

Where Next for Microbiome Research?

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Metabolic network modeling of microbial communities. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2015, 7, 317-334.	6.6	95
2	The role of breast-feeding in infant immune system: a systems perspective on the intestinal microbiome. <i>Microbiome</i> , 2015, 3, 41.	4.9	81
3	From next-generation sequencing to systematic modeling of the gut microbiome. <i>Frontiers in Genetics</i> , 2015, 6, 219.	1.1	99
4	Lungs, Microbes and the Developing Neonate. <i>Neonatology</i> , 2015, 107, 337-343.	0.9	24
5	Lung Microbiomes: New Frontiers?. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015, 191, 870-871.	2.5	0
6	Increasing Metagenomic Resolution of Microbiome Interactions Through Functional Phylogenomics and Bacterial Sub-Communities. <i>Frontiers in Genetics</i> , 2016, 7, 4.	1.1	8
7	Characterization of the Gut Microbiome Using 16S or Shotgun Metagenomics. <i>Frontiers in Microbiology</i> , 2016, 7, 459.	1.5	659
8	A Mutational Hotspot and Strong Selection Contribute to the Order of Mutations Selected for during <i>Escherichia coli</i> Adaptation to the Gut. <i>PLoS Genetics</i> , 2016, 12, e1006420.	1.5	47
9	Microbial contributions to chronic inflammation and metabolic disease. <i>Current Opinion in Clinical Nutrition and Metabolic Care</i> , 2016, 19, 257-262.	1.3	19
10	Divergent selection-induced obesity alters the composition and functional pathways of chicken gut microbiota. <i>Genetics Selection Evolution</i> , 2016, 48, 93.	1.2	41
11	Overview and Update in Geriatric Dermatology. <i>Current Geriatrics Reports</i> , 2016, 5, 275-282.	1.1	0
12	Metabolic Model-Based Integration of Microbiome Taxonomic and Metabolomic Profiles Elucidates Mechanistic Links between Ecological and Metabolic Variation. <i>MSystems</i> , 2016, 1, .	1.7	167
13	The Role of Antibiotics in Gut Microbiota Modulation: The Eubiotic Effects of Rifaximin. <i>Digestive Diseases</i> , 2016, 34, 269-278.	0.8	105
14	High definition for systems biology of microbial communities: metagenomics gets genome-centric and strain-resolved. <i>Current Opinion in Biotechnology</i> , 2016, 39, 174-181.	3.3	30
15	The science, development, and commercialization of postharvest biocontrol products. <i>Postharvest Biology and Technology</i> , 2016, 122, 22-29.	2.9	271
16	The evolution of cooperation within the gut microbiota. <i>Nature</i> , 2016, 533, 255-259.	13.7	483
17	Details Matter: Designing Skin Microbiome Studies. <i>Journal of Investigative Dermatology</i> , 2016, 136, 900-902.	0.3	37
18	Plant Microbiota Interactions as a Driver of the Mineral Turnover in the Rhizosphere. <i>Advances in Applied Microbiology</i> , 2016, 95, 1-67.	1.3	105

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19	Effects of host genetics and environment on egg-associated microbiotas in brown trout (<i>Salmo trutta</i>). <i>Journal of Experimental Biology</i> , 2016, 219, 107-115.	2.0	28
20	Getting Personal About Nutrition. <i>Trends in Molecular Medicine</i> , 2016, 22, 83-85.	3.5	11
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22	Investigating a holobiont: Microbiota perturbations and transkingdom networks. <i>Gut Microbes</i> , 2016, 7, 126-135.	4.3	38
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26	Microbiome engineering: Current applications and its future. <i>Biotechnology Journal</i> , 2017, 12, 1600099.	1.8	137
27	The microbiome in allergic disease: Current understanding and future opportunities-2017 PRACTALL document of the American Academy of Allergy, Asthma & Immunology and the European Academy of Allergy and Clinical Immunology. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 1099-1110.	1.5	264
28	The microbiome in respiratory medicine: current challenges and future perspectives. <i>European Respiratory Journal</i> , 2017, 49, 162086.	3.1	194
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30	Communicating the promise, risks, and ethics of large-scale, open space microbiome and metagenome research. <i>Microbiome</i> , 2017, 5, 132.	4.9	26
31	Recurrent Reverse Evolution Maintains Polymorphism after Strong Bottlenecks in Commensal Gut Bacteria. <i>Molecular Biology and Evolution</i> , 2017, 34, 2879-2892.	3.5	38
32	Genome-driven evolutionary game theory helps understand the rise of metabolic interdependencies in microbial communities. <i>Nature Communications</i> , 2017, 8, 1563.	5.8	130
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39	A phylogenetic transform enhances analysis of compositional microbiota data. <i>ELife</i> , 2017, 6, .	2.8	247
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67	The use of next generation sequencing for improving food safety: Translation into practice. <i>Food Microbiology</i> , 2019, 79, 96-115.	2.1	225
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