Danilo Ercolini

List of Publications by Year in descending order

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		9234	16605
172	17,970	74	123
papers	citations	h-index	g-index
175	175	175	19313
all docs	docs citations	times ranked	citing authors

#	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	Membrane Toxicity of Antimicrobial Compounds from Essential Oils. Journal of Agricultural and Food Chemistry, 2007, 55, 4863-4870.	2.4	499
5	Bacterial populations and the volatilome associated to meat spoilage. Food Microbiology, 2015, 45, 83-102.	2.1	462
6	Spoilage microbiota associated to the storage of raw meat in different conditions. International Journal of Food Microbiology, 2012, 157, 130-141.	2.1	454
7	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
8	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
9	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
10	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
11	The Prevotella copri Complex Comprises Four Distinct Clades Underrepresented in Westernized Populations. Cell Host and Microbe, 2019, 26, 666-679.e7.	5.1	274
12	Prevotella diversity, niches and interactions with the human host. Nature Reviews Microbiology, 2021, 19, 585-599.	13.6	248
13	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
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

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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	Spoilage-related microbiota associated with chilled beef stored in air or vacuum pack. Food Microbiology, 2011, 28, 84-93.	2.1	184
21	Biochemical and sensory characteristics of traditional fermented sausages of Vallo di Diano (Southern Italy) as affected by the use of starter cultures. Meat Science, 2007, 76, 295-307.	2.7	183
22	Microbial Ecology Dynamics during Rye and Wheat Sourdough Preparation. Applied and Environmental Microbiology, 2013, 79, 7827-7836.	1.4	183
23	The Potential of a Polyphasic PCR-DGGEApproach 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
24	Exploring the Sources of Bacterial Spoilers in Beefsteaks by Culture-Independent High-Throughput Sequencing. PLoS ONE, 2013, 8, e70222.	1.1	176
25	"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
26	A global metagenomic map of urban microbiomes and antimicrobial resistance. Cell, 2021, 184, 3376-3393.e17.	13.5	164
27	Selection of Lactobacillus strains from fermented sausages for their potential use as probiotics. Meat Science, 2004, 67, 309-317.	2.7	162
28	Lactic acid bacteria and their controversial role in fresh meat spoilage. Meat Science, 2015, 109, 66-74.	2.7	162
29	Antimicrobial activity of a nisin-activated plastic film for food packaging. Letters in Applied Microbiology, 2005, 41, 464-469.	1.0	157
30	Metatranscriptomics reveals temperature-driven functional changes in microbiome impacting cheese maturation rate. Scientific Reports, 2016, 6, 21871.	1.6	149
31	Proteolytic and lipolytic starter cultures and their effect on traditional fermented sausages ripening and sensory traits. Food Microbiology, 2008, 25, 335-347.	2.1	145
32	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
33	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
34	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
35	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
36	Organic farming induces changes in soil microbiota that affect agro-ecosystem functions. Soil Biology and Biochemistry, 2016, 103, 327-336.	4.2	137

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37	Application of FISH technology for microbiological analysis: current state and prospects. Applied Microbiology and Biotechnology, 2006, 73, 485-494.	1.7	134
38	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
39	Molecular identification of mesophilic and psychrotrophic bacteria from raw cow's milk. Food Microbiology, 2009, 26, 228-231.	2.1	133
40	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
41	Changes in the proteome of <i>Salmonella enterica</i> serovar Thompson as stress adaptation to sublethal concentrations of thymol. Proteomics, 2010, 10, 1040-1049.	1.3	131
42	Molecular evaluation of microbial diversity occurring in different types of Mozzarella cheese. Journal of Applied Microbiology, 2001, 90, 414-420.	1.4	126
43	Yeast dynamics during spontaneous wine fermentation of the Catalanesca grape. International Journal of Food Microbiology, 2007, 117, 201-210.	2.1	126
44	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
45	Atomic force microscopy analysis shows surface structure changes in carvacrol-treated bacterial cells. Research in Microbiology, 2011, 162, 164-172.	1.0	125
46	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
47	Development of polythene films for food packaging activated with an antilisterial bacteriocin from Lactobacillus curvatus 32Y. Journal of Applied Microbiology, 2004, 97, 314-322.	1.4	124
48	PCR detection of staphylococcal enterotoxin genes in Staphylococcus spp. strains isolated from meat and dairy products. Evidence for new variants of seG and seI in S. aureus AB-8802. Journal of Applied Microbiology, 2004, 97, 719-730.	1.4	124
49	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
50	Bacteriophage Therapy of <i>Salmonella enterica:</i> A Fresh Appraisal of Bacteriophage Therapy. Journal of Infectious Diseases, 2010, 201, 52-61.	1.9	118
51	Development of spoilage microbiota in beef stored in nisin activated packaging. Food Microbiology, 2010, 27, 137-143.	2.1	115
52	Diet influences the functions of the human intestinal microbiome. Scientific Reports, 2020, 10, 4247.	1.6	115
53	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
54	Recent Past, Present, and Future of the Food Microbiome. Annual Review of Food Science and Technology, 2018, 9, 589-608.	5.1	113

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55	PCR-DGGE fingerprints of microbial succession during a manufacture of traditional water buffalo mozzarella cheese. Journal of Applied Microbiology, 2004, 96, 263-270.	1.4	112
56	Gut microbiota signatures in cystic fibrosis: Loss of host CFTR function drives the microbiota enterophenotype. PLoS ONE, 2018, 13, e0208171.	1.1	107
57	Food Design To Feed the Human Gut Microbiota. Journal of Agricultural and Food Chemistry, 2018, 66, 3754-3758.	2.4	104
58	Behaviour of Brochothrix thermosphacta in presence of other meat spoilage microbial groups. Food Microbiology, 2006, 23, 797-802.	2.1	102
59	Unusual sub-genus associations of faecal Prevotella and Bacteroides with specific dietary patterns. Microbiome, 2016, 4, 57.	4.9	101
60	Saliva from Obese Individuals Suppresses the Release of Aroma Compounds from Wine. PLoS ONE, 2014, 9, e85611.	1.1	98
61	Different Amplicon Targets for Sequencing-Based Studies of Fungal Diversity. Applied and Environmental Microbiology, 2017, 83, .	1.4	97
62	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
63	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
64	Behavior of Variable V3 Region from 16S rDNA of Lactic Acid Bacteria in Denaturing Gradient Gel Electrophoresis. Current Microbiology, 2001, 42, 199-202.	1.0	95
65	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
66	Salivary Microbiota and Metabolome Associated with Celiac Disease. Applied and Environmental Microbiology, 2014, 80, 3416-3425.	1.4	93
67	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
68	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
69	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
70	Bacteriophage P22 to challenge Salmonella in foods. International Journal of Food Microbiology, 2014, 191, 69-74.	2.1	84
71	Effect of a bacteriocin-activated polythene film on Listeria monocytogenes as evaluated by viable staining and epifluorescence microscopy. Journal of Applied Microbiology, 2006, 100, 765-772.	1.4	83
72	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

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73	Large-scale mapping of microbial diversity in artisanal Brazilian cheeses. Food Microbiology, 2019, 80, 40-49.	2.1	83
74	<i>Lactobacillus</i> Strain Diversity Based on Partial <i>hsp60</i> Gene Sequences and Design of PCR-Restriction Fragment Length Polymorphism Assays for Species Identification and Differentiation. Applied and Environmental Microbiology, 2008, 74, 208-215.	1.4	82
75	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
76	Gut Microbiota as a Target for Preventive and Therapeutic Intervention against Food Allergy. Nutrients, 2017, 9, 672.	1.7	81
77	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
78	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
79	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
80	Gut Microbiome as Target for Innovative Strategies Against Food Allergy. Frontiers in Immunology, 2019, 10, 191.	2.2	75
81	NaOH-Debittering Induces Changes in Bacterial Ecology during Table Olives Fermentation. PLoS ONE, 2013, 8, e69074.	1.1	75
82	Activities of strains of Brochothrix thermosphacta in vitro and in meat. Food Research International, 2014, 62, 366-374.	2.9	74
83	Zooming into food-associated microbial consortia: a â€~cultural' evolution. Current Opinion in Food Science, 2015, 2, 43-50.	4.1	73
84	Newly Explored Faecalibacterium Diversity Is Connected to Age, Lifestyle, Geography, and Disease. Current Biology, 2020, 30, 4932-4943.e4.	1.8	72
85	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
86	Relationships Between Flavoring Capabilities, Bacterial Composition, and Geographical Origin of Natural Whey Cultures Used for Traditional Water-Buffalo Mozzarella Cheese Manufacture. Journal of Dairy Science, 2003, 86, 486-497.	1.4	67
87	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
88	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
89	A Few Pseudomonas Oligotypes Dominate in the Meat and Dairy Processing Environment. Frontiers in Microbiology, 2017, 8, 264.	1.5	64
90	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

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91	Technological and Molecular Diversity of Lactobacillus plantarum Strains Isolated from Naturally Fermented Sourdoughs. Systematic and Applied Microbiology, 2004, 27, 443-453.	1.2	59
92	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
93	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
94	Differential protein expression patterns between planktonic and biofilm cells of Salmonella enterica serovar Enteritidis PT4 on stainless steel surface. International Journal of Food Microbiology, 2013, 162, 105-113.	2.1	54
95	Diversity of <i>Staphylococcus</i> Species Strains Based on Partial <i>kat</i> (Catalase) Gene Sequences and Design of a PCR-Restriction Fragment Length Polymorphism Assay for Identification and		

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109	Development of a fluorescence in situ hybridization method for cheese using a 16S rRNA probe. Journal of Microbiological Methods, 2003, 52, 267-271.	0.7	42
110	PCR-based detection of enterotoxigenic Staphylococcus aureus in the early stages of raw milk cheese making. Journal of Applied Microbiology, 2004, 96, 1090-1096.	1.4	42
111	Presence of endophytic bacteria in Vitis vinifera leaves as detected by fluorescence in situ hybridization. Annals of Microbiology, 2010, 60, 161-167.	1.1	42
112	Animal Rennets as Sources of Dairy Lactic Acid Bacteria. Applied and Environmental Microbiology, 2014, 80, 2050-2061.	1.4	42
113	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
114	The Vaginal Microbiome: A Long Urogenital Colonization Throughout Woman Life. Frontiers in Cellular and Infection Microbiology, 2021, 11, 686167.	1.8	42
115	Different Lactobacillus populations dominate in "Chorizo de León―manufacturing performed in different production plants. Food Microbiology, 2018, 70, 94-102.	2.1	41
116	Stool microRNA profiles reflect different dietary and gut microbiome patterns in healthy individuals. Gut, 2022, 71, 1302-1314.	6.1	39
117	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
118	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
119	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
120	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
121	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
122	Characterization of Bacteriocin-Coated Antimicrobial Polyethylene Films by Atomic Force Microscopy. Journal of Food Science, 2008, 73, T48-T54.	1.5	33
123	Characterization of Streptococcus thermophilus lytic bacteriophages from mozzarella cheese plants. International Journal of Food Microbiology, 2010, 138, 137-144.	2.1	33
124	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
125	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
126	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

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127	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
128	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
129	Rapid and Reliable Identification of Staphylococcus equorum by a Species-Specific PCR Assay Targeting the sodA Gene. Systematic and Applied Microbiology, 2004, 27, 696-702.	1.2	30
130	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
131	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
132	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
133	Diversity of Salmonella spp. serovars isolated from the intestines of water buffalo calves with gastroenteritis. BMC Veterinary Research, 2012, 8, 201.	0.7	29
134	Psychobiotics, gut microbiota and fermented foods can help preserving mental health. Food Research International, 2022, 152, 110892.	2.9	26
135	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
136	Laboratory medicine: health evaluation in elite athletes. Clinical Chemistry and Laboratory Medicine, 2019, 57, 1450-1473.	1.4	25
137	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
138	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
139	Response of Escherichia coli O157:H7, Listeria monocytogenes, Salmonella Typhimurium, and Staphylococcus aureus to the Thermal Stress Occurring in Model Manufactures of Grana Padano Cheese. Journal of Dairy Science, 2005, 88, 3818-3825.	1.4	24
140	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
141	Expression of DnaK, HtpG, GroEL and Tf chaperones and the corresponding encoding genes during growth of Salmonella Thompson in presence of thymol alone or in combination with salt and cold stress. Food Research International, 2013, 52, 153-159.	2.9	22
142	Bacterial biogeographical patterns in a cooking center for hospital foodservice. International Journal of Food Microbiology, 2015, 193, 99-108.	2.1	22
143	Structure of association networks in food bacterial communities. Food Microbiology, 2018, 73, 49-60.	2.1	22
144	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

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145	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
146	Outlook on next-generation probiotics from the human gut. Cellular and Molecular Life Sciences, 2022, 79, 76.	2.4	22
147	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
148	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
149	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
150	Coating-Activation and Antimicrobial Efficacy of Different Polyethylene Films with a Nisin-Based Solution. Food and Bioprocess Technology, 2013, 6, 2770-2779.	2.6	20
151	Effect of polythene film activated with enterocin EJ97 in combination with EDTA against Bacillus coagulans. LWT - Food Science and Technology, 2010, 43, 514-518.	2.5	19
152	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
153	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
154	Pseudomonas fragi Strains Isolated from Meat Do Not Produce N-Acyl Homoserine Lactones as Signal Molecules. Journal of Food Protection, 2009, 72, 2597-2601.	0.8	18
155	Link between Geographical Origin and Occurrence of Brucella abortus Biovars in Cow and Water Buffalo Herds. Applied and Environmental Microbiology, 2013, 79, 1039-1043.	1.4	17
156	Dairy Products. , 2008, , 31-90.		16
157	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
158	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
159	Presence and characterisation of verotoxin producing E. coli in fresh Italian pork sausages, and preparation and use of an antibiotic-resistant strain for challenge studies. Meat Science, 2005, 70, 181-188.	2.7	14
160	Exciting strainâ€level resolution studies of the food microbiome. Microbial Biotechnology, 2017, 10, 54-56.	2.0	14
161	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
162	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

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163	Secrets of the cheese microbiome. Nature Food, 2020, 1, 466-467.	6.2	9
164	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
165	Identification and Characterization of Human Observational Studies in Nutritional Epidemiology on Gut Microbiomics for Joint Data Analysis. Nutrients, 2021, 13, 3292.	1.7	6
166	Distribution of Antibiotic Resistance Genes in the Saliva of Healthy Omnivores, Ovo-Lacto-Vegetarians, and Vegans. Genes, 2020, 11, 1088.	1.0	5
167	Conditions for conjugative transposon transfer in Lactococcus lactis. Letters in Applied Microbiology, 2000, 31, 343-348.	1.0	4
168	Food Neophobia and scarce olfactory performances are linked to oral microbiota. Food Research International, 2022, 155, 111092.	2.9	3
169	FISH in Food Microbiology. , 2009, , 395-408.		2
170	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
171	Food Microbial Ecology in the â€~Omics' Era. , 2016, , .		1
172	Microbiome and Diet. , 2018, , 79-88.		1