Environmental Microbiology</i> , 2007, 73, 4417-4424.	3.1	23
78	Expression of the cationic antimicrobial peptide lactoferricin fused with the anionic peptide in <i>Escherichia coli</i> . <i>Applied Microbiology and Biotechnology</i> , 2006, 72, 330-338.	3.6	47
79	Sequence Analysis of Two Cryptic Plasmids from <i>Bifidobacterium longum</i> DJO10A and Construction of a Shuttle Cloning Vector. <i>Applied and Environmental Microbiology</i> , 2006, 72, 527-535.	3.1	59
80	Prophage-Like Elements in <i>Bifidobacteria</i> : Insights from Genomics, Transcription, Integration, Distribution, and Phylogenetic Analysis. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8692-8705.	3.1	70