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408	Simultaneous removal of nitrate, nitrobenzene and aniline from groundwater in a vertical baffled biofilm reactor. 2022 , 309, 136746	0
407	Postmortem submersion interval estimation of cadavers recovered from freshwater based on gut microbial community succession. 13,	o
406	Identification of Gut Microbiota Affecting Fiber Digestibility in Pigs. 2022, 44, 4557-4569	1
405	Sex Difference is a Determinant of Gut Microbes and Their Metabolites SCFAs/MCFAs in High Fat Diet Fed Rats. 2022 , 79,	1
404	Baseline gut microbial profiles are associated with the efficacy of Bacillus subtilis and Enterococcus faecium in IBS-D. 1-10	0
403	Alterations of bacteriome, mycobiome and metabolome characteristics in PCOS patients with normal/overweight individuals. 2022 , 15,	o
402	Gut Microbiome and Its Cofactors Are Linked to Lipoprotein Distribution Profiles. 2022, 10, 2156	1
401	C-section delivery induces gut barrier-microbiota imbalances in early life and leads to higher sensitivity to inflammation.	О
400	Breast cancer patients from the Midwest region of the United States have reduced levels of short-chain fatty acid-producing gut bacteria.	0
399	Microbiome-Metabolome Analysis of the Immune Microenvironment of the Cecal Contents, Soft Feces, and Hard Feces of Hyplus Rabbits. 2022 , 2022, 1-16	1
398	Screening Salamanders for Symbionts. 2023 , 425-442	O
397	The role of macrophyte-associated microbiomes in lacustrine wetlands: an example of the littoral zone of lake Atitlan, Guatemala.	О
396	Fish disease prevention via microbial dysbiosis-associated biomarkers in aquaculture.	0
395	A Study on the Possibility of Early Warning for Cochlodinium polykrikoides Blooms, Using Molecular Methods. 2022 , 14, 3115	o
394	Prophylactic effect of pectic oligosaccharides against poly I: C- induced virus-like infection in BALB/c mice.	0
393	Insight in the mechanism of alkali treatment methods effecting dewatered sludge fermentation from microbial characteristics. 2022 , 108861	0
392	The oral microbiome in treatment $na \overline{u}e$ paediatric IBD patients exhibits dysbiosis related to disease severity that resolves following therapy.	0
391	Dietary coated essential oil and organic acid mixture supplementation improves health of broilers infected with avian pathogenic Escherichia coli. 2022 ,	O

390	Influence of Rosaceous Species and Driving Factors on Differentiation of Rhizospheric Bacteria in a Deciduous Broad-Leaved Forest. 2022 , 79,	O
389	Effects of Lysophosphatidylcholine on Intestinal Health of Turbot Fed High-Lipid Diets. 2022 , 14, 4398	1
388	TangNaiKang, herbal formulation, alleviates obesity in diabetic SHR/cp rats through modulation of gut microbiota and related metabolic functions. 2022 , 60, 2002-2010	0
387	Echinococcus granulosus sensu stricto and antigen B may decrease inflammatory bowel disease through regulation of M1/2 polarization. 2022 , 15,	O
386	Butyrate Mitigates Lipopolysaccharide-Induced Intestinal Morphological Changes in Weanling Piglets by Regulating the Microbiota and Energy Metabolism, and Alleviating Inflammation and Apoptosis. 2022 , 10, 2001	О
385	Funneliformis mosseae Inoculation Enhances Cucurbita pepo L. Plant Growth and Fruit Yield by Reshaping Rhizosphere Microbial Community Structure. 2022 , 14, 932	O
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382	Gut microbiota differs between two cold-climate lizards distributed in thermally different regions. 2022 , 22,	0
381	A novel non-invasive biomarker based on oral microbiome dysbiosis for detection of Community-Acquired Pneumonia.	O
380	Expression Analysis and the Roles of the Sec1 Gene in Regulating the Composition of Mouse Gut Microbiota. 2022 , 13, 1858	0
379	Brain signatures of chronic gut inflammation.	О
378	Metagenomics analysis on the microbiota of chicken manure anaerobic digestion materials in biogas production.	О
377	High-throughput sequencing-based metagenomic and transcriptomic analysis of intestine in piglets infected with salmonella.	О
376	Lactobacillus acidophilus CICC 6075 alleviates obesity in mice through modulation of gut microbiota dysbiosis.	0
375	Analysis of the Microbiomes on Two Cultural Heritage Sites. 1-10	O
374	Effect of Diet on the Midgut Microbial Composition and Host Immunity of the Fall Armyworm, Spodoptera frugiperda. 2022 , 11, 1602	О
373	Effects of Microbial Transfer during Food-Gut-Feces Circulation on the Health of Bombyx mori.	1

372	Clostridium butyricum and Bifidobacterium pseudolongum Attenuate the Development of Cardiac Fibrosis in Mice.	O
371	Effects of different composting methods on antibiotic-resistant bacteria, antibiotic resistance genes, and microbial diversity in dairy cattle manures. 2022 ,	O
370	How the flow and sediment pulse influencing the distribution and functional gene composition of bacterial communities? Case study of the lower Yellow River, China. 2022 , 145, 109599	О
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368	Impact of static magnetic field on electron transport and microbial community shifts in the nitritation sequencing batch reactor. 2022 , 10, 108774	0
367	Enrichment of DNRA bacteria: Shift of microbial community and its combination with anammox to promote TN removal. 2022 , 10, 108867	O
366	Polyethylene microplastic and biochar interactively affect the global warming potential of soil greenhouse gas emissions. 2022 , 315, 120433	O
365	Influence of low-energy electron beam irradiation on the quality and shelf-life of vacuum-packaged pork stored under chilled and superchilled conditions. 2023 , 195, 109019	O
364	Alterations in gut microbiota are related to metabolite profiles in spinal cord injury. 2023, 18, 1076	1
363	Responses of soil microbial community structure, potential ecological functions, and soil physicochemical properties to different cultivation patterns in cucumber. 2023 , 429, 116237	O
362	Arsenic shapes the microbial community structures in tungsten mine waste rocks. 2023, 216, 114573	0
361	Mechanistic study of the effect of leachate recirculation ratios on the carboxylic acid productions during a two-phase food waste anaerobic digestion. 2023 , 453, 139800	O
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359	Engineering demonstration of the remediation of urban water using a novel MES enhanced ecological floating bed: From construction to long-term performance. 2023 , 454, 140024	O
358	Dietary Lactobacillus reuteri prevent from inflammation mediated apoptosis of liver via improving intestinal microbiota and bile acid metabolism. 2023 , 404, 134643	O
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356	Mechanism of sulfur-oxidizing inoculants and nitrate on regulating sulfur functional genes and bacterial community at the thermophilic compost stage. 2023 , 326, 116733	0
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354	Structure and impact of root-associated fungi in treatment wetland mesocosms. 2023, 858, 159958	O
353	Are neuromodulation interventions associated with changes in the gut microbiota? A systematic review. 2023 , 223, 109318	1
352	Unravelling Diabetes-related Pathways Using 16S rRNA Microbiome Data from Human Gut and Nasal Cavity. 2022 ,	0
351	Soil microbial communities and their co-occurrence networks in response to long-term PbIn contaminated soil in southern China.	O
350	Flow drag force contributes high bio-treatment efficiency in a circulating fluidized bed reactor: Mechanism of selective separation of functional decayed sludge. 2022 , 140448	О
349	Mimicking seasonal changes in light-dark cycle and ambient temperature modulates gut microbiome in mice under the same dietary regimen.	O
348	Treatment with atypical rhizobia, Pararhizobium giardinii and Ochrobactrum sp. modulate the rhizospheric bacterial community, and enhances Lens culinaris growth in fallow-soil. 2022 , 127255	O
347	A systematic review of breast milk microbiota composition and the evidence for transfer to and colonisation of the infant gut. 1-18	1
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345	Bioorganic fertilizer promotes pakchoi growth and shapes the soil microbial structure. 13,	O
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335	Effects of Organic Base Fertilizer and Inorganic Topdressing on Alfalfa Productivity and the Soil Bacterial Community in Saline Soil of the Huanghe River Delta in China. 2022 , 12, 2811	O
334	Microbial community shifts in pearl millet root zone soils with Guiera senegalensis intercropping along a rainfall and soil type gradient in the Sahel.	0
333	Dysbiosis and reduced small intestinal function are required to induce intestinal insufficiency in mice.	Ο
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331	Revealing the Pathogenesis of Salt-Sensitive Hypertension in Dahl Salt-Sensitive Rats through Integrated Multi-Omics Analysis. 2022 , 12, 1076	1
330	Effects of combined antibiotics on nitrification, bacteria and antibiotic resistance genes in activated sludge: Insights from legacy effect of antibiotics. 2022 ,	O
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327	A novel non-invasive biomarker based on oral microbiome dysbiosis for detection of Community-Acquired Pneumonia.	0
326	Axillary fossaa microbial dysbiosis and its relationship with axillary osmidrosis patients. 2022, 105886	O
325	Modeling interaction networks between host, diet, and bacteria predicts obesogenesis in a mouse model. 9,	O
324	Differential patterns and assembly processes of bacterial communities from distinct microhabitats in a subtropical estuary. 9,	О
323	Effects of melittin on laying performance and intestinal barrier function of quails. 2022, 102355	O
322	Seasonal characterization of the prokaryotic microbiota of full-scale anaerobic UASB reactors treating domestic sewage in southern Brazil.	О
321	Insufficient or excessive dietary carbohydrates affect gut health through change in gut microbiota and regulation of gene expression of gut epithelial cells in grass carp (Ctenopharyngodon idella). 2022 ,	1
320	Variations in leaf phyllosphere microbial communities and development of tobacco brown spot before and after fungicide application. 13,	0
319	Early life microbiota transplantation from highly feed-efficient broiler improved weight gain by reshaping the gut microbiota in laying chicken. 13,	0

318	Composition and dynamics of bacterial communities during flotation in a coal preparation plant. 2023 , 385, 135691	O
317	Multi-omics reveals the mechanisms of DEHP driven pulmonary toxicity in ovalbumin-sensitized mice. 2023 , 249, 114355	O
316	Cryptosporidium infection induced the dropping of SCFAS and dysbiosis in intestinal microbiome of Tibetan pigs. 2023 , 174, 105922	1
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313	Escape and functional alterations of microbial aerosol particles containing Pseudomonas sp. during wastewater treatment. 2023 , 219, 115129	O
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311	Effects of different management practices on soil microbial community structure and function in alpine grassland. 2023 , 327, 116859	1
310	Precursor-derived in-water peracetic acid impacts on broiler performance, gut microbiota, and antimicrobial resistance genes. 2023 , 102, 102368	0
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304	Synergistic changes of rhizosphere bacterial community and soil properties in greenhouse soils under long-term tomato monoculture. 2023 , 183, 104738	0
303	Comparative Study of the Gut Microbiota Community between the Farmed and Wild Mastacembelus armatus (Zig-Zag Eel). 2022 , 12, 1193	O
302	Exploring the value of microorganisms in the appendix for inferring postmortem interval in SpragueDawley rats using high-throughput sequencing.	O
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300	Scrophulariae Radix-Atractylodes sinensis pair and metformin inhibit inflammation by modulating gut microbiota of high-fat diet/streptozotocin-induced diabetes in rats. 13,	O
299	Effects of diurnal temperature fluctuations on growth performance, energy metabolism, stress response, and gut microbes of juvenile mud crab Scylla paramamosain. 9,	O
298	Catchment characteristics and seasonality control the composition of microbial assemblages exported from three outlet glaciers of the Greenland Ice Sheet. 13,	O
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292	Response of Soil Bacteria of Dicranopteris dichotoma Populations to Vegetation Restoration in Red Soil Region of China.	O
291	Effects of Circadian Rhythm and Feeding Modes on Rumen Fermentation and Microorganisms in Hu Sheep. 2022 , 10, 2308	O
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289	Gut microbiome alterations in ICU patients with enteral nutrition-related diarrhea. 13,	1
288	The divergent effects of moderate climate warming on the gut microbiota and energetic state of cold-climate lizards from open and semi-closed microhabitats. 13,	O
287	Gut microbiota in hypertensive patients with versus without obstructive sleep apnea. 2022 , 24, 1598-1605	1
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279	The microbial community dynamics of cocaine sensitization in two behaviorally divergent strains of collaborative cross mice.	O
278	Underdevelopment of gut microbiota in failure to thrive infants of up to 12 months of age. 12,	0
277	Analysis of endophyte diversity of Rheum palmatum among different tissues and ages. 2023, 205,	Ο
276	Comparison of soil microbial community structure and function for karst tiankeng with different degrees of degradation. 2022 , 12,	Ο
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273	How elevated nitrogen load affects bacterial community structure and nitrogen cycling services in coastal water. 13,	O
272	Insights into the bacterial community compositions of peanut worm (Sipunculus nudus) and their association with the surrounding environment. 9,	1
271	Dietary Use of Methionine Sources and Bacillus amyloliquefaciens CECT 5940 Influences Growth Performance, Hepatopancreatic Histology, Digestion, Immunity, and Digestive Microbiota of Litopenaeus vannamei Fed Reduced Fishmeal Diets. 2023 , 13, 43	O
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269	The microbiome® fiber degradation profile and its relationship with the host diet. 2022 , 20,	O
268	A core microbiome in the hyphosphere of arbuscular mycorrhizal fungi has functional significance in organic phosphorus mineralization.	0
267	Adeno-associated virus vector intraperitoneal injection induces colonic mucosa and submucosa transduction and alters the diversity and composition of the faecal microbiota in rats. 12,	O
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263	Alterations of the vaginal microbiome in healthy pregnant women positive for group B Streptococcus colonization during the third trimester. 2022 , 22,	O
262	Live yeast supplementation altered the bacterial community composition and function in rumen and hindgut and alleviated the detrimental effects of heat stress on dairy cows.	0
261	A Randomized Placebo Controlled Clinical Trial of a Metabolic Shifting Probiotic, Sugar Shift, for the Treatment of T2DM.	O
260	Temporal and Spatial Variations of the Bacterial Diversity in a Deep Alkaline Lake. 2022, 14, 4097	O
259	Effects of rearing system and antibiotic treatment on immune function, gut microbiota and metabolites of broiler chickens. 2022 , 13,	O
258	Global Distribution of Carbohydrate Utilization Potential in the Prokaryotic Tree of Life. 2022, 7,	0
257	First Insight into the Formation of In Vivo Transformation Products of 2-Ethylhexyl diphenyl phosphate in Zebrafish and Prediction of Their Potential Toxicities.	O
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255	Effects of fermentation medium on cigar filler. 10,	Ο
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	Enhanced bioremediation of cyclohexaneacetic acid in offshore sediments with green synthetic	
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254 253 252	Enhanced bioremediation of cyclohexaneacetic acid in offshore sediments with green synthetic iron oxide and Pseudoalteromonas sp More microbial manipulation and plant defense than soil fertility for biochar in food production: A field experiment of replanted ginseng with different biochars. 13, HIV-Positive Patients on Antiretroviral Therapy Have an Altered Mucosal Intestinal but Not Oral Microbiome. Intestinal bacterial community composition of juvenile Chinese mitten crab Eriocheir sinensis under	0 0
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244	The diversity and function of the in-situ fungal communities in response to polycyclic aromatic hydrocarbons in the urban wetland. 2023 , 205,	О
243	Gut microbiota profiling variated during colorectal cancer development in mouse. 2022 , 23,	О
242	Spatiotemporal and ontogenetic variation, microbial selection, and predicted Bd-inhibitory function in the skin-associated microbiome of a Rocky Mountain amphibian. 13,	О
241	Gut Microbiota, Intestinal Morphometric Characteristics, and Gene Expression in Relation to the Growth Performance of Chickens. 2022 , 12, 3474	O
240	Effects of microbiota-directed supplementary foods on gut microbiota in fecal colonized mice of healthy infants. 2022 , 99, 105346	О
239	Oral Microbiome in Nonsmoker Patients with Oral Cavity Squamous Cell Carcinoma, Defined by Metagenomic Shotgun Sequencing. 2022 , 14, 6096	O
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236	Dietary supplemental coated essential oils and organic acids mixtures improves growth performance and gut health along with reduces Salmonella load of broiler chickens infected with Salmonella Enteritidis.	О
235	Accuracy of mutual predictions of plant and microbial communities vary along a successional gradient in an alpine glacier forefield. 13,	О
234	A clinically validated human saliva metatranscriptomic test for global systems biology studies.	0
233	An update on the biological characteristics and functions of tuft cells in the gut. 10,	O
232	Gut microbiota signatures in tissues of the colorectal polyp and normal colorectal mucosa, and faeces. 12,	О
231	Breast cancer patients from the Midwest region of the United States have reduced levels of short-chain fatty acid-producing gut bacteria. 2023 , 13,	O
230	Mechanism of Enhancing Pyrazines in Daqu via Inoculating Bacillus licheniformis with Strains Specificity. 2023 , 12, 304	О
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227	Tumor-associated microbiota in colorectal cancer with vascular tumor-thrombus and neural invasion and association with clinical prognosis.	О
226	Gastric microbiota in gastric cancer: Different roles of Helicobacter pylori and other microbes. 12,	О
225	Early infancy dysbiosis in food protein-induced enterocolitis syndrome: a prospective cohort study.	O
224	Effect of disease severity on the structure and diversity of the phyllosphere microbial community in tobacco. 13,	0
223	Roles of vaginal flora in human papillomavirus infection, virus persistence and clearance. 12,	1
222	Microbial community and predictive functionalities associated with the marine sediment of Coastal Gujarat.	0
221	Construction of Model Animals to Explore Intestinal Microbiome for Detection of Breast Cancer.	O
220	Microbiome Data Analysis and Interpretation: Correlation Inference and Dynamic Pattern Discovery. 2023 , 119-144	0
219	Edwardsiella ictaluri Almost Completely Occupies the Gut Microbiota of Fish Suffering from Enteric Septicemia of Catfish (Esc). 2023 , 8, 30	O
218	A specific tongue microbiota signature is found in patients displaying an improvement of orosensory lipid perception after a sleeve gastrectomy. 9,	О
217	MetaFunc: Taxonomic and Functional Analyses of High Throughput Sequencing for Microbiomes. 1-41	О
216	Startup of a large height-diameter ratio bioreactor by alternate feeding: performance of partial nitrification and enrichment of ammonia-oxidizing bacteria (AOB). 1-9	О
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211	Microbiome and metabolic features of tissues and feces reveal diagnostic biomarkers for colorectal cancer. 14,	O

210	Starvation alters gut microbiome and mitigates off-flavors in largemouth bass (Micropterus salmoides).	0
209	Host-microbiota interactions and responses of Metapenaeus ensis infected with decapod iridescent virus 1. 13,	O
208	Facilitating effects of the reductive soil disinfestation process combined with Paenibacillus sp. amendment on soil health and physiological properties of Momordica charantia. 13,	0
207	Potential of shrimp waste meal and insect exuviae as sustainable sources of chitin for fish feeds. 2023 , 739256	O
206	Benefits of Huang Lian mediated by gut microbiota on HFD/STZ-induced type 2 diabetes mellitus in mice. 14,	O
205	Enrichment cultivation of VOC-degrading bacteria using diffusion bioreactor and development of bacterial-immobilized biochar for VOC bioremediation. 2023 , 121089	O
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201	The effect of biochar on nitrogen availability and bacterial community in farmland. 2023, 73,	O
200	The role of protein contents in promoting wastewater phosphorus and bioenergy recovery during anaerobic digestion. 2023 , 169, 106694	О
199	Organic vegetable juice supplement alleviates hyperlipidemia in diet-induced obese mice and modulates microbial community in continuous colon simulation system.	O
198	Exploring and comparing the impacts of low temperature to endogenous and exogenous partial denitrification: The nitrite supply, transcription mechanism, and microbial dynamics. 2023 , 370, 128568	O
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193	Di-n-butyl phthalate stress induces changes in the core bacterial community associated with nitrogen conversion during agricultural waste composting. 2023 , 446, 130695	O

192	Interaction among biofilter microbiome, fecal metabolome and water quality and regulation of sewage discharge in the recirculating aquaculture system of Apostichopus japonicus. 2023 , 330, 117100	O
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188	Effects of Trace Elements Supplementation on Methane Enhancement and Microbial Community Dynamics in Mesophilic Anaerobic Digestion of Food Waste.	0
187	New Insights into the Effect of Fipronil on the Soil Bacterial Community. 2023 , 11, 52	O
186	A New Phylogeny-Driven Random Forest-Based Classification Approach for Functional Metagenomics. 2022 ,	О
185	Host niche, genotype, and field location shape the diversity and composition of the soybean microbiome. 2023 ,	O
184	The therapeutic role of microbial metabolites in human health and diseases. 2023, 1-38	0
183	Structure and Function Analysis of Cultivated Meconopsis integrifolia Soil Microbial Community Based on High-Throughput Sequencing and Culturability. 2023 , 12, 160	O
182	Effect of Methionine Hydroxy Analog on Hu Sheep Digestibility, Rumen Fermentation, and Rumen Microbial Community In Vitro. 2023 , 13, 169	0
181	EasyAmplicon: An easy-to-use, open-source, reproducible, and community-based pipeline for amplicon data analysis in microbiome research.	O
180	Metagenomics for the identification and characterization of microorganisms in fermented foods. 2023 , 347-359	О
179	Enhancing Biobased Volatile Fatty Acids Production from Olive Mill Solid Waste by Optimization of pH and Substrate to Inoculum Ratio. 2023 , 11, 338	O
178	Functional metagenomics profiling of symbiotic microbiome. 2023 , 691-713	0
177	Orofacial clefts alter early life oral microbiome maturation towards higher levels of potentially pathogenic species: A prospective observational study. 2023 , 15,	O
176	Heavy metals potentially drive co-selection of antibiotic resistance genes by shifting soil bacterial communities in paddy soils along middle and lower Yangtze River. 2023 ,	О
175	Black Lycium barbarum polysaccharide attenuates LPS-induced intestine damage via regulation gut microbiota. 13,	0

174	High-Dose Vitamin E Supplementation Can Alleviate the Negative Effect of Subacute Ruminal Acidosis in Dairy Cows. 2023 , 13, 486	О
173	Dietary Sodium Butyrate Improves Intestinal Health of Triploid Oncorhynchus mykiss Fed a Low Fish Meal Diet. 2023 , 12, 145	О
172	Comprehensive evaluation of shotgun metagenomics, amplicon sequencing, and harmonization of these platforms for epidemiological studies. 2023 , 3, 100391	О
171	Potential targeted therapy based on deep insight into the relationship between the pulmonary microbiota and immune regulation in lung fibrosis. 14,	О
170	A High Dose of Dietary Berberine Improves Gut Wall Morphology, Despite an Expansion of Enterobacteriaceae and a Reduction in Beneficial Microbiota in Broiler Chickens.	О
169	Adding a polyphenol-rich fiber bundle to food impacts the gastrointestinal microbiome and metabolome in dogs. 9,	1
168	Impact of Pipe Material and Temperature on Drinking Water Microbiome and Prevalence of Legionella, Mycobacterium, and Pseudomonas Species. 2023 , 11, 352	О
167	Vertical organization of microbial communities in Salineta hypersaline wetland, Spain. 14,	O
166	Advancing CAR T cell therapy through the use of multidimensional omics data.	2
165	Comparing the differences of prokaryotic microbial community between pit walls and bottom from Chinese liquor revealed by 16S rRNA gene sequencing. 2023 , 18,	O
164	Genomics of microbial communities in African lakes. 2023 , 73-95	0
163	Changes in the oral and nasal microbiota in pediatric obstructive sleep apnea. 2023, 15,	O
162	The Gut Microbiota B rain Axis during Aging, Mild Cognitive Impairment and Dementia: Role of Tau Protein, EAmyloid and LPS in Serum and Curli Protein in Stool. 2023 , 15, 932	О
161	Microbiota-directed biotherapeutics: considerations for quality and functional assessment. 2023 , 15,	O
160	Acute toxic effects of microcystin-LR on crayfish (Procambarus clarkii): Insights from antioxidant system, histopathology and intestinal flora.	О
159	Impact of neoadjuvant therapy on gut microbiome in patients with resectable/borderline resectable pancreatic ductal adenocarcinoma. 2023 ,	O
158	Composition and function of the skin microbiota were altered of red leg syndrome in cultured bullfrog (Rana catesbeiana). 2023 , 29, 101487	О
157	Microbiome Metabolome Integration Platform (MMIP): a web-based platform for microbiome and metabolome data integration and feature identification.	О

156	Plant growth stages covered the legacy effect of rotation systems on microbial community structure and function in wheat rhizosphere.	О
155	Insights into the Gut Microbiota of the Freshwater Crab Sinopotamon planum across Three Seasons and Its Associations with the Surrounding Aquatic Microbiota. 2023 , 15, 519	O
154	Alterations in gut microbiota and urine metabolomics in infants with yin-deficiency constitution aged 0½ years. 2023 , 9, e14684	O
153	Effects of Phage Cocktail, Probiotics, and Their Combination on Growth Performance and Gut Microbiota of Broiler Chickens. 2023 , 13, 1328	O
152	Effect of yeast species and processing on intestinal microbiota of Atlantic salmon (Salmo salar) fed soybean meal-based diets in seawater. 2023 , 5,	O
151	An efficient continuous quorum quenching feed to mitigate membrane biofouling in membrane bioreactors: Strain 1A1 (extracellular) versus strain BH4 (intracellular). 2023 , 52, 103594	O
150	Dissipation kinetics of chlorpyrifos and 3,5,6 trichloro-2-pyridinol under vegetation of different aromatic grasses: Linkage with enzyme kinetics and microbial community of soil. 2023 , 448, 130960	О
149	Sustained detoxification of 1,2-dichloroethane to ethylene by a symbiotic consortium containing Dehalococcoides species. 2023 , 325, 121443	О
148	Temporal variations, distribution, and dissemination of antibiotic resistance genes and changes of bacterial communities in a biofloc-based zero-water-exchange mariculture system. 2023 , 256, 114904	0
147	Revealed mechanism of micron-pore size of 3D bio-anode on the behavior of biofilm and system performance in microbial electrochemical system. 2023 , 464, 142736	O
146	Sources and succession of microorganisms in industrial coal flotation system. 2023 , 342, 127917	0
145	Alterations in hepatic transcriptome and cecum microbiota underlying potential ways to prevent early fatty liver in laying hens. 2023 , 102, 102593	O
144	An innovative way to treat cash crop wastes: The fermentation characteristics and functional microbial community using different substrates to produce Agricultural Jiaosu. 2023 , 227, 115727	0
143	Impact of persistent rain on microplastics distribution and plastisphere community: A field study in the Pearl River, China. 2023 , 879, 163066	O
142	Comparison of culturable and non-culturable bacterial diversity through metagenomic sequencing from the mangrove sediments in Kannur district, Kerala, India. 2023 , 27, 100175	0
141	Recovery of electron and carbon source from agricultural waste corncob by microbial electrochemical system to enhance wastewater denitrification. 2023 , 878, 162926	O
140	First insight into the sex-dependent accumulation, tissue distribution and potential toxicities of 2-ethylhexyl diphenyl phosphate and its metabolites in adult zebrafish. 2023 , 452, 131299	0
139	The structural and functional shift in the soil rhizosphere and raspberry shoot microbiomes underlies changes caused by phytopathogens contamination and naturalization strategies implementation. 2023 , 186, 104810	0

138	Community rRNA operon copy number of soil bacteria decreases with soil depth and ecosystem succession in postglacial ecosystems. 2023 , 186, 104817	0
137	Potential roles of the rhizospheric bacterial community in assisting Miscanthus floridulus in remediating multi-metal(loid)s contaminated soils. 2023 , 227, 115749	0
136	Optimized soil bacterial structure following grazing exclusion promotes soil nutrient cycling and plant growth. 2023 , 213, 104977	О
135	Microalgae-based constructed wetland system enhances nitrogen removal and reduce carbon emissions: Performance and mechanisms. 2023 , 877, 162883	O
134	Weathering extents and anthropogenic influences shape the soil bacterial community along a subsurface zonation. 2023 , 876, 162570	0
133	DNRA and ANRA-centered microbial mechanism of biogas slurry on soil nitrogen leaching: An indication from a laboratory study. 2023 , 189, 104905	O
132	Long-term integrated rice-crayfish culture disrupts the microbial communities in paddy soil. 2023 , 29, 101515	0
131	Combined toxic effects of nanoplastics and norfloxacin on mussel: Leveraging biochemical parameters and gut microbiota. 2023 , 880, 163304	O
130	Primary nephrotic syndrome relapse within 1 year after glucocorticoid therapy in children is associated with gut microbiota composition at syndrome onset.	О
129	(Meta)genomics -assisted screening of novel antibacterial lactic acid bacteria strains from traditional fermented milk from Western China and their bioprotective effects on cheese. 2023 , 175, 114507	O
128	External sodium acetate improved Cr(VI) stabilization in a Cr-spiked soil during chemical-microbial reduction processes: Insights into Cr(VI) reduction performance, microbial community and metabolic functions. 2023 , 251, 114566	О
127	Interactions between dissolved organic matter and the microbial community are modified by microplastics and heat waves. 2023 , 448, 130868	O
126	Maternal and host effects mediate the adaptive expansion and contraction of the microbiome during ontogeny in a holometabolous, polyphagous insect. 2023 , 37, 929-946	О
125	Sacubitril/valsartan mitigated intermittent hypoxia related intestinal microbiota alteration and aortic injury.	O
124	Effect of azoxystrobin on tobacco leaf microbial composition and diversity. 13,	О
123	Cyprinid herpesvirus 2 infection changes microbiota and metabolites in the gibel carp (Carassius auratus gibelio) midgut. 12,	0
122	Natural variation of Macrocystis pyrifera gametophyte germplasm culture microbiomes and applications for improving yield in offshore farms. 2023 , 59, 402-417	0
121	Growth Stages and Inter-Species Gut Microbiota Composition and Function in Captive Red Deer (Cervus elaphus alxaicus) and Blue Sheep (Pseudois nayaur). 2023 , 13, 553	O

120	Comparative Analyses of Soil Bacterial Colonies of Two Types of Chinese Ginger after a Major Flood Disaster. 2023 , 11,	О
119	Prebiotic mechanisms of resistant starches from dietary beans and pulses on gut microbiome and metabolic health in a humanized murine model of aging. 10,	O
118	The differences in main components, enzyme activity, and microbial composition between substandard and normal jiuyao.	О
117	Colonizing microbiota is associated with clinical outcomes in diabetic wound healing. 2023, 194, 114727	О
116	Contaminants from a former Croatian coal sludge dictate the structure of microbiota in the estuarine (Ra Bay) sediment and soil. 14,	О
115	Carrot genotypes differentially alter soil bacterial communities and decomposition of plant residue in soil.	O
114	Periodontal treatment and microbiome-targeted therapy in management of periodontitis-related nonalcoholic fatty liver disease with oral and gut dysbiosis. 29, 967-996	О
113	Trait biases in microbial reference genomes. 2023 , 10,	О
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109	Maternal IT cells shape offspring pulmonary type 2 immunity in a microbiota-dependent manner. 2023 , 42, 112074	О
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107	Bio-organic fertilizers improve Dendrocalamus farinosus growth by remolding the soil microbiome and metabolome. 14,	O
106	A pilot study exploring the association of bronchial bacterial microbiota and recurrent wheezing in infants with atopy. 13,	О
105	Mimicking seasonal changes in light-dark cycle and ambient temperature modulates gut microbiome in mice under the same dietary regimen. 2023 , 18, e0278013	O
104	Identifying the Novel Gut Microbial Metabolite Contributing to Metabolic Syndrome in Children Based on Integrative Analyses of Microbiome-Metabolome Signatures. 2023 , 11,	0
103	Gut Microbiome Composition Reveals the Distinctiveness between the Bengali people and the Indigenous Ethnicities in Bangladesh.	O

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101	Role of the rhizosphere bacterial community in assisting phytoremediation in a lead-zinc area. 13,	O
100	Bacterial Communities and Diversity of Western Ghats Soil: A Study of a Biodiversity Hotspot. 2023 , 80,	О
99	Lactiplantibacillus pentosus P2020 protects the hyperuricemia and renal inflammation in mice. 10,	O
98	Roe Deer Produce Less Methane and Harbor Distinct Gut Microbiota. 2023 , 9, 186	0
97	Microbial Diversity and Flavor Regularity of Soy Milk Fermented Using Kombucha. 2023, 12, 884	O
96	Full-Length 16S rRNA Gene Analysis Using Long-Read Nanopore Sequencing for Rapid Identification of Bacteria from Clinical Specimens. 2023 , 193-213	0
95	Dynamic variation of Paris polyphylla root-associated microbiome assembly with planting years. 2023 , 257,	O
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89	Gamma-delta T cells modulate the microbiota and fecal micro-RNAs to maintain mucosal tolerance. 2023 , 11,	O
88	Network analysis of 16S rRNA sequences suggests microbial keystone taxa contribute to marine N2O cycling. 2023 , 6,	O
87	Effects of Florfenicol on Intestinal Histology, Apoptosis and Gut Microbiota of Chinese Mitten Crab (Eriocheir sinensis). 2023 , 24, 4412	O
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85	High-Grain Diet Feeding Altered Blood Metabolites, Rumen Microbiome, and Metabolomics of Yaks. 2023 , 9, 215	O

84	Effect of pressure treatment on Microcystis blooms and the subsequent succession of bacterial community. 2023 , 71, 103023	0
83	Thermal Selection of Microbial Communities and Preservation of Microbial Function in Guaymas Basin Hydrothermal Sediments. 2023 , 89,	Ο
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77	Intestine microbiota and SCFAs response in naturally Cryptosporidium-infected plateau yaks. 13,	Ο
76	Insights from Bacterial 16S rRNA Gene into Bacterial Genera and Predicted Metabolic Pathways Associated with Stool Consistency in Rectal Cancer Patients: A Proof of Concept. 109980042311596	0
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72	Diel modifications in the oral and anal microflora of the Pygoscelis papua Penguins. 2023, 54, 351-368	0
71	Identification of Distinct Vaginal Microbiota Signatures Contributing Toward Preterm Birth Using an Integrative Computational Approach. 2023 , 51, 109-123	O
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69	Effects of Bacillus coagulans and Lactobacillus plantarum on the Fermentation Characteristics, Microbial Community, and Functional Shifts during Alfalfa Silage Fermentation. 2023 , 13, 932	O
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67	Effect of Different Host Plants on the Diversity of Gut Bacterial Communities of Spodoptera frugiperda (J. E. Smith, 1797). 2023 , 14, 264	O

66	Bovine Colostrum Supplementation Modulates the Intestinal Microbial Community in Rabbits. 2023 , 13, 976	О
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64	N 2 O emission associated with shifts of bacterial communities in riparian wetland during the spring thawing periods. 2023 , 13,	0
63	Microbiome and function alterations in the gastric mucosa of asymptomatic patients with Helicobacter pylori infection.	o
62	Impact of high altitude on composition and functional profiling of oral microbiome in Indian male population. 2023 , 13,	0
61	Effects of paddy field non-grainization consolidation on sustainable eco-functions protection of soil bacterial: Empirical evidence from Zhejiang province, China. 11,	o
60	Bacterial Diversity Analysis of Chaozhou Sauerkraut Based on High-Throughput Sequencing of Different Production Methods. 2023 , 9, 282	0
59	Biogas Residues Improved Microbial Diversity and Disease Suppression Function under Extent Indigenous Soil Microbial Biomass. 2023 , 13, 774	o
58	Changes in the gut microbiota composition of healthy young volunteers after administration of Lacticaseibacillus rhamnosus LRa05: A placebo-controlled study. 10,	0
57	Different and unified responses of soil bacterial and fungal community composition and predicted functional potential to 3 years drought stress in a semiarid alpine grassland. 14,	O
56	Gut microbiome variation in pulmonary TB patients with diabetes or HIV comorbidities. 2,	0
55	Fermented cottonseed and rapeseed meals outperform soybean meal in improving performance, rumen fermentation, and bacterial composition in Hu sheep. 14,	o
54	Changes of intestinal microbiota in the giant salamander (Andrias davidianus) during growth based on high-throughput sequencing. 14,	0
53	Intratumoral Bacteria Dysbiosis Is Associated with Human Papillary Thyroid Cancer and Correlated with Oncogenic Signaling Pathways. 2023 ,	o
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49	Artificial Cultivation Changes Foliar Endophytic Fungal Community of the Ornamental Plant Lirianthe delavayi. 2023 , 11, 775	О

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46	Significant antimicrobial-producing vegetation uniquely shapes the stormwater biofilter microbiome with implications for enhanced faecal pathogen inactivation. 2023 , 2, e0000094	0
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40	Core Microbiomes. 2023 , 240-271	0
39	Microbial diversity and metabolic function in duodenum, jejunum and ileum of emu (Dromaius novaehollandiae). 2023 , 13,	О
38	Effective Biocorrosive Control in Oil Industry Facilities: 16S rRNA Gene Metabarcoding for Monitoring Microbial Communities in Produced Water. 2023 , 11, 846	0
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33	Alterations of commensal microbiota are associated with pancreatic cancer. 039361552311667	О
32	Potential of Medicago sativa and Perilla frutescens for overcoming the soil sickness caused by ginseng cultivation. 14,	0
31	Evolving approaches to profiling the microbiome in skin disease. 14,	О

30	Carapace microbiota in American lobsters (Homarus americanus) associated with epizootic shell disease and the green gland. 14,	O
29	Bacillus- and Lactobacillus-Based Dietary Synbiotics Are Associated with Shifts in the Oropharyngeal, Proximal Colonic, and Vaginal Microbiomes of Korean Native Black Pigs. 2023 , 9, 359	O
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27	Association between gut microbiota and anxiety symptoms: A large population-based study examining sex differences. 2023 , 333, 21-29	O
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25	Decreasing lactate input for cost-effective sulfidogenic metal removal in sulfate-rich effluents: Mechanistic insights from (bio)chemical kinetics to microbiome response. 2023 , 330, 138662	O
24	Non-rhizobial nodule endophytes improve nodulation, change root exudation pattern and promote the growth of lentil, for prospective application in fallow soil. 14,	0
23	Bacillus paralicheniformis RP01 Enhances the Expression of Growth-Related Genes in Cotton and Promotes Plant Growth by Altering Microbiota inside and outside the Root. 2023 , 24, 7227	Ο
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19	Dietary and Sexual Correlates of Gut Microbiota in the Japanese Gecko, Gekko japonicus (Schlegel, 1836). 2023 , 13, 1365	O
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17	Deep relationships between bacterial community and polycyclic aromatic hydrocarbons in soil profiles near typical coking plants.	О
16	Integrating Multi-Omics Data to Construct Reliable Interconnected Models of Signaling, Gene Regulatory, and Metabolic Pathways. 2023 , 139-151	0
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14	Effects of inorganic and compost tea fertilizers application on the taxonomic and functional microbial diversity of the purslane rhizosphere. 14,	0
13	Practical value of microorganisms for forensic purposes (on the example of microbial flora of bony remnants from the historic burial site). 2023 , 66, 30	Ο

12	Ecological and dynamic analysis of gut microbiota in the early stage of azomethane-dextran sodium sulfate model in mice. 13,	O
11	Liuwei Dihuang formula ameliorates chronic stress-induced emotional and cognitive impairments in mice by elevating hippocampal O-GlcNAc modification. 17,	O
10	Prokaryotic diversity and community structure in the rhizosphere of Lantana weed (Lantana camara L.). 14,	O
9	Pre-aeration promotes nutrient removal in a pilot-scale duckweed-based pond by influencing the duckweed growth and bacterial community. 2023 , 53, 103734	O
8	Microbiome Diversity and Cellulose Decomposition Processes by Microorganisms on the Ancient Wooden Seawall of Qiantang River of Hangzhou, China.	0
7	Saccharomyces cerevisiae Culture Dose Response Effects on Ruminal Nutrient Digestibility and Microbial Community: An In Vitro Study. 2023 , 9, 411	O
6	Metatranscriptomic analysis of the gut microbiome of black soldier fly larvae reared on lignocellulose-rich fiber diets unveils key lignocellulolytic enzymes. 14,	0
5	Application of Clostridium butyricum, Rummeliibacillus suwonensis, and Issatchenkia orientalis for Nongxiangxing baijiu fermentation: Improves the microbial communities and flavor of upper fermented grain. 2023 , 169, 112885	O
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3	Sampling period and disease severity of bacterial wilt significantly affected the bacterial community structure and functional prediction in the sesame rhizosphere soil. 2023 , 26, 100704	O
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1	Bacterial Communities Vary from Different Scleractinian Coral Species and between Bleached and Non-Bleached Corals.	O