

Beyond the Venn diagram: the hunt for a core microbiome

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Metagenomics Potential for Bioremediation. , 2012, , 1-11.		1
2	Fundamentals of Microbial Community Resistance and Resilience. <i>Frontiers in Microbiology</i> , 2012, 3, 417.	1.5	1,131
3	Bacterial Community Structure in the Drinking Water Microbiome Is Governed by Filtration Processes. <i>Environmental Science & Technology</i> , 2012, 46, 8851-8859.	4.6	366
4	Bacterial community structure and its relationship to soil physico-chemical characteristics in alder stands with different management histories. <i>Ecological Engineering</i> , 2012, 49, 10-17.	1.6	63
5	The Human Microbiome Project: A Community Resource for the Healthy Human Microbiome. <i>PLoS Biology</i> , 2012, 10, e1001377.	2.6	369
6	Mycangia of Ambrosia Beetles Host Communities of Bacteria. <i>Microbial Ecology</i> , 2012, 64, 784-793.	1.4	60
7	Low sequencing efforts bias analyses of shared taxa in microbial communities. <i>Folia Microbiologica</i> , 2012, 57, 409-413.	1.1	27
8	Large-Scale Survey of Gut Microbiota Associated With MHE Via 16S rRNA-Based Pyrosequencing. <i>American Journal of Gastroenterology</i> , 2013, 108, 1601-1611.	0.2	149
9	Temporal variability and coherence of euphotic zone bacterial communities over a decade in the Southern California Bight. <i>ISME Journal</i> , 2013, 7, 2259-2273.	4.4	162
10	Land-use change and soil type are drivers of fungal and archaeal communities in the Pampa biome. <i>World Journal of Microbiology and Biotechnology</i> , 2013, 29, 223-233.	1.7	40
11	The Gordian Knot of dysbiosis, obesity and NAFLD. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2013, 10, 637-644.	8.2	134
12	The inconstant gut microbiota of <i>Drosophila</i> species revealed by 16S rRNA gene analysis. <i>ISME Journal</i> , 2013, 7, 1922-1932.	4.4	281
13	Distinct bacterial community structure of 3 tropical volcanic soils from banana plantations contaminated with chlordecone in Guadeloupe (French West Indies). <i>Chemosphere</i> , 2013, 92, 787-794.	4.2	15
14	The saliva microbiome of Pan and Homo. <i>BMC Microbiology</i> , 2013, 13, 204.	1.3	34
15	Next generation sequencing shows high variation of the intestinal microbial species composition in Atlantic cod caught at a single location. <i>BMC Microbiology</i> , 2013, 13, 248.	1.3	98
16	Microbial community structure in vineyard soils across altitudinal gradients and in different seasons. <i>FEMS Microbiology Ecology</i> , 2013, 84, 588-602.	1.3	64
17	Small core communities and high variability in bacteria associated with the introduced ascidian <i>Styela plicata</i> . <i>Symbiosis</i> , 2013, 59, 35-46.	1.2	24
18	The canine and feline skin microbiome in health and disease. <i>Veterinary Dermatology</i> , 2013, 24, 137.	0.4	56

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19	Effects of nitrogen addition on soil microbial diversity and methane cycling capacity depend on drainage conditions in a pine forest soil. <i>Soil Biology and Biochemistry</i> , 2013, 62, 119-128.	4.2	20
20	Co-evolution in context: The importance of studying gut microbiomes in wild animals. <i>Microbiome Science and Medicine</i> , 2013, 1, .	0.3	138
21	454 Pyrosequencing Analysis of Fungal Assemblages from Geographically Distant, Disparate Soils Reveals Spatial Patterning and a Core Mycobiome. <i>Diversity</i> , 2013, 5, 73-98.	0.7	82
22	Unexpected Diversity during Community Succession in the Apple Flower Microbiome. <i>MBio</i> , 2013, 4, .	1.8	210
23	Parallel changes of taxonomic interaction networks in lacustrine bacterial communities induced by a polymetallic perturbation. <i>Evolutionary Applications</i> , 2013, 6, 643-659.	1.5	30
24	Aquacultured Rainbow Trout (<i>Oncorhynchus mykiss</i>) Possess a Large Core Intestinal Microbiota That Is Resistant to Variation in Diet and Rearing Density. <i>Applied and Environmental Microbiology</i> , 2013, 79, 4974-4984.	1.4	191
25	Different bacterial communities in ectomycorrhizae and surrounding soil. <i>Scientific Reports</i> , 2013, 3, 3471.	1.6	77
26	Gut microbiota dysbiosis and bacterial community assembly associated with cholesterol gallstones in large-scale study. <i>BMC Genomics</i> , 2013, 14, 669.	1.2	168
27	A Multifactor Analysis of Fungal and Bacterial Community Structure in the Root Microbiome of Mature <i>Populus deltoides</i> Trees. <i>PLoS ONE</i> , 2013, 8, e76382.	1.1	315
28	Exploring the Dynamic Core Microbiome of Plaque Microbiota during Head-and-Neck Radiotherapy Using Pyrosequencing. <i>PLoS ONE</i> , 2013, 8, e56343.	1.1	74
29	Analyses of the Stability and Core Taxonomic Memberships of the Human Microbiome. <i>PLoS ONE</i> , 2013, 8, e63139.	1.1	184
30	Shifts in the Microbial Community Composition of Gulf Coast Beaches Following Beach Oiling. <i>PLoS ONE</i> , 2013, 8, e74265.	1.1	72
31	Soil-Borne Bacterial Structure and Diversity Does Not Reflect Community Activity in Pampa Biome. <i>PLoS ONE</i> , 2013, 8, e76465.	1.1	52
32	Same, same but different: symbiotic bacterial associations in GBR sponges. <i>Frontiers in Microbiology</i> , 2012, 3, 444.	1.5	52
33	Bespoke microbiome therapy to manage plant diseases. <i>Frontiers in Microbiology</i> , 2013, 4, 355.	1.5	77
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36	Investigation of bacterial diversity in the feces of cattle fed different diets1. <i>Journal of Animal Science</i> , 2014, 92, 683-694.	0.2	134

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37	Pinus flexilis and Piceae engelmannii share a simple and consistent needle endophyte microbiota with a potential role in nitrogen fixation. <i>Frontiers in Microbiology</i> , 2014, 5, 333.	1.5	81
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40	Comparative analysis of the human saliva microbiome from different climate zones: Alaska, Germany, and Africa. <i>BMC Microbiology</i> , 2014, 14, 316.	1.3	134
41	Metagenomic analyses of bacteria on human hairs: a qualitative assessment for applications in forensic science. <i>Investigative Genetics</i> , 2014, 5, 16.	3.3	69
42	Microbial cargo: do bacteria on symbiotic propagules reinforce the microbiome of lichens?. <i>Environmental Microbiology</i> , 2014, 16, 3743-3752.	1.8	78
43	Core functional traits of bacterial communities in the Upper Mississippi River show limited variation in response to land cover. <i>Frontiers in Microbiology</i> , 2014, 5, 414.	1.5	95
44	Bacteria in Soil. , 2014, , .		0
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50	Interactions in the microbiome: communities of organisms and communities of genes. <i>FEMS Microbiology Reviews</i> , 2014, 38, 90-118.	3.9	174
51	Establishing a core microbiome in acetate-fed microbial fuel cells. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 4187-4196.	1.7	65
52	Association of dietary type with fecal microbiota in vegetarians and omnivores in Slovenia. <i>European Journal of Nutrition</i> , 2014, 53, 1051-1064.	1.8	155
53	Quantitative divergence of the bacterial root microbiota in <i>Arabidopsis thaliana</i> relatives. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 585-592.	3.3	539
54	Diversity and structure of bacterial communities associated with <sc>P</sc> <sc>hanerochaete chrysosporium</sc> during wood decay. <i>Environmental Microbiology</i> , 2014, 16, 2238-2252.	1.8	51

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55	Diazotrophic potential among bacterial communities associated with wild and cultivated <i>Agave</i> species. <i>FEMS Microbiology Ecology</i> , 2014, 90, 844-857.	1.3	71
56	Discovering new indicators of fecal pollution. <i>Trends in Microbiology</i> , 2014, 22, 697-706.	3.5	136
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62	Planting increases the abundance and structure complexity of soil core functional genes relevant to carbon and nitrogen cycling. <i>Scientific Reports</i> , 2015, 5, 14345.	1.6	26
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70	Pyrosequencing Reveals Changes in Soil Bacterial Communities after Conversion of Yungas Forests to Agriculture. <i>PLoS ONE</i> , 2015, 10, e0119426.	1.1	48
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86	Microbiota of the Major South Atlantic Reef Building Coral <i>Mussismilia</i> . Microbial Ecology, 2015, 69, 267-280.	1.4	26
87	Microbial communities and their predicted metabolic characteristics in deep fracture groundwaters of the crystalline bedrock at Olkiluoto, Finland. Biogeosciences, 2016, 13, 6031-6047.	1.3	42
88	Characterization of the Core and Caste-Specific Microbiota in the Termite, <i>Reticulitermes flavipes</i> . Frontiers in Microbiology, 2016, 7, 171.	1.5	71
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96	Analysis of single root tip microbiomes suggests that distinctive bacterial communities are selected by <i>Pinus sylvestris</i> roots colonized by different ectomycorrhizal fungi. <i>Environmental Microbiology</i> , 2016, 18, 1470-1483.	1.8	79
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99	Oral microbial biofilm models and their application to the testing of anticariogenic agents. <i>Journal of Dentistry</i> , 2016, 50, 1-11.	1.7	36
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110	Metagenomic applications in environmental monitoring and bioremediation. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2016, 43, 1345-1354.	1.4	102
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118	Elevated nutrients change bacterial community composition and connectivity: high throughput sequencing of young marine biofilms. <i>Biofouling</i> , 2016, 32, 57-69.	0.8	87
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121	Ecological patterns, diversity and core taxa of microbial communities in groundwater-fed rapid gravity filters. <i>ISME Journal</i> , 2016, 10, 2209-2222.	4.4	125
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127	Fish intestinal microbiome: diversity and symbiosis unravelled by metagenomics. <i>Journal of Applied Microbiology</i> , 2017, 123, 2-17.	1.4	290
128	Proteotyping of laboratory-scale biogas plants reveals multiple steady-states in community composition. <i>Anaerobe</i> , 2017, 46, 56-68.	1.0	33
129	Ecological patterns of seed microbiome diversity, transmission, and assembly. <i>Current Opinion in Microbiology</i> , 2017, 37, 15-22.	2.3	331
130	Seasonal variation in the copepod gut microbiome in the subtropical North Atlantic Ocean. <i>Environmental Microbiology</i> , 2017, 19, 3087-3097.	1.8	53
131	Signature of Microbial Dysbiosis in Periodontitis. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	91
132	Intraspecific Variation in the Skin-Associated Microbiome of a Terrestrial Salamander. <i>Microbial Ecology</i> , 2017, 74, 745-756.	1.4	53
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143	Defining the Core Citrus Leaf- and Root-Associated Microbiota: Factors Associated with Community Structure and Implications for Managing Huanglongbing (Citrus Greening) Disease. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	78
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145	Culturable bacterial communities associated to Brazilian Oscarella species (Porifera: Tj ETQq0 0 0 rgBT /Overlock 10,7f 50 742 Td (Hom	0.7	20
146	Bacterial microbiomes of individual ectomycorrhizal <i>Pinus sylvestris</i> roots are shaped by soil horizon and differentially sensitive to nitrogen addition. <i>Environmental Microbiology</i> , 2017, 19, 4736-4753.	1.8	35
147	Xerotolerance of <i>Penicillium</i> and <i>Phialocephala</i> fungi, dominant taxa of fine lateral roots of woody plants in the intermountain Pacific Northwest, USA. <i>Rhizosphere</i> , 2017, 4, 94-103.	1.4	12
148	Group Living and Male Dispersal Predict the Core Gut Microbiome in Wild Baboons. <i>Integrative and Comparative Biology</i> , 2017, 57, 770-785.	0.9	69
149	Actinobacterial Rare Biospheres and Dark Matter Revealed in Habitats of the Chilean Atacama Desert. <i>Scientific Reports</i> , 2017, 7, 8373.	1.6	65
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151	The Microbial Ecosystem Distinguishes Chronically Diseased Tissue from Adjacent Tissue in the Sigmoid Colon of Chronic, Recurrent Diverticulitis Patients. <i>Scientific Reports</i> , 2017, 7, 8467.	1.6	41
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153	The Hibernator Microbiome: Host-Bacterial Interactions in an Extreme Nutritional Symbiosis. <i>Annual Review of Nutrition</i> , 2017, 37, 477-500.	4.3	58
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