

Tatsuya Unno

List of Publications by Year in descending order

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Version: 2024-02-01

85
papers

3,087
citations

159358

30
h-index

168136

53
g-index

87
all docs

87
docs citations

87
times ranked

4901
citing authors

#	ARTICLE	IF	CITATIONS
1	Dietary regulations for microbiota dysbiosis among post-menopausal women with type 2 diabetes. <i>Critical Reviews in Food Science and Nutrition</i> , 2023, 63, 9961-9976.	5.4	11
2	Effects of β -glucan, probiotics, and synbiotics on obesity-associated colitis and hepatic manifestations in C57BL/6J mice. <i>European Journal of Nutrition</i> , 2022, 61, 793-807.	1.8	19
3	Higher abundance of core antimicrobial resistant genes in effluent from wastewater treatment plants. <i>Water Research</i> , 2022, 208, 117882.	5.3	51
4	Dichloromethane fraction of <i>Citrus grandis</i> induces apoptosis in a human colorectal cancer cell lines via apoptotic signaling pathway. <i>Journal of Functional Foods</i> , 2022, 88, 104903.	1.6	1
5	<i>Schizophyllum commune</i> -derived β -glucan improves intestinal health demonstrating protective effects against constipation and common metabolic disorders. <i>Applied Biological Chemistry</i> , 2022, 65, .	0.7	10
6	Differences in the Effects of Calcium and Magnesium Ions on the Anammox Granular Properties to Alleviate Salinity Stress. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 19.	1.3	11
7	Metagenomic investigation of the seasonal distribution of bacterial community and antibiotic-resistant genes in Day River Downstream, Ninh Binh, Vietnam. <i>Applied Biological Chemistry</i> , 2022, 65, .	0.7	5
8	Survey of Bacterial Phylogenetic Diversity During the Glacier Melting Season in an Arctic Fjord. <i>Microbial Ecology</i> , 2021, 81, 579-591.	1.4	9
9	Metagenomic exploration of antibiotic resistome in treated wastewater effluents and their receiving water. <i>Science of the Total Environment</i> , 2021, 765, 142755.	3.9	33
10	A Korean-Style Balanced Diet Has a Potential Connection with Ruminococcaceae Enterotype and Reduction of Metabolic Syndrome Incidence in Korean Adults. <i>Nutrients</i> , 2021, 13, 495.	1.7	36
11	Microbial source tracking using metagenomics and other new technologies. <i>Journal of Microbiology</i> , 2021, 59, 259-269.	1.3	13
12	Effects of digested Cheonggukjang on human microbiota assessed by in vitro fecal fermentation. <i>Journal of Microbiology</i> , 2021, 59, 217-227.	1.3	12
13	<i>In vitro</i> investigation of food effects on human gut microbiota. <i>Journal of Applied Biological Chemistry</i> , 2021, 64, 75-81.	0.2	2
14	Tetracycline-resistant bacteria and ribosomal protection protein genes in soils from selected agricultural fields and livestock farms. <i>Applied Biological Chemistry</i> , 2021, 64, .	0.7	9
15	Comparison of the Gut Microbiota of Jeju and Thoroughbred Horses in Korea. <i>Veterinary Sciences</i> , 2021, 8, 81.	0.6	4
16	Fish farm effluents as a source of antibiotic resistance gene dissemination on Jeju Island, South Korea. <i>Environmental Pollution</i> , 2021, 276, 116764.	3.7	31
17	Comparison of the Fecal Microbiota of Horses with Intestinal Disease and Their Healthy Counterparts. <i>Veterinary Sciences</i> , 2021, 8, 113.	0.6	12
18	Dietary Intervention Induced Distinct Repercussions in Response to the Individual Gut Microbiota as Demonstrated by the In Vitro Fecal Fermentation of Beef. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 6841.	1.3	1

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19	A hybrid DNA sequencing approach is needed to properly link genotype to phenotype in multi-drug resistant bacteria. <i>Environmental Pollution</i> , 2021, 289, 117856.	3.7	1
20	Synbiotic supplementation with prebiotic <i>Schizophyllum commune</i> derived β -(1,3/1,6)-glucan and probiotic concoction benefits gut microbiota and its associated metabolic activities. <i>Applied Biological Chemistry</i> , 2021, 64, .	0.7	11
21	Differences in fecal and cecal microbiota in C57BL/6J mice fed normal and high fat diet. <i>Journal of Applied Biological Chemistry</i> , 2021, 64, 399-405.	0.2	0
22	Improvement effect of cooked soybeans on HFD-deteriorated large intestinal health in rat model. <i>Journal of Applied Biological Chemistry</i> , 2021, 64, 383-389.	0.2	0
23	Seasonal Mixing-Driven System in Estuarineâ€œCoastal Zone Triggers an Ecological Shift in Bacterial Assemblages Involved in Phytoplankton-Derived DMSP Degradation. <i>Microbial Ecology</i> , 2020, 79, 12-20.	1.4	5
24	Dietary intervention using (1,3)/(1,6)- β -glucan, a fungus-derived soluble prebiotic ameliorates high-fat diet-induced metabolic distress and alters beneficially the gut microbiota in mice model. <i>European Journal of Nutrition</i> , 2020, 59, 2617-2629.	1.8	32
25	Sex Differences in Gut Microbiota. <i>World Journal of Men's Health</i> , 2020, 38, 48.	1.7	340
26	Anti-Inflammatory Properties and Gut Microbiota Modulation of <i>Porphyra tenera</i> Extracts in Dextran Sodium Sulfate-Induced Colitis in Mice. <i>Antioxidants</i> , 2020, 9, 988.	2.2	26
27	<i>Dendropanax morbifera</i> Leaf Extracts Improved Alcohol Liver Injury in Association with Changes in the Gut Microbiota of Rats. <i>Antioxidants</i> , 2020, 9, 911.	2.2	12
28	Intervention with kimchi microbial community ameliorates obesity by regulating gut microbiota. <i>Journal of Microbiology</i> , 2020, 58, 859-867.	1.3	19
29	Probiotic <i>Lactobacillus fermentum</i> strain JDFM216 improves cognitive behavior and modulates immune response with gut microbiota. <i>Scientific Reports</i> , 2020, 10, 21701.	1.6	38
30	<i>Codium fragile</i> Ameliorates High-Fat Diet-Induced Metabolism by Modulating the Gut Microbiota in Mice. <i>Nutrients</i> , 2020, 12, 1848.	1.7	27
31	Effects of fermented coffee on human gut microbiota. <i>Journal of Applied Biological Chemistry</i> , 2020, 63, 83-87.	0.2	1
32	<i>Cupriavidus</i> sp. strain Ni-2 resistant to high concentration of nickel and its genes responsible for the tolerance by genome comparison. <i>Archives of Microbiology</i> , 2019, 201, 1323-1331.	1.0	8
33	Korean Traditional Medicine (<i>Jakyakgamcho-tang</i>) Ameliorates Colitis by Regulating Gut Microbiota. <i>Metabolites</i> , 2019, 9, 226.	1.3	11
34	Comparison of de-novo assembly tools for plasmid metagenome analysis. <i>Genes and Genomics</i> , 2019, 41, 1077-1083.	0.5	6
35	Baicalein Suppresses Stem Cell-Like Characteristics in Radio- and Chemoresistant MDA-MB-231 Human Breast Cancer Cells through Up-Regulation of IFIT2. <i>Nutrients</i> , 2019, 11, 624.	1.7	57
36	High genetic diversity of <i>Vibrio parahaemolyticus</i> isolated from tidal water and mud of southern coast of South Korea. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	3

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37	Investigation of MiSeq reproducibility on biomarker identification. Applied Biological Chemistry, 2019, 62, .	0.7	2
38	In-situ microbial colonization and its potential contribution on biofilm formation in subsurface sediments. Journal of Applied Biological Chemistry, 2019, 62, 51-56.	0.2	6
39	Effect of mushroom (Schizophyllum spp.) derived β -glucan on low-fiber diet induced gut dysbiosis. Journal of Applied Biological Chemistry, 2019, 62, 211-217.	0.2	5
40	Comparison of mice gut microbiota before and after fasting for a day. Journal of Applied Biological Chemistry, 2019, 62, 333-337.	0.2	0
41	Current understanding of microbiota- and dietary-therapies for treating inflammatory bowel disease. Journal of Microbiology, 2018, 56, 189-198.	1.3	97
42	Vertical and Horizontal Distribution of Bacterial Communities in Alluvial Groundwater of the Nakdong River Bank. Geomicrobiology Journal, 2018, 35, 74-80.	1.0	9
43	Prevalence of antibiotic resistance genes from effluent of coastal aquaculture, South Korea. Environmental Pollution, 2018, 233, 1049-1057.	3.7	127
44	Nobiletin Enhances Chemosensitivity to Adriamycin through Modulation of the Akt/GSK3 β /E-cadherin/Catenin/MYCN/MRP1 Signaling Pathway in A549 Human Non-Small-Cell Lung Cancer Cells. Nutrients, 2018, 10, 1829.	1.7	34
45	Fecal pollution: new trends and challenges in microbial source tracking using next-generation sequencing. Environmental Microbiology, 2018, 20, 3132-3140.	1.8	56
46	Application of laser-induced breakdown spectroscopy to Arctic sediments in the Chukchi Sea. Spectrochimica Acta, Part B: Atomic Spectroscopy, 2018, 146, 84-92.	1.5	11
47	Metagenomic analysis reveals the prevalence and persistence of antibiotic- and heavy metal-resistance genes in wastewater treatment plant. Journal of Microbiology, 2018, 56, 408-415.	1.3	69
48	Bacterial Communities in Ground-and Surface Water Mixing Zone Induced by Seasonal Heavy Extraction of Groundwater. Geomicrobiology Journal, 2018, 35, 768-774.	1.0	17
49	Comparison of gut microbiome between low fiber and high fat diet fed mice. Journal of Applied Biological Chemistry, 2018, 61, 165-172.	0.2	2
50	Emergence of <i>Klebsiella variicola</i> positive for NDM-9, a variant of New Delhi metallo- β -lactamase, in an urban river in South Korea. Journal of Antimicrobial Chemotherapy, 2017, 72, dkw547.	1.3	42
51	Investigation of microbial communities in water dispensers. Applied Biological Chemistry, 2017, 60, 667-672.	0.7	2
52	Genes and Gut Bacteria Involved in Luminal Butyrate Reduction Caused by Diet and Loperamide. Genes, 2017, 8, 350.	1.0	41
53	Isolation of salt-tolerant bacteria from rhizosphere and rhizoplane of halophyte plant Suaeda japonica in Gochang-Buan tidal flat. Journal of Applied Biological Chemistry, 2017, 60, 125-131.	0.2	0
54	Laminarin favorably modulates gut microbiota in mice fed a high-fat diet. Food and Function, 2016, 7, 4193-4201.	2.1	74

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55	Effects of the Antibiotics Growth Promoter Tylosin on Swine Gut Microbiota. <i>Journal of Microbiology and Biotechnology</i> , 2016, 26, 876-882.	0.9	35
56	Metagenomics analysis of methane metabolisms in manure fertilized paddy soil. <i>Korean Journal of Microbiology</i> , 2016, 52, 157-165.	0.2	0
57	Freeze-drying feces reduces illumina-derived artefacts on 16S rRNA-based microbial community analysis. <i>Journal of Applied Biological Chemistry</i> , 2016, 59, 299-304.	0.2	0
58	Dynamic changes in the population structure of <i>Escherichia coli</i> in the Yeongsan River basin of South Korea. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv127.	1.3	6
59	Influence of seawater intrusion on microbial communities in groundwater. <i>Science of the Total Environment</i> , 2015, 532, 337-343.	3.9	38
60	Changes in human gut microbiota influenced by probiotic fermented milk ingestion. <i>Journal of Dairy Science</i> , 2015, 98, 3568-3576.	1.4	60
61	Analysis of swine fecal microbiota at various growth stages. <i>Archives of Microbiology</i> , 2015, 197, 753-759.	1.0	68
62	Dynamic changes in short- and long-term bacterial composition following fecal microbiota transplantation for recurrent <i>Clostridium difficile</i> infection. <i>Microbiome</i> , 2015, 3, 10.	4.9	218
63	Impacts of Initial Fertilizers and Irrigation Systems on Paddy Methanogens and Methane Emission. <i>Water, Air, and Soil Pollution</i> , 2015, 226, 1.	1.1	12
64	Comparison of Fecal Microbial Communities between White and Black Pigs. <i>Journal of Applied Biological Chemistry</i> , 2015, 58, 369-375.	0.2	8
65	Effects of Antibiotic Growth Promoter and Characterization of Ecological Succession in Swine Gut Microbiota. <i>Journal of Microbiology and Biotechnology</i> , 2015, 25, 431-438.	0.9	36
66	Differences in swine gut microbiota in southern region of Republic of Korea. <i>Korean Journal of Microbiology</i> , 2015, 51, 81-85.	0.2	2
67	Species and genus level resolution analysis of gut microbiota in <i>Clostridium difficile</i> patients following fecal microbiota transplantation. <i>Microbiome</i> , 2014, 2, 13.	4.9	98
68	Seasonal and Genotypic Changes in <i>Escherichia coli</i> Phylogenetic Groups in the Yeongsan River Basin of South Korea. <i>PLoS ONE</i> , 2014, 9, e100585.	1.1	19
69	Comparison Analysis of Swine Gut Microbiota between Landrace and Yorkshire at Various Growth Stages. <i>Korean Journal of Microbiology</i> , 2014, 50, 308-312.	0.2	0
70	Comparative genomics of the core and accessory genomes of 48 <i>Sinorhizobium</i> strains comprising five genospecies. <i>Genome Biology</i> , 2013, 14, R17.	13.9	164
71	Anti-viral activity of blue chanterelle (<i>Polyozellus multiplex</i>) that inhibits $\hat{\pm}$ -glucosidase. <i>Food Science and Biotechnology</i> , 2013, 22, 747-750.	1.2	5
72	Application of Illumina next-generation sequencing to characterize the bacterial community of the Upper Mississippi River. <i>Journal of Applied Microbiology</i> , 2013, 115, 1147-1158.	1.4	209

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73	Pathogenic <i>Escherichia coli</i> Strains Producing Extended-Spectrum β -Lactamases in the Yeongsan River Basin of South Korea. <i>Environmental Science & Technology</i> , 2013, 47, 1128-1136.	4.6	42
74	High-throughput DNA sequence analysis reveals stable engraftment of gut microbiota following transplantation of previously frozen fecal bacteria. <i>Gut Microbes</i> , 2013, 4, 125-135.	4.3	262
75	Use of Pyrosequencing for Characterizing Microbial Community at Phylum Level in Yeongsan River Watershed during Early Summer. <i>Korean Journal of Microbiology</i> , 2013, 49, 150-155.	0.2	0
76	Toward The Fecal Microbiome Project. <i>Korean Journal of Microbiology</i> , 2013, 49, 415-418.	0.2	0
77	Integrated Online System for a Pyrosequencing-Based Microbial Source Tracking Method that Targets Bacteroidetes 16S rDNA. <i>Environmental Science & Technology</i> , 2012, 46, 93-98.	4.6	34
78	Genotypic and Phenotypic Trends in Antibiotic Resistant Pathogenic <i>Escherichia coli</i> Isolated from Humans and Farm Animals in South Korea. <i>Microbes and Environments</i> , 2011, 26, 198-204.	0.7	14
79	Prevalence of season-specific <i>Escherichia coli</i> strains in the Yeongsan River Basin of South Korea. <i>Environmental Microbiology</i> , 2011, 13, 3103-3113.	1.8	15
80	The occurrence of virulence traits among high-level aminoglycosides resistant <i>Enterococcus</i> isolates obtained from feces of humans, animals, and birds in South Korea. <i>International Journal of Food Microbiology</i> , 2011, 144, 387-392.	2.1	45
81	Isoeugenol monooxygenase and its putative regulatory gene are located in the eugenol metabolic gene cluster in <i>Pseudomonas nitroreducens</i> Jin1. <i>Archives of Microbiology</i> , 2010, 192, 201-209.	1.0	18
82	High diversity and abundance of antibiotic-resistant <i>Escherichia coli</i> isolated from humans and farm animal hosts in Jeonnam Province, South Korea. <i>Science of the Total Environment</i> , 2010, 408, 3499-3506.	3.9	22
83	Use of Barcoded Pyrosequencing and Shared OTUs To Determine Sources of Fecal Bacteria in Watersheds. <i>Environmental Science & Technology</i> , 2010, 44, 7777-7782.	4.6	108
84	Absence of <i>Escherichia coli</i> Phylogenetic Group B2 Strains in Humans and Domesticated Animals from Jeonnam Province, Republic of Korea. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5659-5666.	1.4	46
85	Metabolic Characterization of Newly Isolated <i>Pseudomonas nitroreducens</i> Jin1 Growing on Eugenol and Isoeugenol. <i>Journal of Agricultural and Food Chemistry</i> , 2007, 55, 8556-8561.	2.4	33