## Chien-Shun Chiou

List of Publications by Year in descending order

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97 papers

2,362 citations

28 h-index 253896 43 g-index

98 all docs 98 docs citations

98 times ranked 2874 citing authors

#	Article	IF	CITATIONS
1	cgMLST@Taiwan: A web service platform for Vibrio cholerae cgMLST profiling and global strain tracking. Journal of Microbiology, Immunology and Infection, 2022, 55, 102-106.	1.5	5
2	Antimicrobial Resistance in Campylobacter coli and Campylobacter jejuni from Human Campylobacteriosis in Taiwan, 2016 to 2019. Antimicrobial Agents and Chemotherapy, 2022, 66, AAC0173621.	1.4	15
3	Changing epidemiology of shigellosis in Taiwan, 2010-2019: an emerging threat to HIV-infected patients and men who have sex with men. Emerging Microbes and Infections, 2022, 11, 498-506.	3.0	5
4	Association between Escherichia coli with Notl-restriction resistance and urinary tract infections. Journal of Microbiology, Immunology and Infection, 2022, 55, 686-694.	1.5	0
5	A nosocomial salmonellosis outbreak caused by blaOXA-48–carrying, extensively drug-resistant Salmonella enterica serovar Goldcoast in a hospital respiratory care ward in Taiwan. Journal of Global Antimicrobial Resistance, 2022, 29, 331-338.	0.9	3
6	Demographic Features of Invasive Meningococcal Disease in Taiwan, 1993 to 2020, and Genetic Characteristics of Neisseria meningitidis Isolates, 2003 to 2020. Microbiology Spectrum, 2022, 10, .	1.2	3
7	The first imported case of extensively drug-resistant Salmonella enterica serotype Typhi infection in Taiwan and the antimicrobial therapy. Journal of Microbiology, Immunology and Infection, 2021, 54, 740-744.	1.5	18
8	Integrative and Conjugative Element-Mediated Azithromycin Resistance in Multidrug-Resistant Salmonella enterica Serovar Albany. Antimicrobial Agents and Chemotherapy, 2021, 65, .	1.4	7
9	Colonization dynamics of Klebsiella pneumoniae in the pet animals and human owners in a single household. Veterinary Microbiology, 2021, 256, 109050.	0.8	6
10	Microbiological and genomic investigations of invasive Salmonella enterica serovar Panama from a large outbreak in Taiwan. Journal of the Formosan Medical Association, 2021, 121, 660-660.	0.8	1
11	Assessment of metrics in next-generation sequencing experiments for use in core-genome multilocus sequence type. PeerJ, 2021, 9, e11842.	0.9	2
12	Two ST11 <i>Klebsiella pneumoniae</i> strains exacerbate colorectal tumorigenesis in a colitis-associated mouse model. Gut Microbes, 2021, 13, 1980348.	4.3	12
13	RamAp, an efflux pump regulator carried by an IncHI2 plasmid. Antimicrobial Agents and Chemotherapy, 2021, , AAC0115221.	1.4	3
14	Emergence of <i>Vibrio cholerae </i> O1 Sequence Type 75 in Taiwan. Emerging Infectious Diseases, 2020, 26, 164-166.	2.0	8
15	Meningococcal disease surveillance in the Asia–Pacific region (2020): The global meningococcal initiative. Journal of Infection, 2020, 81, 698-711.	1.7	51
16	Investigation of a salmonellosis outbreak linked to French toast sandwich with the use of surveillance camera, Taiwan, 2018. Epidemiology and Infection, 2020, 148, e100.	1.0	0
17	Genomic diversity of Salmonella enterica -The UoWUCC 10K genomes project. Wellcome Open Research, 2020, 5, 223.	0.9	38
18	Emergence of Multidrug-Resistant Salmonella enterica Serovar Goldcoast Strains in Taiwan and International Spread of the ST358 Clone. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	14

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19	Transmission and evolution of OXA-48-producing Klebsiella pneumoniae ST11 in a single hospital in Taiwan. Journal of Antimicrobial Chemotherapy, 2019, 75, 318-326.	1.3	16
20	Cocarriage of Distinct <i>bla</i> <sub>KPC-2</sub> and <i>bla</i> <sub>OXA-48</sub> Plasmids in a Single Sequence Type 11 Carbapenem-Resistant Klebsiella pneumoniae Isolate. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	16
21	New Multidrug-Resistant <i>Salmonella enterica </i> Serovar Anatum Clone, Taiwan, 2015–2017. Emerging Infectious Diseases, 2019, 25, 144-147.	2.0	23
22	Salmonella enterica serotype typhimurium and S. Stanley differ in genomic evolutionary patterns and early immune responses in human THP-1 cell line and CD14+ monocytes. Comparative Immunology, Microbiology and Infectious Diseases, 2019, 63, 10-16.	0.7	3
23	Shigellosis outbreak among MSM living with HIV: a case–control study in Taiwan, 2015–2016. Sexually Transmitted Infections, 2019, 95, 67-70.	0.8	24
24	Draft genome sequence of CTX-M-type $\hat{l}^2$ -lactamase-producing Klebsiella quasipneumoniae subsp. similipneumoniae isolated from a Box turtle. Journal of Global Antimicrobial Resistance, 2018, 12, 235-236.	0.9	8
25	The association of Salmonella enterica from aquatic environmental and clinical samples in Taiwan. Science of the Total Environment, 2018, 624, 106-113.	3.9	9
26	Genetic Relationships among Multidrug-Resistant Salmonella enterica Serovar Typhimurium Strains from Humans and Animals. Antimicrobial Agents and Chemotherapy, 2018, 62, .	1.4	17
27	Clonal dissemination of carbapenemase-producing Klebsiella pneumoniae: Two distinct sub-lineages of Sequence Type 11 carrying blaKPC-2 and blaOXA-48. International Journal of Antimicrobial Agents, 2018, 52, 658-662.	1.1	30
28	Molecular characterization of antimicrobial susceptibility of Salmonella isolates: First identification of a plasmid carrying qnrD or oqxAB in Taiwan. Journal of Microbiology, Immunology and Infection, 2017, 50, 214-223.	1.5	19
29	Dissemination of <i>mcr-1</i> -Carrying Plasmids among Colistin-Resistant Salmonella Strains from Humans and Food-Producing Animals in Taiwan. Antimicrobial Agents and Chemotherapy, 2017, 61, .	1.4	49
30	Highly prevalent emmSTG840.0 and emmSTC839.0 types of erythromycin non-susceptible group G Streptococcus isolated from bacteremia in southern Taiwan. Journal of Microbiology, Immunology and Infection, 2017, 50, 831-838.	1.5	6
31	Azithromycin-Nonsusceptible <i>Shigella flexneri</i> 3a in Men Who Have Sex with Men, Taiwan, 2015–2016. Emerging Infectious Diseases, 2016, 23, 345-346.	2.0	28
32	Construction of a Pan-Genome Allele Database of Salmonella enterica Serovar Enteritidis for Molecular Subtyping and Disease Cluster Identification. Frontiers in Microbiology, 2016, 7, 2010.	1.5	17
33	PGAdb-builder: A web service tool for creating pan-genome allele database for molecular fine typing. Scientific Reports, 2016, 6, 36213.	1.6	62
34	Global phylogeography and evolutionary history of Shigella dysenteriae type 1. Nature Microbiology, 2016, 1, 16027.	5.9	65
35	<i>Clostridium difficile</i> PCR Ribotype 027 Emerges in Taiwan. Japanese Journal of Infectious Diseases, 2015, 68, 338-340.	0.5	5
36	Chromosome-Mediated Multidrug Resistance in Salmonella enterica Serovar Typhi. Antimicrobial Agents and Chemotherapy, 2015, 59, 721-723.	1.4	18

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37	Usefulness of pulsed-field gel electrophoresis profiles for the determination of Salmonella serovars. International Journal of Food Microbiology, 2015, 214, 1-3.	2.1	16
38	Molecular typing and epidemiology of Clostridium difficile in respiratory care wards of central Taiwan. Journal of Microbiology, Immunology and Infection, 2015, 48, 65-71.	1.5	10
39	Liver abscess caused by Klebsiella pneumoniae in a red-footed tortoise. Journal of Microbiology, Immunology and Infection, 2015, 48, 347-349.	1.5	3
40	Clustered Regularly Interspaced Short Palindromic Repeats Are emm Type-Specific in Highly Prevalent Group A Streptococci. PLoS ONE, 2015, 10, e0145223.	1.1	5
41	An Association of Genotypes and Antimicrobial Resistance Patterns among Salmonella Isolates from Pigs and Humans in Taiwan. PLoS ONE, 2014, 9, e95772.	1.1	44
42	A Large Outbreak of Salmonellosis Associated with Sandwiches Contaminated with Multiple Bacterial Pathogens Purchased via an Online Shopping Service. Foodborne Pathogens and Disease, 2014, 11, 230-233.	0.8	9
43	Antimicrobial Resistance in Salmonella enterica Serovar Typhi Isolates from Bangladesh, Indonesia, Taiwan, and Vietnam. Antimicrobial Agents and Chemotherapy, 2014, 58, 6501-6507.	1.4	55
44	Prolonged clonal spreading and dynamic changes in antimicrobial resistance of Escherichia coli ST68 among patients who stayed in a respiratory care ward. Journal of Medical Microbiology, 2014, 63, 1531-1541.	0.7	7
45	Infrequent cross-transmission of Shigella flexneri 2a strains among villages of a mountainous township in Taiwan with endemic shigellosis. BMC Infectious Diseases, 2013, 13, 354.	1.3	6
46	Suitable restriction enzyme for standardization of pulsed-field gel electrophoresis protocol and interlaboratory comparison of Acinetobacter baumannii. Journal of Microbiology, Immunology and Infection, 2013, 46, 195-201.	1.5	9
47	A simple approach to obtain comparable Shigella sonnei MLVA results across laboratories. International Journal of Medical Microbiology, 2013, 303, 678-684.	1.5	8
48	Multidrug-resistant Salmonella enterica serovar Panama carrying class 1 integrons is invasive in Taiwanese children. Journal of the Formosan Medical Association, 2013, 112, 269-275.	0.8	15
49	Human isolates of Salmonella enterica serovar Typhimurium from Taiwan displayed significantly higher levels of antimicrobial resistance than those from Denmark. International Journal of Food Microbiology, 2013, 161, 69-75.	2.1	22
50	Molecular characterization of clinical and environmental Vibrio parahaemolyticus isolates in Taiwan. International Journal of Food Microbiology, 2013, 165, 18-26.	2.1	28
51	Detection of Salmonella in Chicken Meat by Insulated Isothermal PCR. Journal of Food Protection, 2013, 76, 1322-1329.	0.8	21
52	Salmonella enterica Serovar Typhi Variants in Long-Term Carriers. Journal of Clinical Microbiology, 2013, 51, 669-672.	1.8	12
53	Use of multilocus variable-number tandem repeat analysis in molecular subtyping of Salmonella enterica serovar Typhi isolates. Journal of Medical Microbiology, 2012, 61, 223-232.	0.7	16
54	Comparison of the pulsed field gel electrophoresis patterns and virulence profiles of the multidrug resistant strains of Salmonella enterica serovar Schwarzengrund isolated from chicken meat and humans in Taiwan. Food Research International, 2012, 45, 978-983.	2.9	6

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55	Combined rpo B duplex PCR and hsp65 PCR restriction fragment length polymorphism with capillary electrophoresis as an effective algorithm for identification of Mycobacterial species from clinical isolates. BMC Microbiology, 2012, 12, 137.	1.3	9
56	Reduction of Salmonella enterica serovar Choleraesuis carrying large virulence plasmids after the foot and mouth disease outbreak in swine in southern Taiwan, and their independent evolution in human and pig. Journal of Microbiology, Immunology and Infection, 2012, 45, 418-425.	1.5	8
57	Comparison of multilocus variable-number tandem repeat analysis and pulsed-field gel electrophoresis in molecular subtyping of Salmonella enterica serovars Paratyphi A. Diagnostic Microbiology and Infectious Disease, 2011, 69, 1-6.	0.8	22
58	Global Distribution of <i>Shigella sonnei </i> Clones. Emerging Infectious Diseases, 2011, 17, 1910-1912.	2.0	24
59	Characterization of 13 multi-drug resistant Salmonella serovars from different broiler chickens associated with those of human isolates. BMC Microbiology, 2010, 10, 86.	1.3	27
60	Development and evaluation of multilocus variable number tandem repeat analysis for fine typing and phylogenetic analysis of Salmonella enterica serovar Typhimurium. International Journal of Food Microbiology, 2010, 142, 67-73.	2.1	32
61	Prevalence and Antimicrobial Susceptibility of Salmonellae Isolates from Reptiles in Taiwan. Journal of Veterinary Diagnostic Investigation, 2010, 22, 44-50.	0.5	39
62	Molecular epidemiology of Mycobacterium abscessus infections in a subtropical chronic ventilatory setting. Journal of Medical Microbiology, 2010, 59, 1203-1211.	0.7	19
63	Identification of prophage gene z2389 in Escherichia coli EDL933 encoding a DNA cytosine methyltransferase for full protection of Notl sites. International Journal of Medical Microbiology, 2010, 300, 296-303.	1.5	3
64	Multilocus variable-number tandem repeat analysis as a molecular tool for subtyping and phylogenetic analysis of bacterial pathogens. Expert Review of Molecular Diagnostics, 2010, 10, 5-7.	1.5	19
65	Utility of Multilocus Variable-Number Tandem-Repeat Analysis as a Molecular Tool for Phylogenetic Analysis of <i>Shigella sonnei </i> ). Journal of Clinical Microbiology, 2009, 47, 1149-1154.	1.8	38
66	Association of the shuffling of Streptococcus pyogenes clones and the fluctuation of scarlet fever cases between 2000 and 2006 in central Taiwan. BMC Microbiology, 2009, 9, 115.	1.3	10
67	Clonal dissemination of the multi-drug resistant Salmonella enterica serovar Braenderup, but not the serovar Bareilly, of prevalent serogroup C1 Salmonella from Taiwan. BMC Microbiology, 2009, 9, 264.	1.3	20
68	Multilocus variable-number tandem repeat analysis for molecular typing and phylogenetic analysis of Shigella flexneri. BMC Microbiology, 2009, 9, 278.	1.3	27
69	PCR detection of Staphylococcal enterotoxins (SEs) N, O, P, Q, R, U, and survey of SE types in Staphylococcus aureus isolates from food-poisoning cases in Taiwan. International Journal of Food Microbiology, 2008, 121, 66-73.	2.1	132
70	Foodborne disease outbreaks caused by sucrose-nonfermenting and $\hat{l}^2$ -galactosidase-deficient variants of Vibrio cholerae. International Journal of Food Microbiology, 2008, 122, 148-155.	2.1	10
71	Microarray for molecular typing of Salmonella enterica serovars. Molecular and Cellular Probes, 2008, 22, 238-243.	0.9	46
72	Evaluation of restriction enzymes for standardizing pulsed-field gel electrophoresis protocol for rapid subtyping of Vibrio parahaemolyticus. Diagnostic Microbiology and Infectious Disease, 2008, 61, 251-255.	0.8	7

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73	Prevalence and Characterization of Multidrug-Resistant (Type ACSSuT) <i>Salmonella enterica</i> Serovar Typhimurium Strains in Isolates from Four Gosling Farms and a Hatchery Farm. Journal of Clinical Microbiology, 2008, 46, 522-526.	1.8	32
74	Emergence of Qnr determinants in human Salmonella isolates in Taiwan. Journal of Antimicrobial Chemotherapy, 2008, 62, 1269-1272.	1.3	35
75	VNTRDB: a bacterial variable number tandem repeat locus database. Nucleic Acids Research, 2007, 35, D416-D421.	6.5	33
76	Multilocus Variable-Number Tandem-Repeat Analysis for Molecular Typing of <i>Shigella sonnei</i> Journal of Clinical Microbiology, 2007, 45, 3574-3580.	1.8	56
77	Suitable restriction enzymes for pulsed-field gel electrophoresis analysis of Candida tropicalis. Diagnostic Microbiology and Infectious Disease, 2007, 57, 451-454.	0.8	6
78	Epidemiology and evolution of genotype and antimicrobial resistance of an imported Shigella sonnei clone circulating in central Taiwan. Diagnostic Microbiology and Infectious Disease, 2007, 58, 469-475.	0.8	37
79	A pulsed-field gel electrophoresis typing scheme for Vibrio parahaemolyticus isolates from fifteen countries. International Journal of Food Microbiology, 2007, 114, 280-287.	2.1	25
80	A simple and low-cost paper-bridged method for Salmonella phase reversal. Diagnostic Microbiology and Infectious Disease, 2006, 54, 315-317.	0.8	11
81	The suitable restriction enzymes for pulsed-field gel electrophoresis analysis of Bordetella pertussis. Diagnostic Microbiology and Infectious Disease, 2006, 56, 217-219.	0.8	7
82	Molecular epidemiology and emergence of worldwide epidemic clones of Neisseria meningitidis in Taiwan. BMC Infectious Diseases, 2006, 6, 25.	1.3	54
83	Use of a multilocus variable-number tandem repeat analysis method for molecular subtyping and phylogenetic analysis of Neisseria meningitidis isolates. BMC Microbiology, 2006, 6, 44.	1.3	31
84	Usefulness of Inter-IS 1 Spacer Polymorphisms for Subtyping of Shigella sonnei Isolates. Journal of Clinical Microbiology, 2006, 44, 3928-3933.	1.8	9
85	Cephalosporin and Ciprofloxacin Resistance in <i>Salmonella</i> , Taiwan. Emerging Infectious Diseases, 2005, 18, 947-950.	2.0	27
86	Epidemiologic Relationship between Fluoroquinolone-Resistant Salmonella enterica Serovar Choleraesuis Strains Isolated from Humans and Pigs in Taiwan (1997 to 2002). Journal of Clinical Microbiology, 2005, 43, 2798-2804.	1.8	27
87	Epidemiology and Molecular Characterization of Streptococcus pyogenes Recovered from Scarlet Fever Patients in Central Taiwan from 1996 to 1999. Journal of Clinical Microbiology, 2004, 42, 3998-4006.	1.8	41
88	Use of novel PCR primers specific to the genes of staphylococcal enterotoxin G, H, I for the survey of Staphylococcus aureus strains isolated from food-poisoning cases and food samples in Taiwan. International Journal of Food Microbiology, 2004, 92, 189-197.	2.1	66
89	Conversion of Shigella flexneriserotype 2a to serotype Y in a shigellosis patient due to a single amino acid substitution in the protein product of the bacterial glucosyltransferasegtrllgene. FEMS Microbiology Letters, 2003, 224, 277-283.	0.7	10
90	Molecular Epidemiology of Shigella in a Taiwan Township during 1996 to 2000. Journal of Clinical Microbiology, 2003, 41, 3078-3088.	1.8	11

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91	Development and use of PCR primers for the investigation of C1, C2 and C3 enterotoxin types of Staphylococcus aureus strains isolated from food-borne outbreaks. International Journal of Food Microbiology, 2001, 71, 63-70.	2.1	33
92	Molecular Epidemiology of a Shigella flexneri Outbreak in a Mountainous Township in Taiwan, Republic of China. Journal of Clinical Microbiology, 2001, 39, 1048-1056.	1.8	41
93	Vibrio parahaemolyticus Serovar O3:K6 as Cause of Unusually High Incidence of Food-Borne Disease Outbreaks in Taiwan from 1996 to 1999. Journal of Clinical Microbiology, 2000, 38, 4621-4625.	1.8	112
94	Characteristics of Vibrio parahaemolyticus O3:K6 from Asia. Applied and Environmental Microbiology, 2000, 66, 3981-3986.	1.4	153
95	Comparison of Pulsed-Field Gel Electrophoresis and Coagulase Gene Restriction Profile Analysis Techniques in the Molecular Typing of Staphylococcus aureus. Journal of Clinical Microbiology, 2000, 38, 2186-2190.	1.8	43
96	Cloning and characterization of the carp prolactin gene. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1991, 1088, 315-318.	2.4	17
97	The complete nucleotide sequence of the growth-hormone gene from the common carp (Cyprinus) Tj ETQq $1\ 1$	0.784314 2.4	rgBT_/Overloc