

Ilias Lagkouvardos

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

5,424
citations

109321

35
h-index

144013

57
g-index

64
all docs

64
docs citations

64
times ranked

8088
citing authors

#	ARTICLE	IF	CITATIONS
1	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, .	2.1	3
2	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, .	2.1	2
3	Processing Matters in Nutrient-Matched Laboratory Diets for Mice’s Microbiome. <i>Animals</i> , 2021, 11, 862.	2.3	5
4	Recent advances in culture-based gut microbiome research. <i>International Journal of Medical Microbiology</i> , 2021, 311, 151485.	3.6	15
5	Endophytic Bacterial Isolates From Halophytes Demonstrate Phytopathogen Biocontrol and Plant Growth Promotion Under High Salinity. <i>Frontiers in Microbiology</i> , 2021, 12, 681567.	3.5	25
6	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.	11.1	33
7	Alteration of Intestinal Microbiome of <i>Clostridioides difficile</i> -Infected Hamsters during the Treatment with Specific Cow Antibodies. <i>Antibiotics</i> , 2021, 10, 724.	3.7	1
8	MiMiC: a bioinformatic approach for generation of synthetic communities from metagenomes. <i>Microbial Biotechnology</i> , 2021, 14, 1757-1770.	4.2	12
9	Handling of spurious sequences affects the outcome of high-throughput 16S rRNA gene amplicon profiling. <i>ISME Communications</i> , 2021, 1, .	4.2	60
10	Seasonal dynamics in the number and composition of coliform bacteria in drinking water reservoirs. <i>Science of the Total Environment</i> , 2021, 787, 147539.	8.0	20
11	Infusion of donor feces affects the gut-brain axis in humans with metabolic syndrome. <i>Molecular Metabolism</i> , 2020, 42, 101076.	6.5	50
12	A Novel Primer Mixture for GH48 Genes: Quantification and Identification of Truly Cellulolytic Bacteria in Biogas Fermenters. <i>Microorganisms</i> , 2020, 8, 1297.	3.6	3
13	Integrated microbiota and metabolite profiles link Crohn’s disease to sulfur metabolism. <i>Nature Communications</i> , 2020, 11, 4322.	12.8	79
14	A collection of bacterial isolates from the pig intestine reveals functional and taxonomic diversity. <i>Nature Communications</i> , 2020, 11, 6389.	12.8	269
15	An Integrated Metagenome Catalog Reveals New Insights into the Murine Gut Microbiome. <i>Cell Reports</i> , 2020, 30, 2909-2922.e6.	6.4	85
16	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, .	0.6	1
17	Impact of Laparoscopic Sleeve Gastrectomy on Gut Permeability in Morbidly Obese Subjects. <i>Obesity Surgery</i> , 2019, 29, 2132-2143.	2.1	17
18	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.	6.5	102

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19	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.	11.1	481
20	Activated ATF6 Induces Intestinal Dysbiosis and Innate Immune Response to Promote Colorectal Tumorigenesis. <i>Gastroenterology</i> , 2018, 155, 1539-1552.e12.	1.3	85
21	In-vivo shift of the microbiota in oral biofilm in response to frequent sucrose consumption. <i>Scientific Reports</i> , 2018, 8, 14202.	3.3	47
22	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.	4.5	22
23	Oral versus intravenous iron replacement therapy distinctly alters the gut microbiota and metabolome in patients with IBD. <i>Gut</i> , 2017, 66, 863-871.	12.1	237
24	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. <i>Microbial Ecology</i> , 2017, 74, 1-5.	2.8	73
25	Cultured microbes represent a substantial fraction of the human and mouse gut microbiota. <i>Gut Microbes</i> , 2017, 8, 493-503.	9.8	79
26	From complex gut communities to minimal microbiomes via cultivation. <i>Current Opinion in Microbiology</i> , 2017, 38, 148-155.	5.1	23
27	Deciphering interactions between the gut microbiota and the immune system via microbial cultivation and minimal microbiomes. <i>Immunological Reviews</i> , 2017, 279, 8-22.	6.0	101
28	Effect of caloric restriction on gut permeability, inflammation markers, and fecal microbiota in obese women. <i>Scientific Reports</i> , 2017, 7, 11955.	3.3	119
29	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.	4.7	124
30	Determinants of postprandial plasma bile acid kinetics in human volunteers. <i>American Journal of Physiology - Renal Physiology</i> , 2017, 313, G300-G312.	3.4	38
31	Rhea: a transparent and modular R pipeline for microbial profiling based on 16S rRNA gene amplicons. <i>PeerJ</i> , 2017, 5, e2836.	2.0	325
32	Gut barrier impairment by high-fat diet in mice depends on housing conditions. <i>Molecular Nutrition and Food Research</i> , 2016, 60, 897-908.	3.3	49
33	Microbiome sequencing: challenges and opportunities for molecular medicine. <i>Expert Review of Molecular Diagnostics</i> , 2016, 16, 795-805.	3.1	33
34	Comparative genomics and physiology of the butyrate-producing bacterium <i>Intestinimonas butyriciproducens</i> . <i>Environmental Microbiology Reports</i> , 2016, 8, 1024-1037.	2.4	104
35	Dietary fat and gut microbiota interactions determine diet-induced obesity in mice. <i>Molecular Metabolism</i> , 2016, 5, 1162-1174.	6.5	170
36	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.	13.3	465

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37	IMNGS: A comprehensive open resource of processed 16S rRNA microbial profiles for ecology and diversity studies. Scientific Reports, 2016, 6, 33721.	3.3	330
38	Mining gut microbiome oligopeptides by functional metaproteome display. Scientific Reports, 2016, 6, 34337.	3.3	19
39	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.	2.9	54
40	The mouse gut microbiome revisited: From complex diversity to model ecosystems. International Journal of Medical Microbiology, 2016, 306, 316-327.	3.6	70
41	A <i>Rickettsiales</i> symbiont of amoebae with ancient features. Environmental Microbiology, 2016, 18, 2326-2342.	3.8	73
42	Dysbiotic gut microbiota causes transmissible Crohn's disease-like ileitis independent of failure in antimicrobial defence. Gut, 2016, 65, 225-237.	12.1	317
43	Physiological relevance of food grade microcapsules: Impact of milk protein based microcapsules on inflammation in mouse models for inflammatory bowel diseases. Molecular Nutrition and Food Research, 2015, 59, 1629-1634.	3.3	5
44	Gut metabolites and bacterial community networks during a pilot intervention study with flaxseeds in healthy adult men. Molecular Nutrition and Food Research, 2015, 59, 1614-1628.	3.3	95
45	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.	4.7	42
46	Cyanate as an energy source for nitrifiers. Nature, 2015, 524, 105-108.	27.8	231
47	<i>Murimonas intestini</i> gen. nov., sp. nov., an acetate-producing bacterium of the family Lachnospiraceae isolated from the mouse gut. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 870-878.	1.7	25
48	The giant ciliate <i>Zoothamnium niveum</i> and its thiotrophic epibiont <i>Candidatus Thiobios zoothamnicoli</i> : a model system to study interspecies cooperation. Frontiers in Microbiology, 2014, 5, 145.	3.5	27
49	Life in an unusual intracellular niche: a bacterial symbiont infecting the nucleus of amoebae. ISME Journal, 2014, 8, 1634-1644.	9.8	51
50	Integrating metagenomic and amplicon databases to resolve the phylogenetic and ecological diversity of the <i>Chlamydiae</i> . ISME Journal, 2014, 8, 115-125.	9.8	94
51	Endospores of thermophilic bacteria as tracers of microbial dispersal by ocean currents. ISME Journal, 2014, 8, 1153-1165.	9.8	139
52	Improved axenization method reveals complexity of symbiotic associations between bacteria and acanthamoebae. Environmental Microbiology Reports, 2014, 6, 383-388.	2.4	26
53	Massive Expansion of Ubiquitination-Related Gene Families within the <i>Chlamydiae</i> . Molecular Biology and Evolution, 2014, 31, 2890-2904.	8.9	43
54	Signature Protein of the PVC Superphylum. Applied and Environmental Microbiology, 2014, 80, 440-445.	3.1	20

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55	Interactions of Nitrifying Bacteria and Heterotrophs: Identification of a Micavibrio-Like Putative Predator of Nitrospira spp. Applied and Environmental Microbiology, 2013, 79, 2027-2037.	3.1	90
56	Genome of Acanthamoeba castellanii highlights extensive lateral gene transfer and early evolution of tyrosine kinase signaling. Genome Biology, 2013, 14, R11.	9.6	296
57	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. Applied and Environmental Microbiology, 2013, 79, 1534-1544.	3.1	10