

# Ilias Lagkouvardos

## List of Publications by Year in descending order

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Version: 2024-02-01

57  
papers

5,424  
citations

109137

35  
h-index

143772

57  
g-index

64  
all docs

64  
docs citations

64  
times ranked

8088  
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequence and cultivation study of Muribaculaceae reveals novel species, host preference, and functional potential of this yet undescribed family. <i>Microbiome</i> , 2019, 7, 28.	4.9	481
2	The Mouse Intestinal Bacterial Collection (miBC) provides host-specific insight into cultured diversity and functional potential of the gut microbiota. <i>Nature Microbiology</i> , 2016, 1, 16131.	5.9	465
3	IMNGS: A comprehensive open resource of processed 16S rRNA microbial profiles for ecology and diversity studies. <i>Scientific Reports</i> , 2016, 6, 33721.	1.6	330
4	Rhea: a transparent and modular R pipeline for microbial profiling based on 16S rRNA gene amplicons. <i>PeerJ</i> , 2017, 5, e2836.	0.9	325
5	Dysbiotic gut microbiota causes transmissible Crohn's disease-like ileitis independent of failure in antimicrobial defence. <i>Gut</i> , 2016, 65, 225-237.	6.1	317
6	Genome of <i>Acanthamoeba castellanii</i> highlights extensive lateral gene transfer and early evolution of tyrosine kinase signaling. <i>Genome Biology</i> , 2013, 14, R11.	13.9	296
7	A collection of bacterial isolates from the pig intestine reveals functional and taxonomic diversity. <i>Nature Communications</i> , 2020, 11, 6389.	5.8	269
8	Oral versus intravenous iron replacement therapy distinctly alters the gut microbiota and metabolome in patients with IBD. <i>Gut</i> , 2017, 66, 863-871.	6.1	237
9	Cyanate as an energy source for nitrifiers. <i>Nature</i> , 2015, 524, 105-108.	13.7	231
10	Dietary fat and gut microbiota interactions determine diet-induced obesity in mice. <i>Molecular Metabolism</i> , 2016, 5, 1162-1174.	3.0	170
11	Endospores of thermophilic bacteria as tracers of microbial dispersal by ocean currents. <i>ISME Journal</i> , 2014, 8, 1153-1165.	4.4	139
12	Randomized controlled trial on the impact of early-life intervention with bifidobacteria on the healthy infant fecal microbiota and metabolome. <i>American Journal of Clinical Nutrition</i> , 2017, 106, 1274-1286.	2.2	124
13	Effect of caloric restriction on gut permeability, inflammation markers, and fecal microbiota in obese women. <i>Scientific Reports</i> , 2017, 7, 11955.	1.6	119
14	Comparative genomics and physiology of the butyrate-producing bacterium <i>Intestinimonas butyriciproducens</i> . <i>Environmental Microbiology Reports</i> , 2016, 8, 1024-1037.	1.0	104
15	Synbiotic-driven improvement of metabolic disturbances is associated with changes in the gut microbiome in diet-induced obese mice. <i>Molecular Metabolism</i> , 2019, 22, 96-109.	3.0	102
16	Deciphering interactions between the gut microbiota and the immune system via microbial cultivation and minimal microbiomes. <i>Immunological Reviews</i> , 2017, 279, 8-22.	2.8	101
17	Gut metabolites and bacterial community networks during a pilot intervention study with flaxseeds in healthy adult men. <i>Molecular Nutrition and Food Research</i> , 2015, 59, 1614-1628.	1.5	95
18	Integrating metagenomic and amplicon databases to resolve the phylogenetic and ecological diversity of the <i>Chlamydiae</i> . <i>ISME Journal</i> , 2014, 8, 115-125.	4.4	94

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19	Interactions of Nitrifying Bacteria and Heterotrophs: Identification of a Micavibrio-Like Putative Predator of Nitrospira spp. Applied and Environmental Microbiology, 2013, 79, 2027-2037.	1.4	90
20	Activated ATF6 Induces Intestinal Dysbiosis and Innate Immune Response to Promote Colorectal Tumorigenesis. Gastroenterology, 2018, 155, 1539-1552.e12.	0.6	85
21	An Integrated Metagenome Catalog Reveals New Insights into the Murine Gut Microbiome. Cell Reports, 2020, 30, 2909-2922.e6.	2.9	85
22	Cultured microbes represent a substantial fraction of the human and mouse gut microbiota. Gut Microbes, 2017, 8, 493-503.	4.3	79
23	Integrated microbiota and metabolite profiles link Crohn's disease to sulfur metabolism. Nature Communications, 2020, 11, 4322.	5.8	79
24	A <i>Scytonema</i> symbiont of amoebae with ancient features. Environmental Microbiology, 2016, 18, 2326-2342.	1.8	73
25	Draft Genome of <i>Scalindia rubra</i> , Obtained from the Interface Above the Discovery Deep Brine in the Red Sea, Sheds Light on Potential Salt Adaptation Strategies in Anammox Bacteria. Microbial Ecology, 2017, 74, 1-5.	1.4	73
26	The mouse gut microbiome revisited: From complex diversity to model ecosystems. International Journal of Medical Microbiology, 2016, 306, 316-327.	1.5	70
27	Handling of spurious sequences affects the outcome of high-throughput 16S rRNA gene amplicon profiling. ISME Communications, 2021, 1, .	1.7	60
28	Exclusive enteral nutrition in active pediatric Crohn disease: Effects on intestinal microbiota and immune regulation. Journal of Allergy and Clinical Immunology, 2016, 138, 592-596.	1.5	54
29	Life in an unusual intracellular niche: a bacterial symbiont infecting the nucleus of amoebae. ISME Journal, 2014, 8, 1634-1644.	4.4	51
30	Infusion of donor feces affects the gut-brain axis in humans with metabolic syndrome. Molecular Metabolism, 2020, 42, 101076.	3.0	50
31	Gut barrier impairment by high-fat diet in mice depends on housing conditions. Molecular Nutrition and Food Research, 2016, 60, 897-908.	1.5	49
32	In-vivo shift of the microbiota in oral biofilm in response to frequent sucrose consumption. Scientific Reports, 2018, 8, 14202.	1.6	47
33	Massive Expansion of Ubiquitination-Related Gene Families within the Chlamydiae. Molecular Biology and Evolution, 2014, 31, 2890-2904.	3.5	43
34	Surface-Associated Lipoproteins Link <i>Enterococcus faecalis</i> Virulence to Colitogenic Activity in IL-10-Deficient Mice Independent of Their Expression Levels. PLoS Pathogens, 2015, 11, e1004911.	2.1	42
35	Determinants of postprandial plasma bile acid kinetics in human volunteers. American Journal of Physiology - Renal Physiology, 2017, 313, G300-G312.	1.6	38
36	Microbiome sequencing: challenges and opportunities for molecular medicine. Expert Review of Molecular Diagnostics, 2016, 16, 795-805.	1.5	33

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37	Pre-digest of unprotected DNA by Benzonase improves the representation of living skin bacteria and efficiently depletes host DNA. <i>Microbiome</i> , 2021, 9, 123.	4.9	33
38	The giant ciliate <i>Zoothamnium niveum</i> and its thiotrophic epibiont <i>Candidatus Thiobios zoothamnicoli</i> : a model system to study interspecies cooperation. <i>Frontiers in Microbiology</i> , 2014, 5, 145.	1.5	27
39	Improved axenization method reveals complexity of symbiotic associations between bacteria and acanthamoebae. <i>Environmental Microbiology Reports</i> , 2014, 6, 383-388.	1.0	26
40	<i>Murimonas intestini</i> gen. nov., sp. nov., an acetate-producing bacterium of the family Lachnospiraceae isolated from the mouse gut. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 870-878.	0.8	25
41	Endophytic Bacterial Isolates From Halophytes Demonstrate Phytopathogen Biocontrol and Plant Growth Promotion Under High Salinity. <i>Frontiers in Microbiology</i> , 2021, 12, 681567.	1.5	25
42	From complex gut communities to minimal microbiomes via cultivation. <i>Current Opinion in Microbiology</i> , 2017, 38, 148-155.	2.3	23
43	Increased Pancreatic Protease Activity in Response to Antibiotics Impairs Gut Barrier and Triggers Colitis. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2018, 6, 370-388.e3.	2.3	22
44	Signature Protein of the PVC Superphylum. <i>Applied and Environmental Microbiology</i> , 2014, 80, 440-445.	1.4	20
45	Seasonal dynamics in the number and composition of coliform bacteria in drinking water reservoirs. <i>Science of the Total Environment</i> , 2021, 787, 147539.	3.9	20
46	Mining gut microbiome oligopeptides by functional metaproteome display. <i>Scientific Reports</i> , 2016, 6, 34337.	1.6	19
47	Impact of Laparoscopic Sleeve Gastrectomy on Gut Permeability in Morbidly Obese Subjects. <i>Obesity Surgery</i> , 2019, 29, 2132-2143.	1.1	17
48	Recent advances in culture-based gut microbiome research. <i>International Journal of Medical Microbiology</i> , 2021, 311, 151485.	1.5	15
49	MiMiC: a bioinformatic approach for generation of synthetic communities from metagenomes. <i>Microbial Biotechnology</i> , 2021, 14, 1757-1770.	2.0	12
50	Depletion of Unwanted Nucleic Acid Templates by Selective Cleavage: LNAzymes, Catalytically Active Oligonucleotides Containing Locked Nucleic Acids, Open a New Window for Detecting Rare Microbial Community Members. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1534-1544.	1.4	10
51	Physiological relevance of food grade microcapsules: Impact of milk protein based microcapsules on inflammation in mouse models for inflammatory bowel diseases. <i>Molecular Nutrition and Food Research</i> , 2015, 59, 1629-1634.	1.5	5
52	Processing Matters in Nutrient-Matched Laboratory Diets for Mice's Microbiome. <i>Animals</i> , 2021, 11, 862.	1.0	5
53	A Novel Primer Mixture for GH48 Genes: Quantification and Identification of Truly Cellulolytic Bacteria in Biogas Fermenters. <i>Microorganisms</i> , 2020, 8, 1297.	1.6	3
54	Taxonomy Informed Clustering, an Optimized Method for Purer and More Informative Clusters in Diversity Analysis and Microbiome Profiling. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	3

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55	DivCom: A Tool for Systematic Partition of Groups of Microbial Profiles Into Intrinsic Subclusters and Distance-Based Subgroup Comparisons. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	2
56	Draft Genome Sequence of <i>Paenibacillus polymyxa</i> DSM 292, a Gram-Positive, Spore-Forming Soil Bacterium with High Biotechnological Potential. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
57	Alteration of Intestinal Microbiome of <i>Clostridioides difficile</i> -Infected Hamsters during the Treatment with Specific Cow Antibodies. <i>Antibiotics</i> , 2021, 10, 724.	1.5	1