Liang Xiao

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7581421/publications.pdf

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26	9,638	19	24
papers	citations	h-index	g-index
35	35	35	14058
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Over 50,000 Metagenomically Assembled Draft Genomes for the Human Oral Microbiome Reveal New Taxa. Genomics, Proteomics and Bioinformatics, 2022, 20, 246-259.	6.9	38
2	Mendelian randomization analyses support causal relationships between blood metabolites and the gut microbiome. Nature Genetics, 2022, 54, 52-61.	21.4	134
3	A Bacterial Genome and Culture Collection of Gut Microbial in Weanling Piglet. Microbiology Spectrum, 2022, 10, e0241721.	3.0	3
4	An Expanded Gene Catalog of Mouse Gut Metagenomes. MSphere, 2021, 6, .	2.9	13
5	Taxonomic Description and Genome Sequence of Christensenella intestinihominis sp. nov., a Novel Cholesterol-Lowering Bacterium Isolated From Human Gut. Frontiers in Microbiology, 2021, 12, 632361.	3 . 5	18
6	A genome-wide association study for gut metagenome in Chinese adults illuminates complex diseases. Cell Discovery, 2021, 7, 9.	6.7	49
7	Butyribacter intestini gen. nov., sp. nov., a butyric acid-producing bacterium of the family Lachnospiraceae isolated from human faeces, and reclassification of Acetivibrio ethanolgignens as Acetanaerobacter ethanolgignens gen. nov., comb. nov. Systematic and Applied Microbiology, 2021, 44, 126201.	2.8	21
8	Characterization and description of Faecalibacterium butyricigenerans sp. nov. and F. longum sp. nov., isolated from human faeces. Scientific Reports, 2021, 11, 11340.	3.3	42
9	A transomic cohort as a reference point for promoting a healthy human gut microbiome. Medicine in Microecology, 2021, 8, 100039.	1.6	24
10	Transplantation of microbiota from drug-free patients with schizophrenia causes schizophrenia-like abnormal behaviors and dysregulated kynurenine metabolism in mice. Molecular Psychiatry, 2020, 25, 2905-2918.	7.9	202
11	Metagenome-wide association of gut microbiomeÂfeatures for schizophrenia. Nature Communications, 2020, 11, 1612.	12.8	204
12	Relationship between the Gut Microbiome and Energy/Nutrient Intake in a Confined Bioregenerative Life Support System. Applied and Environmental Microbiology, 2020, 86, .	3.1	8
13	Characterization a Novel Butyric Acid-Producing Bacterium Collinsella aerofaciens Subsp. Shenzhenensis Subsp. Nov Microorganisms, 2019, 7, 78.	3.6	71
14	1,520 reference genomes from cultivated human gut bacteria enable functional microbiome analyses. Nature Biotechnology, 2019, 37, 179-185.	17.5	402
15	A novel affordable reagent for room temperature storage and transport of fecal samples for metagenomic analyses. Microbiome, 2018, 6, 43.	11.1	53
16	High-fat feeding rather than obesity drives taxonomical and functional changes in the gut microbiota in mice. Microbiome, 2017, 5, 43.	11.1	132
17	The gut microbiome in atherosclerotic cardiovascular disease. Nature Communications, 2017, 8, 845.	12.8	1,029
18	A reference gene catalogue of the pig gut microbiome. Nature Microbiology, 2016, 1, 16161.	13.3	416

#	Article	IF	CITATIONS
19	Dysbiosis of the fecal microbiota in the TNBS-induced Crohn's disease mouse model. Applied Microbiology and Biotechnology, 2016, 100, 4485-4494.	3.6	33
20	The complete mitochondrial genome of Pimephales promelas (Cypriniformes: Cyprinidae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3711-3712.	0.7	0
21	Gut microbiome development along the colorectal adenoma–carcinoma sequence. Nature Communications, 2015, 6, 6528.	12.8	1,062
22	The oral and gut microbiomes are perturbed in rheumatoid arthritis and partly normalized after treatment. Nature Medicine, 2015, 21, 895-905.	30.7	1,306
23	Dynamics and Stabilization of the Human Gut Microbiome during the First Year of Life. Cell Host and Microbe, 2015, 17, 690-703.	11.0	2,276
24	A catalog of the mouse gut metagenome. Nature Biotechnology, 2015, 33, 1103-1108.	17.5	422
25	An integrated catalog of reference genes in the human gut microbiome. Nature Biotechnology, 2014, 32, 834-841.	17.5	1,664
26	Efficient and stable metabarcoding sequencing data using a DNBSEQ-G400 sequencer validated by comprehensive community analyses. GigaByte, 0, 2021, 1-15.	0.0	10