

Yun Kit Yeoh

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

35 papers	2,153 citations	18 h-index	41 g-index
41 ext. papers	3,560 ext. citations	9.8 avg, IF	5.2 L-index

#	Paper	IF	Citations
35	Gut microbiota dynamics in a prospective cohort of patients with post-acute COVID-19 syndrome.. <i>Gut</i> , 2022 ,	19.2	41
34	Removing Host-derived DNA Sequences from Microbial Metagenomes via Mapping to Reference Genomes. <i>Methods in Molecular Biology</i> , 2021 , 2232, 147-153	1.4	0
33	Prolonged Impairment of Short-Chain Fatty Acid and L-Isoleucine Biosynthesis in Gut Microbiome in Patients With COVID-19. <i>Gastroenterology</i> , 2021 ,	13.3	17
32	Depicting SARS-CoV-2 faecal viral activity in association with gut microbiota composition in patients with COVID-19. <i>Gut</i> , 2021 , 70, 276-284	19.2	180
31	Effects of different rotational legume crops and residue management regimes on soil microbial properties and functions in a sugarcane farming system. <i>Journal of Plant Nutrition and Soil Science</i> , 2021 , 184, 398-408	2.3	1
30	Temporal landscape of human gut RNA and DNA virome in SARS-CoV-2 infection and severity. <i>Microbiome</i> , 2021 , 9, 91	16.6	13
29	Reply. <i>Gastroenterology</i> , 2021 , 160, 2193-2195	13.3	1
28	Population-Level Configurations of Gut Mycobiome Across 6 Ethnicities in Urban and Rural China. <i>Gastroenterology</i> , 2021 , 160, 272-286.e11	13.3	11
27	Gut microbiota composition reflects disease severity and dysfunctional immune responses in patients with COVID-19. <i>Gut</i> , 2021 , 70, 698-706	19.2	312
26	Longitudinal dynamics of gut bacteriome, mycobiome and virome after fecal microbiota transplantation in graft-versus-host disease. <i>Nature Communications</i> , 2021 , 12, 65	17.4	16
25	Underdevelopment of the gut microbiota and bacteria species as non-invasive markers of prediction in children with autism spectrum disorder. <i>Gut</i> , 2021 ,	19.2	9
24	Alterations in the Gut Virome in Obesity and Type 2 Diabetes Mellitus. <i>Gastroenterology</i> , 2021 , 161, 1257-1269.e13	13.3	13
23	Sa1915 POPULATION-LEVEL CONFIGURATIONS OF GUT MYCOBIOME ACROSS SIX ETHNICITIES IN URBAN AND RURAL CHINA. <i>Gastroenterology</i> , 2020 , 158, S-478-S-479	13.3	4
22	Alterations in Gut Microbiota of Patients With COVID-19 During Time of Hospitalization. <i>Gastroenterology</i> , 2020 , 159, 944-955.e8	13.3	555
21	Swine methicillin-resistant carrying toxic-shock syndrome toxin gene in Hong Kong, China. <i>Emerging Microbes and Infections</i> , 2020 , 9, 1534-1536	18.9	1
20	Epidemiological characteristics of the first 100 cases of coronavirus disease 2019 (COVID-19) in Hong Kong Special Administrative Region, China, a city with a stringent containment policy. <i>International Journal of Epidemiology</i> , 2020 , 49, 1096-1105	7.8	18
19	Southern Chinese populations harbour non-nucleatum <i>Fusobacterium</i> possessing homologues of the colorectal cancer-associated FadA virulence factor. <i>Gut</i> , 2020 , 69, 1998-2007	19.2	16

18	Systematic review of human gut resistome studies revealed variable definitions and approaches. <i>Gut Microbes</i> , 2020 , 12, 1700755	8.8	7
17	Scientific frontiers in faecal microbiota transplantation: joint document of Asia-Pacific Association of Gastroenterology (APAGE) and Asia-Pacific Society for Digestive Endoscopy (APSDE). <i>Gut</i> , 2020 , 69, 83-91	19.2	42
16	Human-Gut-DNA Virome Variations across Geography, Ethnicity, and Urbanization. <i>Cell Host and Microbe</i> , 2020 , 28, 741-751.e4	23.4	30
15	Bacteria pathogens drive host colonic epithelial cell promoter hypermethylation of tumor suppressor genes in colorectal cancer. <i>Microbiome</i> , 2020 , 8, 108	16.6	14
14	Impact of Preservation Method and 16S rRNA Hypervariable Region on Gut Microbiota Profiling. <i>MSystems</i> , 2019 , 4,	7.6	59
13	Impact of inter- and intra-individual variation, sample storage and sampling fraction on human stool microbial community profiles. <i>PeerJ</i> , 2019 , 7, e6172	3.1	14
12	The human oral cavity microbiota composition during acute tonsillitis: a cross-sectional survey. <i>BMC Oral Health</i> , 2019 , 19, 275	3.7	11
11	Diversity of macaque microbiota compared to the human counterparts. <i>Scientific Reports</i> , 2018 , 8, 15573	4.9	24
10	Frequent Genetic Mismatch between Vaccine Strains and Circulating Seasonal Influenza Viruses, Hong Kong, China, 1996-2012. <i>Emerging Infectious Diseases</i> , 2018 , 24, 1825-1834	10.2	5
9	Evolutionary conservation of a core root microbiome across plant phyla along a tropical soil chronosequence. <i>Nature Communications</i> , 2017 , 8, 215	17.4	143
8	Legume crop rotation suppressed nitrifying microbial community in a sugarcane cropping soil. <i>Scientific Reports</i> , 2017 , 7, 16707	4.9	22
7	Crosstalk between sugarcane and a plant-growth promoting Burkholderia species. <i>Scientific Reports</i> , 2016 , 6, 37389	4.9	54
6	Comparative Genomics of Candidate Phylum TM6 Suggests That Parasitism Is Widespread and Ancestral in This Lineage. <i>Molecular Biology and Evolution</i> , 2016 , 33, 915-27	8.3	50
5	The core root microbiome of sugarcanes cultivated under varying nitrogen fertilizer application. <i>Environmental Microbiology</i> , 2016 , 18, 1338-51	5.2	111
4	Introducing BASE: the Biomes of Australian Soil Environments soil microbial diversity database. <i>GigaScience</i> , 2016 , 5, 21	7.6	131
3	Nitrogen fertilizer dose alters fungal communities in sugarcane soil and rhizosphere. <i>Scientific Reports</i> , 2015 , 5, 8678	4.9	105
2	A new species of Burkholderia isolated from sugarcane roots promotes plant growth. <i>Microbial Biotechnology</i> , 2014 , 7, 142-54	6.3	63
1	Dynamics of cathode-associated microbial communities and metabolite profiles in a glycerol-fed bioelectrochemical system. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 4008-14	4.8	53

