Xiaofang Jiang

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A novel Ruminococcus gnavus clade enriched in inflammatory bowel disease patients. Genome Medicine, 2017, 9, 103.	8.2	478
2	Gut microbiota composition and functional changes in inflammatory bowel disease and irritable bowel syndrome. Science Translational Medicine, 2018, 10, .	12.4	351
3	High-throughput sequencing of SARS-CoV-2 in wastewater provides insights into circulating variants. Water Research, 2021, 205, 117710.	11.3	93
4	Invertible promoters mediate bacterial phase variation, antibiotic resistance, and host adaptation in the gut. Science, 2019, 363, 181-187.	12.6	85
5	Comprehensive analysis of chromosomal mobile genetic elements in the gut microbiome reveals phylum-level niche-adaptive gene pools. PLoS ONE, 2019, 14, e0223680.	2.5	59
6	Characterizing Transcriptional Regulatory Sequences in Coronaviruses and Their Role in Recombination. Molecular Biology and Evolution, 2021, 38, 1241-1248.	8.9	46
7	The Capacity to Produce Hydrogen Sulfide (H2S) via Cysteine Degradation Is Ubiquitous in the Human Gut Microbiome. Frontiers in Microbiology, 2021, 12, 705583.	3.5	37
8	KH domain proteins: Another family of bacterial RNA matchmakers?. Molecular Microbiology, 2022, 117, 10-19.	2.5	25
9	The taxonomic distribution of histamine-secreting bacteria in the human gut microbiome. BMC Genomics, 2021, 22, 695.	2.8	22
10	Bacteroidales species in the human gut are a reservoir of antibiotic resistance genes regulated by invertible promoters. Npj Biofilms and Microbiomes, 2022, 8, 1.	6.4	22
11	Taxonomic distribution and evolutionary analysis of the equol biosynthesis gene cluster. BMC Genomics, 2022, 23, 182.	2.8	10
12	Applications of de Bruijn graphs in microbiome research. , 2022, 1, .		2
13	Putative Host-Derived Insertions in the Genomes of Circulating SARS-CoV-2 Variants. MSystems, 2022, , e0017922.	3.8	1