

# Ju-Hoon Lee

## List of Publications by Year in descending order

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80  
papers

2,878  
citations

257101

24  
h-index

189595

50  
g-index

81  
all docs

81  
docs citations

81  
times ranked

3604  
citing authors

#	ARTICLE	IF	CITATIONS
1	Deciphering Diversity Indices for a Better Understanding of Microbial Communities. <i>Journal of Microbiology and Biotechnology</i> , 2017, 27, 2089-2093.	0.9	578
2	Genomic Insights into Bifidobacteria. <i>Microbiology and Molecular Biology Reviews</i> , 2010, 74, 378-416.	2.9	237
3	Role of Probiotics in Human Gut Microbiome-Associated Diseases. <i>Journal of Microbiology and Biotechnology</i> , 2019, 29, 1335-1340.	0.9	221
4	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
5	Biocontrol and Rapid Detection of Food-Borne Pathogens Using Bacteriophages and Endolysins. <i>Frontiers in Microbiology</i> , 2016, 7, 474.	1.5	99
6	Receptor Diversity and Host Interaction of Bacteriophages Infecting <i>Salmonella enterica</i> Serovar Typhimurium. <i>PLoS ONE</i> , 2012, 7, e43392.	1.1	98
7	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.	4.3	85
8	A suggested new bacteriophage genus: <i>Viunalikevirus</i> . <i>Archives of Virology</i> , 2012, 157, 2035-2046.	0.9	77
9	Prophage-Like Elements in Bifidobacteria: Insights from Genomics, Transcription, Integration, Distribution, and Phylogenetic Analysis. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8692-8705.	1.4	70
10	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
11	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.	1.4	59
12	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
13	Isolation and Genome Characterization of the Virulent <i>Staphylococcus aureus</i> Bacteriophage SA97. <i>Viruses</i> , 2015, 7, 5225-5242.	1.5	49
14	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.	1.7	47
15	Complete Genome Sequence of <i>Salmonella</i> Bacteriophage SPN3US. <i>Journal of Virology</i> , 2011, 85, 13470-13471.	1.5	45
16	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
17	Transcription Analysis of a Lantibiotic Gene Cluster from <i>Bifidobacterium longum</i> DJO10A. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5879-5887.	1.4	41
18	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

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19	Metagenomic Approach to Identifying Foodborne Pathogens on Chinese Cabbage. <i>Journal of Microbiology and Biotechnology</i> , 2018, 28, 227-235.	0.9	32
20	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
21	<i>Vibrio vulnificus</i> Bacteriophage SSP002 as a Possible Biocontrol Agent. <i>Applied and Environmental Microbiology</i> , 2014, 80, 515-524.	1.4	31
22	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
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	<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
25	<i>Lelliottia jeotgali</i> sp. nov., isolated from a traditional Korean fermented clam. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1725-1731.	0.8	27
26	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.	1.0	26
27	Characterization of bacteriophage VWP001 and its application for the inhibition of <i>Vibrio vulnificus</i> causing seafood-borne diseases. <i>Food Microbiology</i> , 2021, 94, 103630.	2.1	25
28	Complete Genome Sequence of <i>Bacillus cereus</i> Bacteriophage BCP78. <i>Journal of Virology</i> , 2012, 86, 637-638.	1.5	24
29	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.	1.4	23
30	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.	2.1	23
31	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.	4.2	22
32	Complete Genome Sequence of <i>Pectobacterium carotovorum</i> subsp. <i>carotovorum</i> Bacteriophage My1. <i>Journal of Virology</i> , 2012, 86, 11410-11411.	1.5	21
33	Detection of <i>Bacillus Cereus</i> Using Bioluminescence Assay with Cell Wall-binding Domain Conjugated Magnetic Nanoparticles. <i>Biochip Journal</i> , 2018, 12, 287-293.	2.5	21
34	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
35	Molecular cloning and expression of amylosucrase from highly radiation-resistant <i>Deinococcus radiopugnans</i> . <i>Food Science and Biotechnology</i> , 2014, 23, 2007-2012.	1.2	19
36	Complete genome sequence analysis of bacterial-flagellum-targeting bacteriophage chi. <i>Archives of Virology</i> , 2013, 158, 2179-2183.	0.9	18

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37	Characterization and genome analysis of novel bacteriophages infecting the opportunistic human pathogens <i>Klebsiella oxytoca</i> and <i>K. pneumoniae</i> . <i>Archives of Virology</i> , 2017, 162, 1129-1139.	0.9	18
38	Complete Genome Sequence of <i>Cronobacter sakazakii</i> Temperate Bacteriophage phiES15. <i>Journal of Virology</i> , 2012, 86, 7713-7714.	1.5	17
39	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
40	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.	0.9	16
41	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.	2.1	15
42	Intestinal Microbial Dysbiosis in Beagles Naturally Infected with Canine Parvovirus. <i>Journal of Microbiology and Biotechnology</i> , 2019, 29, 1391-1400.	0.9	15
43	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
44	Characterization and complete genome sequence analysis of <i>Staphylococcus aureus</i> bacteriophage SA12. <i>Virus Genes</i> , 2013, 47, 389-393.	0.7	14
45	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
46	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.	1.6	14
47	Isolation and Characterization of a Novel Broad-host-range Bacteriophage Infecting <i>Salmonella enterica</i> subsp. <i>enterica</i> for Biocontrol and Rapid Detection. <i>Journal of Microbiology and Biotechnology</i> , 2017, 27, 2151-2155.	0.9	14
48	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.	0.9	14
49	Complete Genome Sequence of <i>Cronobacter sakazakii</i> Bacteriophage CR3. <i>Journal of Virology</i> , 2012, 86, 6367-6368.	1.5	13
50	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
51	The complete genome sequence of <i>Cronobacter sakazakii</i> ATCC 29544T, a food-borne pathogen, isolated from a child's throat. <i>Gut Pathogens</i> , 2017, 9, 2.	1.6	12
52	Complete Genome Sequence of <i>Salmonella enterica</i> Serovar Typhimurium Bacteriophage SPN1S. <i>Journal of Virology</i> , 2012, 86, 1284-1285.	1.5	11
53	Complete Genome Sequence of <i>Salmonella enterica</i> Serovar Typhimurium Bacteriophage SPN3UB. <i>Journal of Virology</i> , 2012, 86, 3404-3405.	1.5	11
54	Use of a Novel <i>Escherichia coli</i> - <i>Leuconostoc</i> Shuttle Vector for Metabolic Engineering of <i>Leuconostoc citreum</i> To Overproduce <i>D</i> -Lactate. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1428-1435.	1.4	11

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55	Evaluating the Prevalence of Foodborne Pathogens in Livestock Using Metagenomics Approach. <i>Journal of Microbiology and Biotechnology</i> , 2021, 31, 1701-1708.	0.9	11
56	Complete genome sequence of marine bacterium <i>Pseudoalteromonas phenolica</i> bacteriophage TW1. <i>Archives of Virology</i> , 2014, 159, 159-162.	0.9	10
57	<i>Peptoniphilus faecalis</i> sp. nov., isolated from swine faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	10
58	<i>Peribacillus faecalis</i> sp. nov., a moderately halophilic bacterium isolated from the faeces of a cow. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	9
59	Complete genome sequence of hyperthermophilic archaeon <i>Thermococcus</i> sp. ES1. <i>Journal of Biotechnology</i> , 2014, 174, 14-15.	1.9	7
60	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
61	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.	0.7	7
62	<i>Phocaeicola faecicola</i> sp. nov., isolated from porcine faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	7
63	Genomic Insights of <i>Weissella jogaejeotgali</i> FOL01T Reveals Its Food Fermentation Ability and Human Gut Adaptive Potential for Probiotic Applications in Food Industries. <i>Journal of Microbiology and Biotechnology</i> , 2017, 27, 943-946.	0.9	6
64	Draft genome sequence of <i>Xanthomonas axonopodis</i> pv. <i>glycines 8ra</i> possessing transcription activator-like effectors used for genetic engineering. <i>Journal of Biotechnology</i> , 2014, 179, 15-16.	1.9	5
65	Complete genome sequence of <i>Vibrio parahaemolyticus</i> strain FORC_008, a foodborne pathogen from a flounder fish in South Korea. <i>Pathogens and Disease</i> , 2016, 74, ftw044.	0.8	5
66	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.	0.7	5
67	Potential Survival and Pathogenesis of a Novel Strain, <i>Vibrio parahaemolyticus</i> FORC_022, Isolated From a Soy Sauce Marinated Crab by Genome and Transcriptome Analyses. <i>Frontiers in Microbiology</i> , 2018, 9, 1504.	1.5	5
68	<i>Anaerosporebacter faecicola</i> sp. nov. isolated from faeces of Korean cow. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	5
69	Complete genome sequence of <i>Vibrio parahaemolyticus</i> FORC_023 isolated from raw fish storage water. <i>Pathogens and Disease</i> , 2016, 74, ftw032.	0.8	4
70	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. <i>Journal of Functional Foods</i> , 2018, 49, 96-104.	1.6	3
71	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
72	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.	0.9	3

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73	Analysis of Microbiota in Bellflower Root, <i>Platycodon grandiflorum</i> , Obtained from South Korea. <i>Journal of Microbiology and Biotechnology</i> , 2018, 28, 551-560.	0.9	2
74	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.	1.5	1
75	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.	0.8	1
76	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
77	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.	1.5	1
78	<i>Anaerococcus faecalis</i> sp. nov., Isolated from Swine Faeces. <i>Current Microbiology</i> , 2021, 78, 2589-2594.	1.0	1
79	<i>Faecalicatena faecalis</i> sp. nov., a moderately alkaliphilic bacterial strain isolated from swine faeces. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 2091-2099.	0.7	1
80	Isolation and Characterization of <i>Bifidobacterium longum</i> subsp. <i>longum</i> BCBL-583 for Probiotic Applications in Fermented Foods. <i>Journal of Microbiology and Biotechnology</i> , 2018, 28, 1846-1849.	0.9	1