Ilias Lagkouvardos

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

57	3,021	29	54
papers	citations	h-index	g-index
64 ext. papers	4,643 ext. citations	8.6 avg, IF	5.19 L-index

#	Paper	IF	Citations
57	Recent advances in culture-based gut microbiome research. <i>International Journal of Medical Microbiology</i> , 2021 , 311, 151485	3.7	1
56	Endophytic Bacterial Isolates From Halophytes Demonstrate Phytopathogen Biocontrol and Plant Growth Promotion Under High Salinity. <i>Frontiers in Microbiology</i> , 2021 , 12, 681567	5.7	8
55	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	16.6	2
54	MiMiC: a bioinformatic approach for generation of synthetic communities from metagenomes. <i>Microbial Biotechnology</i> , 2021 , 14, 1757-1770	6.3	О
53	Handling of spurious sequences affects the outcome of high-throughput 16S rRNA gene amplicon profiling. <i>ISME Communications</i> , 2021 , 1,		7
52	Seasonal dynamics in the number and composition of coliform bacteria in drinking water reservoirs. <i>Science of the Total Environment</i> , 2021 , 787, 147539	10.2	5
51	A collection of bacterial isolates from the pig intestine reveals functional and taxonomic diversity. <i>Nature Communications</i> , 2020 , 11, 6389	17.4	26
50	An Integrated Metagenome Catalog Reveals New Insights into the Murine Gut Microbiome. <i>Cell Reports</i> , 2020 , 30, 2909-2922.e6	10.6	44
49	Infusion of donor feces affects the gut-brain axis in humans with metabolic syndrome. <i>Molecular Metabolism</i> , 2020 , 42, 101076	8.8	15
48	A Novel Primer Mixture for GH48 Genes: Quantification and Identification of Truly Cellulolytic Bacteria in Biogas Fermenters. <i>Microorganisms</i> , 2020 , 8,	4.9	1
47	Integrated microbiota and metabolite profiles link CrohnZ disease to sulfur metabolism. <i>Nature Communications</i> , 2020 , 11, 4322	17.4	25
46	Impact of Laparoscopic Sleeve Gastrectomy on Gut Permeability in Morbidly Obese Subjects. <i>Obesity Surgery</i> , 2019 , 29, 2132-2143	3.7	10
45	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	8.8	62
44	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	16.6	202
43	Dysbiotische Verschiebungen der mikrobiellen Gemeinschaft des supragingivalen oralen Biofilms durch hllfigen Saccharosekonsum. <i>Oralprophylaxe Und Kinderzahnheilkunde</i> , 2019 , 41, 157-168	0.1	
42	Acetatifactor 2018 , 1-8		
41	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	7.9	13

(2016-2018)

40	Activated ATF6 Induces Intestinal Dysbiosis and Innate Immune Response to Promote Colorectal Tumorigenesis. <i>Gastroenterology</i> , 2018 , 155, 1539-1552.e12	13.3	51
39	In-vivo shift of the microbiota in oral biofilm in response to frequent sucrose consumption. <i>Scientific Reports</i> , 2018 , 8, 14202	4.9	30
38	Oral versus intravenous iron replacement therapy distinctly alters the gut microbiota and metabolome in patients with IBD. <i>Gut</i> , 2017 , 66, 863-871	19.2	160
37	Draft Genome of Scalindua rubra, 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	4.4	53
36	Cultured microbes represent a substantial fraction of the human and mouse gut microbiota. <i>Gut Microbes</i> , 2017 , 8, 493-503	8.8	57
35	From complex gut communities to minimal microbiomes via cultivation. <i>Current Opinion in Microbiology</i> , 2017 , 38, 148-155	7.9	17
34	Deciphering interactions between the gut microbiota and the immune system via microbial cultivation and minimal microbiomes. <i>Immunological Reviews</i> , 2017 , 279, 8-22	11.3	57
33	Effect of caloric restriction on gut permeability, inflammation markers, and fecal microbiota in obese women. <i>Scientific Reports</i> , 2017 , 7, 11955	4.9	77
32	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	-7286	66
31	Determinants of postprandial plasma bile acid kinetics in human volunteers. <i>American Journal of Physiology - Renal Physiology</i> , 2017 , 313, G300-G312	5.1	25
30	Rhea: a transparent and modular R pipeline for microbial profiling based on 16S rRNA gene amplicons. <i>PeerJ</i> , 2017 , 5, e2836	3.1	172
29	A Rickettsiales symbiont of amoebae with ancient features. <i>Environmental Microbiology</i> , 2016 , 18, 2326	- 4 2	41
28	Dysbiotic gut microbiota causes transmissible Crohn丞 disease-like ileitis independent of failure in antimicrobial defence. <i>Gut</i> , 2016 , 65, 225-37	19.2	220
27	Comparative genomics and physiology of the butyrate-producing bacterium Intestinimonas butyriciproducens. <i>Environmental Microbiology Reports</i> , 2016 , 8, 1024-1037	3.7	52
26	Dietary fat and gut microbiota interactions determine diet-induced obesity in mice. <i>Molecular Metabolism</i> , 2016 , 5, 1162-1174	8.8	108
25	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	26.6	222
24	IMNGS: A comprehensive open resource of processed 16S rRNA microbial profiles for ecology and diversity studies. <i>Scientific Reports</i> , 2016 , 6, 33721	4.9	192
23	Mining gut microbiome oligopeptides by functional metaproteome display. <i>Scientific Reports</i> , 2016 , 6, 34337	4.9	11

22	Exclusive enteral nutrition in active pediatric Crohn disease: Effects on intestinal microbiota and immune regulation. <i>Journal of Allergy and Clinical Immunology</i> , 2016 , 138, 592-6	11.5	39
21	The mouse gut microbiome revisited: From complex diversity to model ecosystems. <i>International Journal of Medical Microbiology</i> , 2016 , 306, 316-327	3.7	50
20	Gut barrier impairment by high-fat diet in mice depends on housing conditions. <i>Molecular Nutrition and Food Research</i> , 2016 , 60, 897-908	5.9	40
19	Microbiome sequencing: challenges and opportunities for molecular medicine. <i>Expert Review of Molecular Diagnostics</i> , 2016 , 16, 795-805	3.8	25
18	Cyanate as an energy source for nitrifiers. <i>Nature</i> , 2015 , 524, 105-8	50.4	160
17	Murimonas intestini 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	2.2	14
16	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, 1629-34	5.9	4
15	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, 1614-28	5.9	65
14	Surface-Associated Lipoproteins Link Enterococcus faecalis Virulence to Colitogenic Activity in IL-10-Deficient Mice Independent of Their Expression Levels. <i>PLoS Pathogens</i> , 2015 , 11, e1004911	7.6	37
13	Signature protein of the PVC superphylum. Applied and Environmental Microbiology, 2014, 80, 440-5	4.8	18
12	The giant ciliate Zoothamnium niveum and its thiotrophic epibiont Candidatus Thiobios zoothamnicoli: a model system to study interspecies cooperation. <i>Frontiers in Microbiology</i> , 2014 , 5, 145	; 5.7	19
11	Life in an unusual intracellular niche: a bacterial symbiont infecting the nucleus of amoebae. <i>ISME Journal</i> , 2014 , 8, 1634-44	11.9	32
10	Integrating metagenomic and amplicon databases to resolve the phylogenetic and ecological diversity of the Chlamydiae. <i>ISME Journal</i> , 2014 , 8, 115-25	11.9	68
9	Endospores of thermophilic bacteria as tracers of microbial dispersal by ocean currents. <i>ISME Journal</i> , 2014 , 8, 1153-65	11.9	85
8	Improved axenization method reveals complexity of symbiotic associations between bacteria and acanthamoebae. <i>Environmental Microbiology Reports</i> , 2014 , 6, 383-8	3.7	18
7	Massive expansion of Ubiquitination-related gene families within the Chlamydiae. <i>Molecular Biology and Evolution</i> , 2014 , 31, 2890-904	8.3	26
6	Interactions of nitrifying bacteria and heterotrophs: identification of a Micavibrio-like putative predator of Nitrospira spp. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 2027-37	4.8	67
5	Genome of Acanthamoeba castellanii highlights extensive lateral gene transfer and early evolution of tyrosine kinase signaling. <i>Genome Biology</i> , 2013 , 14, R11	18.3	205

LIST OF PUBLICATIONS

4	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 4. community members. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 1534-44	8 9	
3	Handling of Spurious Sequences Affects the Outcome of High-Throughput 16S rRNA Gene Amplicon Profiling	2	
2	An integrated metagenome catalog reveals novel insights into the murine gut microbiome	5	
1	Namco: A microbiome explorer	1	