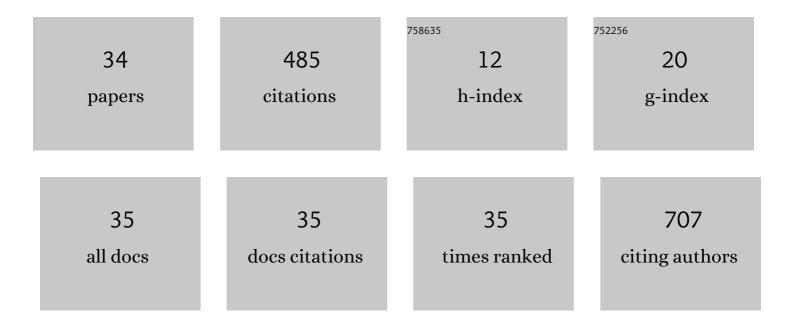
## Eng Guan Chua

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Changes in the rodent gut microbiome following chronic restraint stress and low-intensity rTMS. Neurobiology of Stress, 2022, 17, 100430.	1.9	15
2	Investigating the development of diarrhoea through gene expression analysis in sheep genetically resistant to gastrointestinal helminth infection. Scientific Reports, 2022, 12, 2207.	1.6	4
3	Bacterial communities in the gastrointestinal tract segments of helminth-resistant and helminth-susceptible sheep. Animal Microbiome, 2022, 4, 23.	1.5	6
4	Contribution of the Immune Response in the Ileum to the Development of Diarrhoea caused by Helminth Infection: Studies with the Sheep Model. Functional and Integrative Genomics, 2022, 22, 865-877.	1.4	2
5	Microbiome data reveal significant differences in the bacterial diversity in freshwater rohu ( <i>Labeo) Tj ETQq1 1</i>	0,784314	4 rgBT /Over
6	Comparative Transcriptomic and Molecular Pathway Analyses of HL-CZ Human Pro-Monocytic Cells Expressing SARS-CoV-2 Spike S1, S2, NP, NSP15 and NSP16 Genes. Microorganisms, 2021, 9, 1193.	1.6	9
7	A re-testing range is recommended for 13C- and 14C-urea breath tests for Helicobacter pylori infection in China. Gut Pathogens, 2021, 13, 38.	1.6	6
8	Ethanol extract of mulberry leaves partially restores the composition of intestinal microbiota and strengthens liver glycogen fragility in type 2 diabetic rats. BMC Complementary Medicine and Therapies, 2021, 21, 172.	1.2	17
9	Absence of BapA type III effector protein affects Burkholderia pseudomallei intracellular lifecycle in human host cells. Process Biochemistry, 2021, 108, 48-59.	1.8	1
10	Changes in the Gut Microbiome and Predicted Functional Metabolic Effects in an Australian Parkinson's Disease Cohort. Frontiers in Neuroscience, 2021, 15, 756951.	1.4	15
11	A novel taxon selection method, aimed at minimizing recombination, clarifies the discovery of a new subâ€population of <i>Helicobacter pylori</i> from Australia. Evolutionary Applications, 2020, 13, 278-289.	1.5	6
12	Mutations of Helicobacter pylori RdxA are mainly related to the phylogenetic origin of the strain and not to metronidazole resistance. Journal of Antimicrobial Chemotherapy, 2020, 75, 3152-3155.	1.3	13
13	Actual and estimated adenoma detection rates: a 2â€year monocentric colonoscopic screening outcome in Shenzhen, China. JGH Open, 2020, 4, 707-712.	0.7	1
14	Bacillus mycoides supplemented diet modulates the health status, gut microbiota and innate immune response of freshwater crayfish marron (Cherax cainii). Animal Feed Science and Technology, 2020, 262, 114408.	1.1	3
15	Prevalence and risk factors of <i>Helicobacter pylori</i> infection among children in Kuichong Subdistrict of Shenzhen City, China. PeerJ, 2020, 8, e8878.	0.9	4
16	The Influence of Modernization and Disease on the Gastric Microbiome of Orang Asli, Myanmars and Modern Malaysians. Microorganisms, 2019, 7, 174.	1.6	8
17	High primary resistance to metronidazole and levofloxacin, and a moderate resistance to clarithromycin in Helicobacter pylori isolated from Karnataka patients. Gut Pathogens, 2019, 11, 21.	1.6	30
18	The complete genome and methylome of Helicobacter pylori hpNEAfrica strain HP14039. Gut Pathogens, 2019, 11, 7.	1.6	5

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19	Analysis of core protein clusters identifies candidate variable sites conferring metronidazole resistance in <i>Helicobacter pylori</i> . Gastroenterology Report, 2019, 7, 42-49.	0.6	18
20	Gastric <i>Helicobacter pylori</i> infection perturbs human oral microbiota. PeerJ, 2019, 7, e6336.	0.9	9
21	Draft Genome Sequences of 42 <i>Helicobacter pylori</i> Isolates from Rural Regions of South India. Genome Announcements, 2018, 6, .	0.8	3
22	Metabolomics and 16S rRNA sequencing of human colorectal cancers and adjacent mucosa. PLoS ONE, 2018, 13, e0208584.	1.1	39
23	Quantum changes in <i>Helicobacter pylori</i> gene expression accompany host-adaptation. DNA Research, 2017, 24, dsw046.	1.5	8
24	Helicobacter pylori gene silencing in vivo demonstrates urease is essential for chronic infection. PLoS Pathogens, 2017, 13, e1006464.	2.1	64
25	Assessment of Risk and Sero-Prevalence of Helicobacter pylori Colonization among Remote Orang Asli Tribes in Peninsula Malaysia. PLoS ONE, 2016, 11, e0159830.	1.1	9
26	Comparative Genomics Revealed Multiple Helicobacter pylori Genes Associated with Biofilm Formation In Vitro. PLoS ONE, 2016, 11, e0166835.	1.1	36
27	Fucoidans Disrupt Adherence of <i>Helicobacter pylori</i> to AGS Cells <i>In Vitro</i> . Evidence-based Complementary and Alternative Medicine, 2015, 2015, 1-6.	0.5	26
28	The complete methylome of Helicobacter pylori UM032. BMC Genomics, 2015, 16, 424.	1.2	57
29	Determinants of Proteolysis and Cell-Binding for the Shigella flexneri Cytotoxin, SigA. Current Microbiology, 2015, 71, 613-617.	1.0	4
30	Functional Characterizations of Effector Protein BipC, a Type III Secretion System Protein, in Burkholderia pseudomallei Pathogenesis. Journal of Infectious Diseases, 2015, 211, 827-834.	1.9	21
31	Comparing the genomes of Helicobacter pylori clinical strain UM032 and Mice-adapted derivatives. Gut Pathogens, 2013, 5, 25.	1.6	13
32	Draft Genome Sequences of Helicobacter pylori Isolates from Malaysia, Cultured from Patients with Functional Dyspepsia and Gastric Cancer. Journal of Bacteriology, 2012, 194, 5695-5696.	1.0	7
33	Helicobacter pylori virulence and antibiotic susceptibility pattern in Malaysian patients. International Journal of Infectious Diseases, 2012, 16, e226.	1.5	1
34	Phenotypic Detection of Metallo- <i>β</i> -Lactamase in Imipenem-Resistant <i>Pseudomonas aeruginosa</i> . Scientific World Journal, The, 2012, 2012, 1-7.	0.8	25