

# Mi Young Lim

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9517991/publications.pdf>

Version: 2024-02-01

19  
papers

1,272  
citations

567281

15  
h-index

794594

19  
g-index

19  
all docs

19  
docs citations

19  
times ranked

2500  
citing authors

#	ARTICLE	IF	CITATIONS
1	Association Between Gut Microbiome and Frailty in the Older Adult Population in Korea. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2021, 76, 1362-1368.	3.6	21
2	Gut Microbiome Structure and Association with Host Factors in a Korean Population. <i>MSystems</i> , 2021, 6, e0017921.	3.8	14
3	Diagnostic and prognostic potential of the oral and gut microbiome for lung adenocarcinoma. <i>Clinical and Translational Medicine</i> , 2021, 11, e508.	4.0	12
4	Effect of Saengshik Supplementation on the Gut Microbial Composition of Healthy Korean Adults: A Single-Group Pilot Study. <i>Frontiers in Nutrition</i> , 2021, 8, 743620.	3.7	2
5	Evaluation of fecal DNA extraction protocols for human gut microbiome studies. <i>BMC Microbiology</i> , 2020, 20, 212.	3.3	23
6	The human gut archaeome: identification of diverse haloarchaea in Korean subjects. <i>Microbiome</i> , 2020, 8, 114.	11.1	65
7	Changes in microbiome and metabolomic profiles of fecal samples stored with stabilizing solution at room temperature: a pilot study. <i>Scientific Reports</i> , 2020, 10, 1789.	3.3	22
8	Effects of <i>Lactobacillus pentosus</i> in Children with Allergen-Sensitized Atopic Dermatitis. <i>Journal of Korean Medical Science</i> , 2020, 35, e128.	2.5	18
9	Effect of raw potato starch on the gut microbiome and metabolome in mice. <i>International Journal of Biological Macromolecules</i> , 2019, 133, 37-43.	7.5	35
10	Comparison of DNA extraction methods for human gut microbial community profiling. <i>Systematic and Applied Microbiology</i> , 2018, 41, 151-157.	2.8	133
11	The effects of sequencing platforms on phylogenetic resolution in 16S rRNA gene profiling of human feces. <i>Scientific Data</i> , 2018, 5, 180068.	5.3	22
12	The effect of heritability and host genetics on the gut microbiota and metabolic syndrome. <i>Gut</i> , 2017, 66, 1031-1038.	12.1	283
13	Modeling environmental risk factors of autism in mice induces IBD-related gut microbial dysbiosis and hyperserotonemia. <i>Molecular Brain</i> , 2017, 10, 14.	2.6	56
14	Analysis of the association between host genetics, smoking, and sputum microbiota in healthy humans. <i>Scientific Reports</i> , 2016, 6, 23745.	3.3	58
15	Sub-clinical detection of gut microbial biomarkers of obesity and type 2 diabetes. <i>Genome Medicine</i> , 2016, 8, 17.	8.2	219
16	Enhancement of enteric adenovirus cultivation in a novel Ras-overexpressing cell line. <i>Journal of General Virology</i> , 2014, 95, 171-178.	2.9	2
17	Stability of Gut Enterotypes in Korean Monozygotic Twins and Their Association with Biomarkers and Diet. <i>Scientific Reports</i> , 2014, 4, 7348.	3.3	124
18	Characterization of Ozone Disinfection of Murine Norovirus. <i>Applied and Environmental Microbiology</i> , 2010, 76, 1120-1124.	3.1	59

#	ARTICLE	IF	CITATIONS
19	Disinfection kinetics of murine norovirus using chlorine and chlorine dioxide. Water Research, 2010, 44, 3243-3251.	11.3	104