## Hao Chung The

List of Publications by Year in descending order

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623188 610482 24 995 14 24 citations g-index h-index papers 26 26 26 1544 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Dynamic of the human gut microbiome under infectious diarrhea. Current Opinion in Microbiology, 2022, 66, 79-85.	2.3	23
2	Colonization with Staphylococcus aureus and Klebsiella pneumoniae causes infections in a Vietnamese intensive care unit. Microbial Genomics, $2021, 7, \ldots$	1.0	10
3	Evolutionary histories and antimicrobial resistance in Shigella flexneri and Shigella sonnei in Southeast Asia. Communications Biology, 2021, 4, 353.	2.0	17
4	The Gut Microbiome of Healthy Vietnamese Adults and Children Is a Major Reservoir for Resistance Genes Against Critical Antimicrobials. Journal of Infectious Diseases, 2021, 224, S840-S847.	1.9	3
5	Exploring the Genomic Diversity and Antimicrobial Susceptibility of Bifidobacterium pseudocatenulatum in a Vietnamese Population. Microbiology Spectrum, 2021, 9, e0052621.	1.2	6
6	The identification of novel immunogenic antigens as potential Shigella vaccine components. Genome Medicine, 2021, 13, 8.	3.6	9
7	The evolutionary history of Shigella flexneri serotype 6 in Asia. Microbial Genomics, 2021, 7, .	1.0	3
8	Pathogenic Escherichia coli Possess Elevated Growth Rates under Exposure to Sub-Inhibitory Concentrations of Azithromycin. Antibiotics, 2020, 9, 735.	1.5	5
9	Genomic Serotyping, Clinical Manifestations, and Antimicrobial Resistance of Nontyphoidal <i>Salmonella</i> Gastroenteritis in Hospitalized Children in Ho Chi Minh City, Vietnam. Journal of Clinical Microbiology, 2020, 58, .	1.8	18
10	Commensal Escherichia coli are a reservoir for the transfer of XDR plasmids into epidemic fluoroquinolone-resistant Shigella sonnei. Nature Microbiology, 2020, 5, 256-264.	5.9	43
11	Dissecting the molecular evolution of fluoroquinolone-resistant Shigella sonnei. Nature Communications, 2019, 10, 4828.	5.8	41
12	Azithromycin Resistance in Shigella spp. in Southeast Asia. Antimicrobial Agents and Chemotherapy, 2018, 62, .	1.4	37
13	Assessing gut microbiota perturbations during the early phase of infectious diarrhea in Vietnamese children. Gut Microbes, 2018, 9, 38-54.	4.3	66
14	A Double-blind, Randomized, Placebo-controlled Trial of Lactobacillus acidophilus for the Treatment of Acute Watery Diarrhea in Vietnamese Children. Pediatric Infectious Disease Journal, 2018, 37, 35-42.	1.1	24
15	Out of Asia: the independent rise and global spread of fluoroquinolone-resistant Shigella. Microbial Genomics, 2018, 4, .	1.0	14
16	Recent insights into Shigella: a major contributor to the global diarrhoeal disease burden. Current Opinion in Infectious Diseases, 2018, 31, 449-454.	1.3	134
17	Rapid environmental effects on gut nematode susceptibility in rewilded mice. PLoS Biology, 2018, 16, e2004108.	2.6	97
18	Excess body weight and age associated with the carriage of fluoroquinolone and third-generation cephalosporin resistance genes in commensal Escherichia coli from a cohort of urban Vietnamese children. Journal of Medical Microbiology, 2018, 67, 1457-1466.	0.7	8

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19	South Asia as a Reservoir for the Global Spread of Ciprofloxacin-Resistant Shigella sonnei: A Cross-Sectional Study. PLoS Medicine, 2016, 13, e1002055.	3.9	84
20	Inducible colistin resistance via a disrupted plasmid-borne <i>mcr-1</i> gene in a 2008 Vietnamese <i>Shigella sonnei</i> i>isolate. Journal of Antimicrobial Chemotherapy, 2016, 71, 2314-2317.	1.3	82
21	The genomic signatures of Shigella evolution, adaptation and geographical spread. Nature Reviews Microbiology, 2016, 14, 235-250.	13.6	142
22	Clinical implications of reduced susceptibility to fluoroquinolones in paediatric <i>Shigella sonnei</i> and <i>Shigella flexneri</i> infections. Journal of Antimicrobial Chemotherapy, 2016, 71, 807-815.	1.3	13
23	A highâ€resolution genomic analysis of multidrugâ€resistant hospital outbreaks of <i>Klebsiella pneumoniae</i> . EMBO Molecular Medicine, 2015, 7, 227-239.	3.3	104
24	Introduction and establishment of fluoroquinolone-resistant Shigella sonnei into Bhutan. Microbial Genomics, 2015, 1, e000042.	1.0	11