

Ken-ichi Lee

List of Publications by Year in descending order

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49
papers

1,222
citations

331670

21
h-index

395702

33
g-index

51
all docs

51
docs citations

51
times ranked

1849
citing authors

#	ARTICLE	IF	CITATIONS
1	Cooperative Recognition of Internationally Disseminated Ceftriaxone-Resistant <i>Neisseria gonorrhoeae</i> Strain. <i>Emerging Infectious Diseases</i> , 2018, 24, .	4.3	170
2	Molecular phylogeny of the higher and lower taxonomy of the <i>Fusarium</i> genus and differences in the evolutionary histories of multiple genes. <i>BMC Evolutionary Biology</i> , 2011, 11, 322.	3.2	87
3	Distribution and Relationships of Antimicrobial Resistance Determinants among Extended-Spectrum-Cephalosporin-Resistant or Carbapenem-Resistant <i>Escherichia coli</i> Isolates from Rivers and Sewage Treatment Plants in India. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 2972-2980.	3.2	87
4	Impact of wastewater from different sources on the prevalence of antimicrobial-resistant <i>Escherichia coli</i> in sewage treatment plants in South India. <i>Ecotoxicology and Environmental Safety</i> , 2015, 115, 203-208.	6.0	65
5	Rapid and Effective DNA Extraction Method with Bead Grinding for a Large Amount of Fungal DNA. <i>Journal of Food Protection</i> , 2010, 73, 1077-1084.	1.7	54
6	Clonal expansion and spread of the ceftriaxone-resistant <i>Neisseria gonorrhoeae</i> strain FC428, identified in Japan in 2015, and closely related isolates. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1812-1819.	3.0	50
7	Genomic surveillance of <i>Neisseria gonorrhoeae</i> to investigate the distribution and evolution of antimicrobial-resistance determinants and lineages. <i>Microbial Genomics</i> , 2018, 4, .	2.0	47
8	Characteristics of <i>Salmonella enterica</i> Serovar 4,[5],12:i:- as a Monophasic Variant of Serovar Typhimurium. <i>PLoS ONE</i> , 2014, 9, e104380.	2.5	41
9	Prevalence of <i>Salmonella</i> , <i>Yersinia</i> and <i>Campylobacter</i> spp. in Feral Raccoons (<i>Procyon lotor</i>) and Masked Palm Civets (<i>Paguma larvata</i>) in Japan. <i>Zoonoses and Public Health</i> , 2011, 58, 424-431.	2.2	40
10	A novel multiplex PCR assay for <i>Salmonella</i> subspecies identification. <i>Journal of Applied Microbiology</i> , 2009, 107, 805-811.	3.1	37
11	Variation in Stress Resistance Patterns among <i>stx</i> Genotypes and Genetic Lineages of Shiga Toxin-Producing <i>Escherichia coli</i> O157. <i>Applied and Environmental Microbiology</i> , 2012, 78, 3361-3368.	3.1	37
12	<i>Neisseria cinerea</i> with High Ceftriaxone MIC Is a Source of Ceftriaxone and Cefixime Resistance-Mediating <i>penA</i> Sequences in <i>Neisseria gonorrhoeae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	37
13	Virulence Gene Profiles and Population Genetic Analysis for Exploration of Pathogenic Serogroups of Shiga Toxin-Producing <i>Escherichia coli</i> . <i>Journal of Clinical Microbiology</i> , 2013, 51, 4022-4028.	3.9	33
14	<i>Treponema pallidum</i> genome sequencing from six continents reveals variability in vaccine candidate genes and dominance of Nichols clade strains in Madagascar. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0010063.	3.0	30
15	Population structure of <i>Escherichia coli</i> O26:H11 with recent and repeated <i>stx2</i> acquisition in multiple lineages. <i>Microbial Genomics</i> , 2017, 3, .	2.0	29
16	Differential dynamics and impacts of prophages and plasmids on the pangenome and virulence factor repertoires of Shiga toxin-producing <i>Escherichia coli</i> O145:H28. <i>Microbial Genomics</i> , 2020, 6, .	2.0	28
17	Virulence characteristics of <i>Yersinia pseudotuberculosis</i> isolated from breeding monkeys in Japan. <i>Veterinary Microbiology</i> , 2008, 129, 404-409.	1.9	26
18	Multivariate Analyses Revealed Distinctive Features Differentiating Human and Cattle Isolates of Shiga Toxin-Producing <i>Escherichia coli</i> O157 in Japan. <i>Journal of Clinical Microbiology</i> , 2011, 49, 1495-1500.	3.9	26

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19	Identification of a New Virulent Clade in Enterohemorrhagic <i>Escherichia coli</i> O26:H11/H- Sequence Type 29. <i>Scientific Reports</i> , 2017, 7, 43136.	3.3	25
20	Outbreak of Legionnaire's Disease Caused by <i>Legionella pneumophila</i> Serogroups 1 and 13. <i>Emerging Infectious Diseases</i> , 2017, 23, 349-351.	4.3	25
21	Nationwide investigation of Shiga toxin-producing <i>Escherichia coli</i> among cattle in Japan revealed the risk factors and potentially virulent subgroups. <i>Epidemiology and Infection</i> , 2017, 145, 1557-1566.	2.1	24
22	Evaluation of genetic markers for identifying isolates of the species of the genus <i>Fusarium</i> . <i>Journal of the Science of Food and Agriculture</i> , 2011, 91, 2500-2504.	3.5	23
23	A Geographically Widespread Outbreak Investigation and Development of a Rapid Screening Method Using Whole Genome Sequences of Enterohemorrhagic <i>Escherichia coli</i> O121. <i>Frontiers in Microbiology</i> , 2017, 8, 701.	3.5	23
24	Emergence of Resistance Mutations in <i>Salmonella enterica</i> Serovar Typhi Against Fluoroquinolones. <i>Open Forum Infectious Diseases</i> , 2017, 4, ofx230.	0.9	18
25	Whole-Genome Sequence Analysis of <i>Streptococcus pneumoniae</i> Strains That Cause Hospital-Acquired Pneumonia Infections. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	15
26	Effective Surveillance Using Multilocus Variable-Number Tandem-Repeat Analysis and Whole-Genome Sequencing for Enterohemorrhagic <i>Escherichia coli</i> O157. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	13
27	Phylogenetic and genetic characterization of <i>Treponema pallidum</i> strains from syphilis patients in Japan by whole-genome sequence analysis from global perspectives. <i>Scientific Reports</i> , 2021, 11, 3154.	3.3	12
28	Single Circular Chromosome Identified from the Genome Sequence of the <i>Vibrio cholerae</i> O1 bv. El Tor Ogawa Strain V060002. <i>Genome Announcements</i> , 2018, 6, .	0.8	11
29	<i>Penicillium camemberti</i> and <i>Penicillium roqueforti</i> Enhance the Growth and Survival of Shiga Toxin-Producing <i>Escherichia coli</i> O157 under Mild Acidic Conditions. <i>Journal of Food Science</i> , 2012, 77, M102-7.	3.1	9
30	Extensive amplification of GI-VII-6, a multidrug resistance genomic island of <i>Salmonella enterica</i> serovar Typhimurium, increases resistance to extended-spectrum cephalosporins. <i>Frontiers in Microbiology</i> , 2015, 6, 78.	3.5	9
31	The global population structure and evolutionary history of the acquisition of major virulence factor-encoding genetic elements in Shiga toxin-producing <i>Escherichia coli</i> O121:H19. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
32	Global distribution of epidemic-related Shiga toxin 2 encoding phages among enteroaggregative <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2020, 10, 11738.	3.3	8
33	Additional Og-Typing PCR Techniques Targeting <i>Escherichia coli</i> -Novel and <i>Shigella</i> -Unique O-Antigen Biosynthesis Gene Clusters. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	8
34	Spread and change in stress resistance of <i>Shiga toxin-producing Escherichia coli</i> O157 on fungal colonies. <i>Microbial Biotechnology</i> , 2014, 7, 621-629.	4.2	7
35	Characterization of two <i>Neisseria gonorrhoeae</i> strains with high-level azithromycin resistance isolated in 2015 and 2018 in Japan. <i>Sexually Transmitted Diseases</i> , 2020, Publish Ahead of Print, e85-e87.	1.7	7
36	An outbreak of food poisoning due to <i>Escherichia coli</i> serotype O7:H4 carrying <i>astA</i> for enteroaggregative <i>E. coli</i> heat-stable enterotoxin1 (EAST1). <i>Epidemiology and Infection</i> , 2021, 149, e244.	2.1	7

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37	Seroepidemiological Survey of Pathogenic <i>Yersinia</i> in Breeding Squirrel Monkeys in Japan. <i>Journal of Veterinary Medical Science</i> , 2010, 72, 981-984.	0.9	6
38	Analysis of Consumer Complaints Related to Microbial Contamination in Soft Drinks. <i>Shokuhin Eiseigaku Zasshi Journal of the Food Hygienic Society of Japan</i> , 2009, 50, 315-320.	0.2	5
39	Quantitative Analysis of Mycoflora on Commercial Domestic Fruits in Japan. <i>Journal of Food Protection</i> , 2011, 74, 1488-1499.	1.7	5
40	Survival of Pathogenic <i>Yersinia enterocolitica</i> in Vacuum-packed or Non-vacuum-packed Pork at Low Temperature. <i>Biocontrol Science</i> , 2008, 13, 139-144.	0.8	4
41	Rapid Detection of Shiga Toxin-Producing <i>Escherichia coli</i> in Ground Beef by an Immunochromatography Kit in Combination with Short-Term Enrichment and Treatment for Shiga Toxin Release. <i>Biocontrol Science</i> , 2011, 16, 159-164.	0.8	4
42	Multiple-Locus Variable-Number Tandem Repeat Analysis Scheme for Non-O157 Shiga Toxin-Producing <i>Escherichia coli</i> : Focus on Serogroups O103, O121, O145, O165, and O91. <i>Japanese Journal of Infectious Diseases</i> , 2020, 73, 481-490.	1.2	4
43	Enumeration of Fungi in Fruits by the Most Probable Number Method. <i>Journal of Food Science</i> , 2010, 75, M564-M567.	3.1	3
44	Whole-Genome Sequencing of Shiga Toxin-Producing <i>Escherichia coli</i> OX18 from a Fatal Hemolytic Uremic Syndrome Case. <i>Emerging Infectious Diseases</i> , 2021, 27, 1509-1512.	4.3	3
45	RNA-binding protein Hfq downregulates locus of enterocyte effacement-encoded regulators independent of small regulatory RNA in enterohemorrhagic <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2022, 117, 86-101.	2.5	3
46	Enterohaemorrhagic <i>Escherichia coli</i> O121:H19 acquired an extended-spectrum β -lactamase gene during the development of an outbreak in two nurseries. <i>Microbial Genomics</i> , 2019, 5, .	2.0	3
47	Complete Genome Sequence of an Enterohemorrhagic <i>Escherichia coli</i> O111:H8 Strain Recovered from a Large Outbreak in Japan Associated with Consumption of Raw Beef. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	3
48	Whole-Genome Sequence of CMY-2 β -Lactamase-Producing <i>Salmonella enterica</i> Serovar Typhimurium Strain L-3553. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
49	Complete Genome Sequence of a Sequence Type 4846 <i>Streptococcus pneumoniae</i> Serotype 12F Strain Isolated from a Meningitis Case in Japan. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1