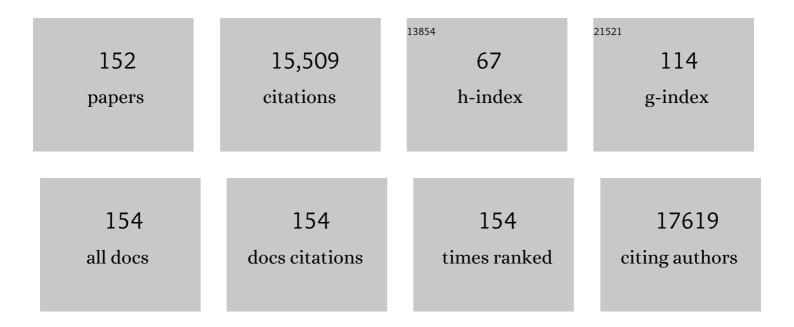
Francesca De Filippis

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4059055/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	A Selected Core Microbiome Drives the Early Stages of Three Popular Italian Cheese Manufactures. PLoS ONE, 2014, 9, e89680.	1.1	1,195
2	High-level adherence to a Mediterranean diet beneficially impacts the gut microbiota and associated metabolome. Gut, 2016, 65, 1812-1821.	6.1	1,092
3	PCR-DGGE fingerprinting: novel strategies for detection of microbes in food. Journal of Microbiological Methods, 2004, 56, 297-314.	0.7	518
4	Bacterial populations and the volatilome associated to meat spoilage. Food Microbiology, 2015, 45, 83-102.	2.1	462
5	Spoilage microbiota associated to the storage of raw meat in different conditions. International Journal of Food Microbiology, 2012, 157, 130-141.	2.1	454
6	High-Throughput Sequencing and Metagenomics: Moving Forward in the Culture-Independent Analysis of Food Microbial Ecology. Applied and Environmental Microbiology, 2013, 79, 3148-3155.	1.4	412
7	Changes in the Spoilage-Related Microbiota of Beef during Refrigerated Storage under Different Packaging Conditions. Applied and Environmental Microbiology, 2006, 72, 4663-4671.	1.4	354
8	Mesophilic and Psychrotrophic Bacteria from Meat and Their Spoilage Potential In Vitro and in Beef. Applied and Environmental Microbiology, 2009, 75, 1990-2001.	1.4	282
9	Mediterranean diet intervention in overweight and obese subjects lowers plasma cholesterol and causes changes in the gut microbiome and metabolome independently of energy intake. Gut, 2020, 69, 1258-1268.	6.1	279
10	The Prevotella copri Complex Comprises Four Distinct Clades Underrepresented in Westernized Populations. Cell Host and Microbe, 2019, 26, 666-679.e7.	5.1	274
11	Prevotella diversity, niches and interactions with the human host. Nature Reviews Microbiology, 2021, 19, 585-599.	13.6	248
12	Whole-grain wheat consumption reduces inflammation in a randomized controlled trial on overweight and obese subjects with unhealthy dietary and lifestyle behaviors: role of polyphenols bound to cereal dietary fiber. American Journal of Clinical Nutrition, 2015, 101, 251-261.	2.2	246
13	Antibiotic-induced microbiota perturbation causes gut endocannabinoidome changes, hippocampal neuroglial reorganization and depression in mice. Brain, Behavior, and Immunity, 2018, 67, 230-245.	2.0	246
14	Bacterial Community Structure and Location in Stilton Cheese. Applied and Environmental Microbiology, 2003, 69, 3540-3548.	1.4	242
15	Distinct Genetic and Functional Traits of Human Intestinal Prevotella copri Strains Are Associated with Different Habitual Diets. Cell Host and Microbe, 2019, 25, 444-453.e3.	5.1	229
16	Monitoring of Microbial Metabolites and Bacterial Diversity in Beef Stored under Different Packaging Conditions. Applied and Environmental Microbiology, 2011, 77, 7372-7381.	1.4	224
17	Bacteria and yeast microbiota in milk kefir grains from different Italian regions. Food Microbiology, 2015, 49, 123-133.	2.1	202
18	Metagenomics insights into food fermentations. Microbial Biotechnology, 2017, 10, 91-102.	2.0	196

#	Article	IF	CITATIONS
19	Large-scale genome-wide analysis links lactic acid bacteria from food with the gut microbiome. Nature Communications, 2020, 11, 2610.	5.8	190
20	Microbial Ecology Dynamics during Rye and Wheat Sourdough Preparation. Applied and Environmental Microbiology, 2013, 79, 7827-7836.	1.4	183
21	The Potential of a Polyphasic PCR-DGCEApproach in Evaluating Microbial Diversity of Natural Whey Cultures for Water-Buffalo Mozzarella Cheese Production: Bias of Culture-Dependent and Culture-Independent Analyses. Systematic and Applied Microbiology, 2001, 24, 610-617.	1.2	176
22	Exploring the Sources of Bacterial Spoilers in Beefsteaks by Culture-Independent High-Throughput Sequencing. PLoS ONE, 2013, 8, e70222.	1.1	176
23	"Remake―by High-Throughput Sequencing of the Microbiota Involved in the Production of Water Buffalo Mozzarella Cheese. Applied and Environmental Microbiology, 2012, 78, 8142-8145.	1.4	165
24	A global metagenomic map of urban microbiomes and antimicrobial resistance. Cell, 2021, 184, 3376-3393.e17.	13.5	164
25	Lactic acid bacteria and their controversial role in fresh meat spoilage. Meat Science, 2015, 109, 66-74.	2.7	162
26	Metatranscriptomics reveals temperature-driven functional changes in microbiome impacting cheese maturation rate. Scientific Reports, 2016, 6, 21871.	1.6	149
27	Different molecular types of Pseudomonas fragi have the same overall behaviour as meat spoilers. International Journal of Food Microbiology, 2010, 142, 120-131.	2.1	145
28	Midgut microbiota and host immunocompetence underlie <i>Bacillus thuringiensis</i> killing mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9486-9491.	3.3	144
29	Overlap of Spoilage-Associated Microbiota between Meat and the Meat Processing Environment in Small-Scale and Large-Scale Retail Distributions. Applied and Environmental Microbiology, 2016, 82, 4045-4054.	1.4	141
30	The food-gut axis: lactic acid bacteria and their link to food, the gut microbiome and human health. FEMS Microbiology Reviews, 2020, 44, 454-489.	3.9	139
31	Organic farming induces changes in soil microbiota that affect agro-ecosystem functions. Soil Biology and Biochemistry, 2016, 103, 327-336.	4.2	137
32	The Intestinal Microbiota of Hermetia illucens Larvae Is Affected by Diet and Shows a Diverse Composition in the Different Midgut Regions. Applied and Environmental Microbiology, 2019, 85, .	1.4	134
33	Molecular identification of mesophilic and psychrotrophic bacteria from raw cow's milk. Food Microbiology, 2009, 26, 228-231.	2.1	133
34	Coexistence of Lactic Acid Bacteria and Potential Spoilage Microbiota in a Dairy Processing Environment. Applied and Environmental Microbiology, 2015, 81, 7893-7904.	1.4	132
35	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. Nature Medicine, 2020, 26, 941-951.	15.2	130
36	Yeast dynamics during spontaneous wine fermentation of the Catalanesca grape. International Journal of Food Microbiology, 2007, 117, 201-210.	2.1	126

#	Article	IF	CITATIONS
37	Taxonomic Structure and Monitoring of the Dominant Population of Lactic Acid Bacteria during Wheat Flour Sourdough Type I Propagation Using <i>Lactobacillus sanfranciscensis</i> Starters. Applied and Environmental Microbiology, 2009, 75, 1099-1109.	1.4	125
38	Spoilage-Related Activity of Carnobacterium maltaromaticum Strains in Air-Stored and Vacuum-Packed Meat. Applied and Environmental Microbiology, 2011, 77, 7382-7393.	1.4	125
39	Different temperatures select distinctive acetic acid bacteria species and promotes organic acids production during Kombucha tea fermentation. Food Microbiology, 2018, 73, 11-16.	2.1	119
40	Development of spoilage microbiota in beef stored in nisin activated packaging. Food Microbiology, 2010, 27, 137-143.	2.1	115
41	Diet influences the functions of the human intestinal microbiome. Scientific Reports, 2020, 10, 4247.	1.6	115
42	The Same Microbiota and a Potentially Discriminant Metabolome in the Saliva of Omnivore, Ovo-Lacto-Vegetarian and Vegan Individuals. PLoS ONE, 2014, 9, e112373.	1.1	115
43	Recent Past, Present, and Future of the Food Microbiome. Annual Review of Food Science and Technology, 2018, 9, 589-608.	5.1	113
44	Organic amendment type and application frequency affect crop yields, soil fertility and microbiome composition. Applied Soil Ecology, 2017, 120, 254-264.	2.1	107
45	Gut microbiota signatures in cystic fibrosis: Loss of host CFTR function drives the microbiota enterophenotype. PLoS ONE, 2018, 13, e0208171.	1.1	107
46	Food Design To Feed the Human Gut Microbiota. Journal of Agricultural and Food Chemistry, 2018, 66, 3754-3758.	2.4	104
47	Unusual sub-genus associations of faecal Prevotella and Bacteroides with specific dietary patterns. Microbiome, 2016, 4, 57.	4.9	101
48	Saliva from Obese Individuals Suppresses the Release of Aroma Compounds from Wine. PLoS ONE, 2014, 9, e85611.	1.1	98
49	Different Amplicon Targets for Sequencing-Based Studies of Fungal Diversity. Applied and Environmental Microbiology, 2017, 83, .	1.4	97
50	Simultaneous Detection of Pseudomonas fragi , P. lundensis , and P. putida from Meat by Use of a Multiplex PCR Assay Targeting the carA Gene. Applied and Environmental Microbiology, 2007, 73, 2354-2359.	1.4	96
51	Monitoring of the microbiota of fermented sausages by culture independent rRNA-based approaches. International Journal of Food Microbiology, 2015, 212, 67-75.	2.1	96
52	Exploring the microbiota dynamics related to vegetable biomasses degradation and study of lignocellulose-degrading bacteria for industrial biotechnological application. Scientific Reports, 2015, 5, 8161.	1.6	95
53	Salivary Microbiota and Metabolome Associated with Celiac Disease. Applied and Environmental Microbiology, 2014, 80, 3416-3425.	1.4	93
54	Specific Signatures of the Gut Microbiota and Increased Levels of Butyrate in Children Treated with Fermented Cow's Milk Containing Heat-Killed Lactobacillus paracasei CBA L74. Applied and Environmental Microbiology, 2017, 83, .	1.4	92

#	Article	IF	CITATIONS
55	Microbial Ecology of the Soppressata of Vallo di Diano, a Traditional Dry Fermented Sausage from Southern Italy, and In Vitro and In Situ Selection of Autochthonous Starter Cultures. Applied and Environmental Microbiology, 2007, 73, 5453-5463.	1.4	89
56	Relationships among house, rind and core microbiotas during manufacture of traditional Italian cheeses at the same dairy plant. Food Microbiology, 2016, 54, 115-126.	2.1	86
57	Bacteriophage P22 to challenge Salmonella in foods. International Journal of Food Microbiology, 2014, 191, 69-74.	2.1	84
58	Microbiota of an Italian Grana-Like Cheese during Manufacture and Ripening, Unraveled by 16S rRNA-Based Approaches. Applied and Environmental Microbiology, 2016, 82, 3988-3995.	1.4	83
59	Large-scale mapping of microbial diversity in artisanal Brazilian cheeses. Food Microbiology, 2019, 80, 40-49.	2.1	83
60	Repeated applications of organic amendments promote beneficial microbiota, improve soil fertility and increase crop yield. Applied Soil Ecology, 2020, 156, 103714.	2.1	82
61	Microbial diversity in Natural Whey Cultures used for the production of Caciocavallo Silano PDO cheese. International Journal of Food Microbiology, 2008, 124, 164-170.	2.1	81
62	Gut Microbiota as a Target for Preventive and Therapeutic Intervention against Food Allergy. Nutrients, 2017, 9, 672.	1.7	81
63	Gut microbiota composition and butyrate production in children affected by non-IgE-mediated cow's milk allergy. Scientific Reports, 2018, 8, 12500.	1.6	80
64	Specific gut microbiome signatures and the associated pro-inflamatory functions are linked to pediatric allergy and acquisition of immune tolerance. Nature Communications, 2021, 12, 5958.	5.8	77
65	Altered gut microbiota and endocannabinoid system tone in vitamin D deficiency-mediated chronic pain. Brain, Behavior, and Immunity, 2020, 85, 128-141.	2.0	76
66	Gut Microbiome as Target for Innovative Strategies Against Food Allergy. Frontiers in Immunology, 2019, 10, 191.	2.2	75
67	NaOH-Debittering Induces Changes in Bacterial Ecology during Table Olives Fermentation. PLoS ONE, 2013, 8, e69074.	1.1	75
68	Activities of strains of Brochothrix thermosphacta in vitro and in meat. Food Research International, 2014, 62, 366-374.	2.9	74
69	Zooming into food-associated microbial consortia: a â€~cultural' evolution. Current Opinion in Food Science, 2015, 2, 43-50.	4.1	73
70	Newly Explored Faecalibacterium Diversity Is Connected to Age, Lifestyle, Geography, and Disease. Current Biology, 2020, 30, 4932-4943.e4.	1.8	72
71	Organic Cultivation of Triticum turgidum subsp. durum Is Reflected in the Flour-Sourdough Fermentation-Bread Axis. Applied and Environmental Microbiology, 2015, 81, 3192-3204.	1.4	68
72	FoodMicrobionet: A database for the visualisation and exploration of food bacterial communities based on network analysis. International Journal of Food Microbiology, 2016, 219, 28-37.	2.1	65

#	Article	IF	CITATIONS
73	A volatilomics approach for off-line discrimination of minced beef and pork meat and their admixture using HS-SPME GC/MS in tandem with multivariate data analysis. Meat Science, 2019, 151, 43-53.	2.7	65
74	Linking bacterial and eukaryotic microbiota to litter chemistry: Combining next generation sequencing with 13C CPMAS NMR spectroscopy. Soil Biology and Biochemistry, 2019, 129, 110-121.	4.2	65
75	A Few Pseudomonas Oligotypes Dominate in the Meat and Dairy Processing Environment. Frontiers in Microbiology, 2017, 8, 264.	1.5	64
76	Dietary Interventions to Modulate the Gut Microbiome—How Far Away Are We From Precision Medicine. Inflammatory Bowel Diseases, 2018, 24, 2142-2154.	0.9	61
77	Technological and Molecular Diversity of Lactobacillus plantarum Strains Isolated from Naturally Fermented Sourdoughs. Systematic and Applied Microbiology, 2004, 27, 443-453.	1.2	59
78	Fluorescence in situ hybridisation detection of Lactobacillus plantarum group on olives to be used in natural fermentations. International Journal of Food Microbiology, 2006, 112, 291-296.	2.1	59
79	Dynamics of bacterial communities and interaction networks in thawed fish fillets during chilled storage in air. International Journal of Food Microbiology, 2019, 293, 102-113.	2.1	55
80	The fate of cigarette butts in different environments: Decay rate, chemical changes and ecotoxicity revealed by a 5-years decomposition experiment. Environmental Pollution, 2020, 261, 114108.	3.7	55
81	Development of a Real-Time PCR assay for the specific detection of Brochothrix thermosphacta in fresh and spoiled raw meat. International Journal of Food Microbiology, 2009, 134, 230-236.	2.1	54
82	The microbiota of high-moisture mozzarella cheese produced with different acidification methods. International Journal of Food Microbiology, 2016, 216, 9-17.	2.1	49
83	Causal Relationship between Microbial Ecology Dynamics and Proteolysis during Manufacture and Ripening of Protected Designation of Origin (PDO) Cheese Canestrato Pugliese. Applied and Environmental Microbiology, 2014, 80, 4085-4094.	1.4	47
84	Impact of Nisin-Activated Packaging on Microbiota of Beef Burgers during Storage. Applied and Environmental Microbiology, 2016, 82, 549-559.	1.4	47
85	Environmental microbiome mapping as a strategy to improve quality and safety in the food industry. Current Opinion in Food Science, 2021, 38, 168-176.	4.1	47
86	Evaluation of microbial diversity during the manufacture of Fior di Latte di Agerola, a traditional raw milk pasta-filata cheese of the Naples area. Journal of Dairy Research, 2006, 73, 264-272.	0.7	46
87	rRNA-based monitoring of the microbiota involved in Fontina PDO cheese production in relation to different stages of cow lactation. International Journal of Food Microbiology, 2014, 185, 127-135.	2.1	46
88	The therapeutic efficacy of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> BBâ€12 [®] in infant colic: A randomised, double blind, placeboâ€controlled trial. Alimentary Pharmacology and Therapeutics, 2020, 51, 110-120.	1.9	46
89	Processing Environment and Ingredients Are Both Sources of Leuconostoc gelidum, Which Emerges as a Major Spoiler in Ready-To-Eat Meals. Applied and Environmental Microbiology, 2015, 81, 3529-3541.	1.4	44
90	Impact of Lactobacillus curvatus 54M16 on microbiota composition and growth of Listeria monocytogenes in fermented sausages. Food Microbiology, 2018, 72, 1-15.	2.1	43

#	Article	IF	CITATIONS
91	Acute and chronic improvement in postprandial glucose metabolism by a diet resembling the traditional Mediterranean dietary pattern: Can SCFAs play a role?. Clinical Nutrition, 2021, 40, 428-437.	2.3	43
92	Animal Rennets as Sources of Dairy Lactic Acid Bacteria. Applied and Environmental Microbiology, 2014, 80, 2050-2061.	1.4	42
93	Coffee prevents fatty liver disease induced by a high-fat diet by modulating pathways of the gut–liver axis. Journal of Nutritional Science, 2019, 8, e15.	0.7	42
94	The Vaginal Microbiome: A Long Urogenital Colonization Throughout Woman Life. Frontiers in Cellular and Infection Microbiology, 2021, 11, 686167.	1.8	42
95	Different Lactobacillus populations dominate in "Chorizo de León―manufacturing performed in different production plants. Food Microbiology, 2018, 70, 94-102.	2.1	41
96	Stool microRNA profiles reflect different dietary and gut microbiome patterns in healthy individuals. Gut, 2022, 71, 1302-1314.	6.1	39
97	Antimicrobial Packaging To Retard the Growth of Spoilage Bacteria and To Reduce the Release of Volatile Metabolites in Meat Stored under Vacuum at 1A°C. Journal of Food Protection, 2013, 76, 52-58.	0.8	38
98	Sequence heterogeneity in the lacSZ operon of Streptococcus thermophilus and its use in PCR systems for strain differentiation. Research in Microbiology, 2005, 156, 161-172.	1.0	36
99	Decarboxylase gene expression and cadaverine and putrescine production by Serratia proteamaculans in vitro and in beef. International Journal of Food Microbiology, 2013, 165, 332-338.	2.1	35
100	Monitoring the mycobiota during Greco di Tufo and Aglianico wine fermentation by 18S rRNA gene sequencing. Food Microbiology, 2017, 63, 117-122.	2.1	35
101	A comparison of bioinformatic approaches for 16S rRNA gene profiling of food bacterial microbiota. International Journal of Food Microbiology, 2018, 265, 9-17.	2.1	35
102	Microbial community dynamics in thermophilic undefined milk starter cultures. International Journal of Food Microbiology, 2016, 217, 59-67.	2.1	34
103	Revealing the microbiota of marketed edible insects through PCR-DGGE, metagenomic sequencing and real-time PCR. International Journal of Food Microbiology, 2018, 276, 54-62.	2.1	34
104	Dynamics of bacterial communities during manufacture and ripening of traditional Caciocavallo of Castelfranco cheese in relation to cows' feeding. Food Microbiology, 2017, 63, 170-177.	2.1	33
105	Mediterranean diet consumption affects the endocannabinoid system in overweight and obese subjects: possible links with gut microbiome, insulin resistance and inflammation. European Journal of Nutrition, 2021, 60, 3703-3716.	1.8	33
106	Conventional farming impairs <i>RhizoctoniaÂsolani</i> disease suppression by disrupting soil food web. Journal of Phytopathology, 2018, 166, 663-673.	0.5	32
107	Advancing integration of data on food microbiome studies: FoodMicrobionet 3.1, a major upgrade of the FoodMicrobionet database. International Journal of Food Microbiology, 2019, 305, 108249.	2.1	32
108	From an imbalance to a new imbalance: Italian-style gluten-free diet alters the salivary microbiota and metabolome of African celiac children. Scientific Reports, 2016, 5, 18571.	1.6	31

#	Article	IF	CITATIONS
109	Metabolic gene-targeted monitoring of non-starter lactic acid bacteria during cheese ripening. International Journal of Food Microbiology, 2017, 257, 276-284.	2.1	31
110	Salivary and fecal microbiota and metabolome of celiac children under gluten-free diet. International Journal of Food Microbiology, 2016, 239, 125-132.	2.1	30
111	Strain-Level Diversity Analysis of Pseudomonas fragi after <i>In Situ</i> Pangenome Reconstruction Shows Distinctive Spoilage-Associated Metabolic Traits Clearly Selected by Different Storage Conditions. Applied and Environmental Microbiology, 2019, 85, .	1.4	30
112	A Mediterranean Diet Intervention Reduces the Levels of Salivary Periodontopathogenic Bacteria in Overweight and Obese Subjects. Applied and Environmental Microbiology, 2020, 86, .	1.4	30
113	Psychobiotics, gut microbiota and fermented foods can help preserving mental health. Food Research International, 2022, 152, 110892.	2.9	26
114	Postprandial Gastrointestinal Function Differs after Acute Administration of Sourdough Compared with Brewer's Yeast Bakery Products in Healthy Adults. Journal of Nutrition, 2018, 148, 202-208.	1.3	25
115	Laboratory medicine: health evaluation in elite athletes. Clinical Chemistry and Laboratory Medicine, 2019, 57, 1450-1473.	1.4	25
116	The Interrelationship Between Microbiota and Peptides During Ripening as a Driver for Parmigiano Reggiano Cheese Quality. Frontiers in Microbiology, 2020, 11, 581658.	1.5	25
117	One ring to rule them all: an ecosystem engineer fungus fosters plant and microbial diversity in a Mediterranean grassland. New Phytologist, 2020, 227, 884-898.	3.5	25
118	A Metagenomic and in Silico Functional Prediction of Gut Microbiota Profiles May Concur in Discovering New Cystic Fibrosis Patient-Targeted Probiotics. Nutrients, 2017, 9, 1342.	1.7	24
119	Bacterial biogeographical patterns in a cooking center for hospital foodservice. International Journal of Food Microbiology, 2015, 193, 99-108.	2.1	22
120	Structure of association networks in food bacterial communities. Food Microbiology, 2018, 73, 49-60.	2.1	22
121	Probiotic potential of a Lactobacillus rhamnosus cheese isolate and its effect on the fecal microbiota of healthy volunteers. Food Research International, 2019, 119, 305-314.	2.9	22
122	Influence of microbial communities on the chemical and sensory features of Falanghina sweet passito wines. Food Research International, 2019, 120, 740-747.	2.9	22
123	Outlook on next-generation probiotics from the human gut. Cellular and Molecular Life Sciences, 2022, 79, 76.	2.4	22
124	Antimicrobial activity of Myrtus communis L. water-ethanol extract against meat spoilage strains of Brochothrix thermosphacta and Pseudomonas fragi in vitro and in meat. Annals of Microbiology, 2015, 65, 841-850.	1.1	21
125	Changes in microbial diversity of brined green asparagus upon treatment with high hydrostatic pressure. International Journal of Food Microbiology, 2016, 216, 1-8.	2.1	21
126	Next-Generation Food Research: Use of Meta-Omic Approaches for Characterizing Microbial Communities Along the Food Chain. Annual Review of Food Science and Technology, 2022, 13, 361-384.	5.1	21

#	Article	IF	CITATIONS
127	Microbial diversity in pitted sweet cherries (Prunus avium L.) as affected by High-Hydrostatic Pressure treatment. Food Research International, 2016, 89, 790-796.	2.9	19
128	Microbiota thrombus colonization may influence athero-thrombosis in hyperglycemic patients with ST segment elevation myocardialinfarction (STEMI). Marianella study. Diabetes Research and Clinical Practice, 2021, 173, 108670.	1.1	19
129	Profiling white wine seed vinegar bacterial diversity through viable counting, metagenomic sequencing and PCR-DGGE. International Journal of Food Microbiology, 2018, 286, 66-74.	2.1	16
130	Pea-Wheat Rotation Affects Soil Microbiota Diversity, Community Structure, and Soilborne Pathogens. Microorganisms, 2022, 10, 370.	1.6	16
131	The Core Human Microbiome: Does It Exist and How Can We Find It? A Critical Review of the Concept. Nutrients, 2022, 14, 2872.	1.7	16
132	Specific microbiome signatures under the canopy of Mediterranean shrubs. Applied Soil Ecology, 2022, 173, 104407.	2.1	15
133	Exciting strainâ€level resolution studies of the food microbiome. Microbial Biotechnology, 2017, 10, 54-56.	2.0	14
134	Contrasting effects of Rhizophagus irregularis versus bacterial and fungal seed endophytes on Trifolium repens plant-soil feedback. Mycorrhiza, 2021, 31, 103-115.	1.3	14
135	Attenuated Lactococcus lactis and Surface Bacteria as Tools for Conditioning the Microbiota and Driving the Ripening of Semisoft Caciotta Cheese. Applied and Environmental Microbiology, 2020, 86, .	1.4	13
136	Riding the wave: Response of bacterial and fungal microbiota associated with the spread of the fairy ring fungus Calocybe gambosa. Applied Soil Ecology, 2021, 163, 103963.	2.1	12
137	Polymorphism of the phosphoserine phosphatase gene in Streptococcus thermophilus and its potential use for typing and monitoring of population diversity. International Journal of Food Microbiology, 2016, 236, 138-147.	2.1	10
138	Rapid onset of effect of benralizumab on respiratory symptoms in a patient with eosinophilic granulomatosis with polyangiitis. Respiratory Medicine Case Reports, 2020, 30, 101050.	0.2	10
139	Secrets of the cheese microbiome. Nature Food, 2020, 1, 466-467.	6.2	9
140	Omics-based monitoring of microbial dynamics across the food chain for the improvement of food safety and quality. Food Research International, 2022, 157, 111242.	2.9	9
141	Host phenotype classification from human microbiome data is mainly driven by the presence of microbial taxa. PLoS Computational Biology, 2022, 18, e1010066.	1.5	9
142	Identification and Characterization of Human Observational Studies in Nutritional Epidemiology on Gut Microbiomics for Joint Data Analysis. Nutrients, 2021, 13, 3292.	1.7	6
143	Draft Genome Sequences of the Aerobic Strains Lactobacillus gasseri AL3 and AL5. Genome Announcements, 2017, 5, .	0.8	5
144	Distribution of Antibiotic Resistance Genes in the Saliva of Healthy Omnivores, Ovo-Lacto-Vegetarians, and Vegans. Genes, 2020, 11, 1088.	1.0	5

#	Article	IF	CITATIONS
145	Food Neophobia and scarce olfactory performances are linked to oral microbiota. Food Research International, 2022, 155, 111092.	2.9	3
146	Metabolic Profiling and Cold-Starvation Stress Response of Oxygen-Tolerant Lactobacillus gasseri Strains Cultured in Batch Bioreactor. Microorganisms, 2019, 7, 200.	1.6	2
147	The Effect of Weaning with Adult Food Typical of the Mediterranean Diet on Taste Development and Eating Habits of Children: A Randomized Trial. Nutrients, 2022, 14, 2486.	1.7	2
148	Microbiome and Diet. , 2018, , 79-88.		1
149	Diet, Health, and the Gut Microbiota. , 2019, , 815-829.		1
150	Editorial: interventions in infantile colic – can efficacy be attributed to treatment or to time? Authors' reply. Alimentary Pharmacology and Therapeutics, 2020, 51, 398-399.	1.9	1
151	Biomarkers of intake of a Mediterranean Diet: Which contribution from the gut microbiota?. Nutrition, Metabolism and Cardiovascular Diseases, 2019, 29, 880.	1.1	0
152	Mediterranean diet diminishes the effects of Crohn's disease and improves its parameters: A systematic review. Nutrition and Health, 0, , 026010602211022.	0.6	0