Danilo Ercolini

List of Publications by Year
in descending order

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172	17,970	9234 74	16605 123
papers	citations	h-index	g-index

175	175	175	19313
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Stool microRNA profiles reflect different dietary and gut microbiome patterns in healthy individuals. Gut, 2022, 71, 1302-1314.	6.1	39
2	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
3	Psychobiotics, gut microbiota and fermented foods can help preserving mental health. Food Research International, 2022, 152, 110892.	2.9	26
4	Outlook on next-generation probiotics from the human gut. Cellular and Molecular Life Sciences, 2022, 79, 76.	2.4	22
5	Food Neophobia and scarce olfactory performances are linked to oral microbiota. Food Research International, 2022, 155, 111092.	2.9	3
6	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
7	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
8	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
9	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
10	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
11	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
12	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
13	Prevotella diversity, niches and interactions with the human host. Nature Reviews Microbiology, 2021, 19, 585-599.	13.6	248
14	A global metagenomic map of urban microbiomes and antimicrobial resistance. Cell, 2021, 184, 3376-3393.e17.	13.5	164
15	The Vaginal Microbiome: A Long Urogenital Colonization Throughout Woman Life. Frontiers in Cellular and Infection Microbiology, 2021, 11, 686167.	1.8	42
16	Identification and Characterization of Human Observational Studies in Nutritional Epidemiology on Gut Microbiomics for Joint Data Analysis. Nutrients, 2021, 13, 3292.	1.7	6
17	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
18	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

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19	The therapeutic efficacy of Bifidobacterium animalis subsp. lactis BBâ€12^{Â®} in infant colic: A randomised, double blind, placeboâ€controlled trial. Alimentary Pharmacology and Therapeutics, 2020, 51, 110-120.	1.9	46
20	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
21	Newly Explored Faecalibacterium Diversity Is Connected to Age, Lifestyle, Geography, and Disease. Current Biology, 2020, 30, 4932-4943.e4.	1.8	72
22	Distribution of Antibiotic Resistance Genes in the Saliva of Healthy Omnivores, Ovo-Lacto-Vegetarians, and Vegans. Genes, 2020, 11, 1088.	1.0	5
23	Secrets of the cheese microbiome. Nature Food, 2020, 1, 466-467.	6.2	9
24	Large-scale genome-wide analysis links lactic acid bacteria from food with the gut microbiome. Nature Communications, 2020, 11, 2610.	5.8	190
25	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
26	Diet influences the functions of the human intestinal microbiome. Scientific Reports, 2020, 10, 4247.	1.6	115
27	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
28	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
29	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
30	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
31	The Prevotella copri Complex Comprises Four Distinct Clades Underrepresented in Westernized Populations. Cell Host and Microbe, 2019, 26, 666-679.e7.	5.1	274
32	Gut Microbiome as Target for Innovative Strategies Against Food Allergy. Frontiers in Immunology, 2019, 10, 191.	2.2	75
33	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
34	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
35	Coffee prevents fatty liver disease induced by a high-fat diet by modulating pathways of the gutâ€“liver axis. Journal of Nutritional Science, 2019, 8, e15.	0.7	42
36	Laboratory medicine: health evaluation in elite athletes. Clinical Chemistry and Laboratory Medicine, 2019, 57, 1450-1473.	1.4	25

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37	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
38	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
39	Large-scale mapping of microbial diversity in artisanal Brazilian cheeses. Food Microbiology, 2019, 80, 40-49.	2.1	83
40	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
41	Strain-Level Diversity Analysis of Pseudomonas fragi after In Situ Pangenome Reconstruction Shows Distinctive Spoilage-Associated Metabolic Traits Clearly Selected by Different Storage Conditions. Applied and Environmental Microbiology, 2019, 85, .	1.4	30
42	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
43	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
44	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
45	Dietary Interventions to Modulate the Gut Microbiomeâ€"How Far Away Are We From Precision Medicine. Inflammatory Bowel Diseases, 2018, 24, 2142-2154.	0.9	61
46	Recent Past, Present, and Future of the Food Microbiome. Annual Review of Food Science and Technology, 2018, 9, 589-608.	5.1	113
47	Structure of association networks in food bacterial communities. Food Microbiology, 2018, 73, 49-60.	2.1	22
48	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
49	Food Design To Feed the Human Gut Microbiota. Journal of Agricultural and Food Chemistry, 2018, 66, 3754-3758.	2.4	104
50	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
51	Different Lactobacillus populations dominate in â€œChorizo de LeÃ³nâ€•manufacturing performed in different production plants. Food Microbiology, 2018, 70, 94-102.	2.1	41
52	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
53	Gut microbiota signatures in cystic fibrosis: Loss of host CFTR function drives the microbiota enterophenotype. PLoS ONE, 2018, 13, e0208171.	1.1	107
54	Microbiome and Diet. , 2018, , 79-88.		1

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55	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
56	Gut microbiota composition and butyrate production in children affected by non-IgE-mediated cowâ€™s milk allergy. Scientific Reports, 2018, 8, 12500.	1.6	80
57	Different Amplicon Targets for Sequencing-Based Studies of Fungal Diversity. Applied and Environmental Microbiology, 2017, 83, .	1.4	97
58	Exciting strainâ€level resolution studies of the food microbiome. Microbial Biotechnology, 2017, 10, 54-56.	2.0	14
59	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
60	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
61	Metagenomics insights into food fermentations. Microbial Biotechnology, 2017, 10, 91-102.	2.0	196
62	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
63	Gut Microbiota as a Target for Preventive and Therapeutic Intervention against Food Allergy. Nutrients, 2017, 9, 672.	1.7	81
64	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
65	A Few Pseudomonas Oligotypes Dominate in the Meat and Dairy Processing Environment. Frontiers in Microbiology, 2017, 8, 264.	1.5	64
66	Food Microbial Ecology in the â€˜Omicsâ€™ Era. , 2016, , .		1
67	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
68	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
69	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
70	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
71	Organic farming induces changes in soil microbiota that affect agro-ecosystem functions. Soil Biology and Biochemistry, 2016, 103, 327-336.	4.2	137
72	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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73	Midgut microbiota and host immunocompetence underlie Bacillus thuringiensis killing mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9486-9491.	3.3	144
74	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
75	Metatranscriptomics reveals temperature-driven functional changes in microbiome impacting cheese maturation rate. Scientific Reports, 2016, 6, 21871.	1.6	149
76	Unusual sub-genus associations of faecal Prevotella and Bacteroides with specific dietary patterns. Microbiome, 2016, 4, 57.	4.9	101
77	Impact of Nisin-Activated Packaging on Microbiota of Beef Burgers during Storage. Applied and Environmental Microbiology, 2016, 82, 549-559.	1.4	47
78	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
79	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
80	High-level adherence to a Mediterranean diet beneficially impacts the gut microbiota and associated metabolome. Gut, 2016, 65, 1812-1821.	6.1	1,092
81	The microbiota of high-moisture mozzarella cheese produced with different acidification methods. International Journal of Food Microbiology, 2016, 216, 9-17.	2.1	49
82	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
83	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
84	Bacteria and yeast microbiota in milk kefir grains from different Italian regions. Food Microbiology, 2015, 49, 123-133.	2.1	202
85	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
86	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
87	Lactic acid bacteria and their controversial role in fresh meat spoilage. Meat Science, 2015, 109, 66-74.	2.7	162
88	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
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	Zooming into food-associated microbial consortia: a â€˜culturalâ€™ evolution. Current Opinion in Food Science, 2015, 2, 43-50.	4.1	73

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91	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
92	Bacterial populations and the volatilome associated to meat spoilage. Food Microbiology, 2015, 45, 83-102.	2.1	462
93	Bacterial biogeographical patterns in a cooking center for hospital foodservice. International Journal of Food Microbiology, 2015, 193, 99-108.	2.1	22
94	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
95	Saliva from Obese Individuals Suppresses the Release of Aroma Compounds from Wine. PLoS ONE, 2014, 9, e85611.	1.1	98
96	Activities of strains of Brochothrix thermosphacta in vitro and in meat. Food Research International, 2014, 62, 366-374.	2.9	74
97	Salivary Microbiota and Metabolome Associated with Celiac Disease. Applied and Environmental Microbiology, 2014, 80, 3416-3425.	1.4	93
98	Bacteriophage P22 to challenge Salmonella in foods. International Journal of Food Microbiology, 2014, 191, 69-74.	2.1	84
99	Animal Rennets as Sources of Dairy Lactic Acid Bacteria. Applied and Environmental Microbiology, 2014, 80, 2050-2061.	1.4	42
100	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
101	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
102	A Selected Core Microbiome Drives the Early Stages of Three Popular Italian Cheese Manufactures. PLoS ONE, 2014, 9, e89680.	1.1	1,195
103	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
104	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
105	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
106	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
107	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
108	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

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109	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
110	Antimicrobial Packaging To Retard the Growth of Spoilage Bacteria and To Reduce the Release of Volatile Metabolites in Meat Stored under Vacuum at 1Â°C. Journal of Food Protection, 2013, 76, 52-58.	0.8	38
111	Microbial Ecology Dynamics during Rye and Wheat Sourdough Preparation. Applied and Environmental Microbiology, 2013, 79, 7827-7836.	1.4	183
112	Exploring the Sources of Bacterial Spoilers in Beefsteaks by Culture-Independent High-Throughput Sequencing. PLoS ONE, 2013, 8, e70222.	1.1	176
113	NaOH-Debittering Induces Changes in Bacterial Ecology during Table Olives Fermentation. PLoS ONE, 2013, 8, e69074.	1.1	75
114	â€œRemakeâ€•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
115	A combination of modified atmosphere and antimicrobial packaging to extend the shelf-life of beefsteaks stored at chill temperature. International Journal of Food Microbiology, 2012, 158, 186-194.	2.1	52
116	Diversity of Salmonella spp. serovars isolated from the intestines of water buffalo calves with gastroenteritis. BMC Veterinary Research, 2012, 8, 201.	0.7	29
117	Spoilage microbiota associated to the storage of raw meat in different conditions. International Journal of Food Microbiology, 2012, 157, 130-141.	2.1	454
118	Atomic force microscopy analysis shows surface structure changes in carvacrol-treated bacterial cells. Research in Microbiology, 2011, 162, 164-172.	1.0	125
119	Spoilage-related microbiota associated with chilled beef stored in air or vacuum pack. Food Microbiology, 2011, 28, 84-93.	2.1	184
120	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
121	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
122	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
123	Development of spoilage microbiota in beef stored in nisin activated packaging. Food Microbiology, 2010, 27, 137-143.	2.1	115
124	Characterization of Streptococcus thermophilus lytic bacteriophages from mozzarella cheese plants. International Journal of Food Microbiology, 2010, 138, 137-144.	2.1	33
125	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
126	Changes in the proteome of Salmonella enterica serovar Thompson as stress adaptation to sublethal concentrations of thymol. Proteomics, 2010, 10, 1040-1049.	1.3	131

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127	Diversity of Staphylococcus Species Strains Based on Partial kat (Catalase) Gene Sequences and Design of a PCR-Restriction Fragment Length Polymorphism Assay for Identification and		

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145	Yeast dynamics during spontaneous wine fermentation of the Catalanesca grape. International Journal of Food Microbiology, 2007, 117, 201-210.	2.1	126
146	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
147	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
148	Application of FISH technology for microbiological analysis: current state and prospects. Applied Microbiology and Biotechnology, 2006, 73, 485-494.	1.7	134
149	Behaviour of Brochothrix thermosphacta in presence of other meat spoilage microbial groups. Food Microbiology, 2006, 23, 797-802.	2.1	102
150	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
151	Genetic Resistance to Brucella abortus in the Water Buffalo (Bubalus bubalis). Infection and Immunity, 2006, 74, 2115-2120.	1.0	51
152	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
153	Antimicrobial activity of a nisin-activated plastic film for food packaging. Letters in Applied Microbiology, 2005, 41, 464-469.	1.0	157
154	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
155	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
156	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
157	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
158	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
159	PCR detection of staphylococcal enterotoxin genes in Staphylococcus spp. strains isolated from meat and dairy products. Evidence for new variants of seG and sel in S. aureus AB-8802. Journal of Applied Microbiology, 2004, 97, 719-730.	1.4	124
160	Technological and Molecular Diversity of Lactobacillus plantarum Strains Isolated from Naturally Fermented Sourdoughs. Systematic and Applied Microbiology, 2004, 27, 443-453.	1.2	59
161	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
162	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

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163	PCR-DGGE fingerprinting: novel strategies for detection of microbes in food. Journal of Microbiological Methods, 2004, 56, 297-314.	0.7	518
164	Selection of Lactobacillus strains from fermented sausages for their potential use as probiotics. Meat Science, 2004, 67, 309-317.	2.7	162
165	Combining Denaturing Gradient Gel Electrophoresis of 16S rDNA V3 Region and 16Sâ€“23S rDNA Spacer Region Polymorphism Analyses for the Identification of Staphylococci from Italian Fermented Sausages. Systematic and Applied Microbiology, 2003, 26, 423-433.	1.2	47
166	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
167	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
168	Bacterial Community Structure and Location in Stilton Cheese. Applied and Environmental Microbiology, 2003, 69, 3540-3548.	1.4	242
169	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
170	Molecular evaluation of microbial diversity occurring in different types of Mozzarella cheese. Journal of Applied Microbiology, 2001, 90, 414-420.	1.4	126
171	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
172	Conditions for conjugative transposon transfer in Lactococcus lactis. Letters in Applied Microbiology, 2000, 31, 343-348.	1.0	4