David A Mills

List of Publications by Year
in descending order

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208	28,367	4942 84	5806 161
papers	citations	h-index	g-index

215	215	215	26659
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. Nature Methods, 2013, 10, 57-59.	9.0	3,402
2	A communal catalogue reveals Earthâ€™s multiscale microbial diversity. Nature, 2017, 551, 457-463.	13.7	1,942
3	Comparative genomics of the lactic acid bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15611-15616.	3.3	1,303
4	Microbial biogeography of wine grapes is conditioned by cultivar, vintage, and climate. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E139-48.	3.3	791
5	The genome sequence of Bifidobacterium longum subsp. infantis reveals adaptations for milk utilization within the infant microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 18964-18969.	3.3	748
6	The Soil Microbiome Influences Grapevine-Associated Microbiota. MBio, 2015, 6, .	1.8	747
7	Human milk glycobiome and its impact on the infant gastrointestinal microbiota. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4653-4658.	3.3	566
8	Sialylated Milk Oligosaccharides Promote Microbiota-Dependent Growth in Models of Infant Undernutrition. Cell, 2016, 164, 859-871.	13.5	497
9	Bacteroides in the Infant Gut Consume Milk Oligosaccharides via Mucus-Utilization Pathways. Cell Host and Microbe, 2011, 10, 507-514.	5.1	474
10	Consumption of Human Milk Oligosaccharides by Gut-Related Microbes. Journal of Agricultural and Food Chemistry, 2010, 58, 5334-5340.	2.4	453
11	Improved Selection of Internal Transcribed Spacer-Specific Primers Enables Quantitative, Ultra-High-Throughput Profiling of Fungal Communities. Applied and Environmental Microbiology, 2013, 79, 2519-2526.	1.4	442
12	Direct profiling of the yeast dynamics in wine fermentations. FEMS Microbiology Letters, 2000, 189, 81-87.	0.7	429
13	Nursing our microbiota: molecular linkages between bifidobacteria and milk oligosaccharides. Trends in Microbiology, 2010, 18, 298-307.	3.5	402
14	Diet shapes the gut microbiome of pigs during nursing and weaning. Microbiome, 2015, 3, 28.	4.9	387
15	Breast Milk Oligosaccharides: Structure-Function Relationships in the Neonate. Annual Review of Nutrition, 2014, 34, 143-169.	4.3	332
16	Prebiotics: why definitions matter. Current Opinion in Biotechnology, 2016, 37, 1-7.	3.3	326
17	Associations among Wine Grape Microbiome, Metabolome, and Fermentation Behavior Suggest Microbial Contribution to Regional Wine Characteristics. MBio, 2016, 7, .	1.8	325
18	Genome analysis of Bifidobacterium bifidum PRL2010 reveals metabolic pathways for host-derived glycan foraging. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 19514-19519.	3.3	324

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19	Maternal fucosyltransferase 2 status affects the gut bifidobacterial communities of breastfed infants. Microbiome, 2015, 3, 13.	4.9	319
20	Glycoprofiling of Bifidobacterial Consumption of Human Milk Oligosaccharides Demonstrates Strain Specific, Preferential Consumption of Small Chain Glycans Secreted in Early Human Lactation. Journal of Agricultural and Food Chemistry, 2007, 55, 8914-8919.	2.4	313
21	Stool Microbiota and Vaccine Responses of Infants. Pediatrics, 2014, 134, e362-e372.	1.0	308
22	Bifidobacterium longum subspecies infantis: champion colonizer of the infant gut. Pediatric Research, 2015, 77, 229-235.	1.1	297
23	In Vitro Fermentation of Breast Milk Oligosaccharides by Bifidobacterium infantis and Lactobacillus gasseri. Applied and Environmental Microbiology, 2006, 72, 4497-4499.	1.4	255
24	Simultaneous consumption of pentose and hexose sugars: an optimal microbial phenotype for efficient fermentation of lignocellulosic biomass. Applied Microbiology and Biotechnology, 2010, 88, 1077-1085.	1.7	234
25	Facility-Specific â€œHouseâ€•Microbiome Drives Microbial Landscapes of Artisan Cheesemaking Plants. Applied and Environmental Microbiology, 2013, 79, 5214-5223.	1.4	232
26	Yeast Diversity and Persistence in Botrytis-Affected Wine Fermentations. Applied and Environmental Microbiology, 2002, 68, 4884-4893.	1.4	228
27	A microbial perspective of human developmental biology. Nature, 2016, 535, 48-55.	13.7	215
28	In vitro fermentability of human milk oligosaccharides by several strains of bifidobacteria. Molecular Nutrition and Food Research, 2007, 51, 1398-1405.	1.5	212
29	Retrohoming of a Bacterial Group II Intron. Cell, 1998, 94, 451-462.	13.5	208
30	Bifidobacteria Isolated From Infants and Cultured on Human Milk Oligosaccharides Affect Intestinal Epithelial Function. Journal of Pediatric Gastroenterology and Nutrition, 2012, 55, 321-327.	0.9	208
31	Bifidobacterium longum subsp. infantis ATCC 15697 Î±-Fucosidases Are Active on Fucosylated Human Milk Oligosaccharides. Applied and Environmental Microbiology, 2012, 78, 795-803.	1.4	204
32	Variation in Consumption of Human Milk Oligosaccharides by Infant Gut-Associated Strains of Bifidobacterium breve. Applied and Environmental Microbiology, 2013, 79, 6040-6049.	1.4	203
33	Maturation of the gut microbiome during the first year of life contributes to the protective farm effect on childhood asthma. Nature Medicine, 2020, 26, 1766-1775.	15.2	202
34	Next-Generation Sequencing Reveals Significant Bacterial Diversity of Botrytized Wine. PLoS ONE, 2012, 7, e36357.	1.1	196
35	Broad Conservation of Milk Utilization Genes in Bifidobacterium longum subsp. infantis as Revealed by Comparative Genomic Hybridization. Applied and Environmental Microbiology, 2010, 76, 7373-7381.	1.4	193
36	Human Milk Oligosaccharides: Evolution, Structures and Bioselectivity as Substrates for Intestinal Bacteria. Nestle Nutrition Workshop Series Paediatric Programme, 2008, 62, 205-222.	1.5	192

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37	Consumption of human milk glycoconjugates by infant-associated bifidobacteria: mechanisms and implications. Microbiology (United Kingdom), 2013, 159, 649-664.	0.7	187
38	Flavonoids and the gastrointestinal tract: Local and systemic effects. Molecular Aspects of Medicine, 2018, 61, 41-49.	2.7	181
39	Oligosaccharide Binding Proteins from Bifidobacterium longum subsp. infantis Reveal a Preference for Host Glycans. PLoS ONE, 2011, 6, e17315.	1.1	179
40	Design and Evaluation of PCR Primers for Analysis of Bacterial Populations in Wine by Denaturing Gradient Gel Electrophoresis. Applied and Environmental Microbiology, 2003, 69, 6801-6807.	1.4	168
41	Monitoring Seasonal Changes in Winery-Resident Microbiota. PLoS ONE, 2013, 8, e66437.	1.1	167
42	Human Milk Glycomics and Gut Microbial Genomics in Infant Feces Show a Correlation between Human Milk Oligosaccharides and Gut Microbiota: A Proof-of-Concept Study. Journal of Proteome Research, 2015, 14, 491-502.	1.8	166
43	An Infant-associated Bacterial Commensal Utilizes Breast Milk Sialyloligosaccharides. Journal of Biological Chemistry, 2011, 286, 11909-11918.	1.6	164
44	The Human Gut Microbiota and Undernutrition. Science Translational Medicine, 2012, 4, 137ps12.	5.8	162
45	Brewhouse-Resident Microbiota Are Responsible for Multi-Stage Fermentation of American Coolship Ale. PLoS ONE, 2012, 7, e35507.	1.1	161
46	The Influence of Milk Oligosaccharides on Microbiota of Infants: Opportunities for Formulas. Annual Review of Food Science and Technology, 2011, 2, 331-351.	5.1	158
47	Persistence of Supplemented Bifidobacterium longum subsp. infantis EVC001 in Breastfed Infants. MSphere, 2017, 2, .	1.3	158
48	Cultivating Healthy Growth and Nutrition through the Gut Microbiota. Cell, 2015, 161, 36-48.	13.5	155
49	Human milk oligosaccharides in premature infants: absorption, excretion, and influence on the intestinal microbiota. Pediatric Research, 2015, 78, 670-677.	1.1	155
50	Growth and Morbidity of Gambian Infants are Influenced by Maternal Milk Oligosaccharides and Infant Gut Microbiota. Scientific Reports, 2017, 7, 40466.	1.6	152
51	Symbiotic Human Gut Bacteria with Variable Metabolic Priorities for Host Mucosal Glycans. MBio, 2015, 6, e01282-15.	1.8	148
52	Genomic analysis of PSU-1 and its relevance to winemaking. FEMS Microbiology Reviews, 2005, 29, 465-475.	3.9	146
53	A Randomized Placeboâ€controlled Comparison of 2 Prebiotic/Probiotic Combinations in Preterm Infants: Impact on Weight Gain, Intestinal Microbiota, and Fecal Shortâ€chain Fatty Acids. Journal of Pediatric Gastroenterology and Nutrition, 2009, 48, 216-225.	0.9	145
54	Comparative transcriptomics reveals key differences in the response to milk oligosaccharides of infant gut-associated bifidobacteria. Scientific Reports, 2015, 5, 13517.	1.6	144

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55	The Impact of the Milk Glycobiome on the Neonate Gut Microbiota. Annual Review of Animal Biosciences, 2015, 3, 419-445.	3.6	143
56	A novel gene cluster allows preferential utilization of fucosylated milk oligosaccharides in Bifidobacterium longum subsp. longum SC596. Scientific Reports, 2016, 6, 35045.	1.6	137
57	Splicing of a group II intron involved in the conjugative transfer of pRS01 in lactococci. Journal of Bacteriology, 1996, 178, 3531-3538.	1.0	128
58	A Molecular Basis for Bifidobacterial Enrichment in the Infant Gastrointestinal Tract. Advances in Nutrition, 2012, 3, 415S-421S.	2.9	128
59	Lacto-N-Tetraose, Fucosylation, and Secretor Status Are Highly Variable in Human Milk Oligosaccharides From Women Delivering Preterm. Journal of Proteome Research, 2012, 11, 4662-4672.	1.8	127
60	Pilot study of probiotic/colostrum supplementation on gut function in children with autism and gastrointestinal symptoms. PLoS ONE, 2019, 14, e0210064.	1.1	126
61	Validating bifidobacterial species and subspecies identity in commercial probiotic products. Pediatric Research, 2016, 79, 445-452.	1.1	125
62	Oligosaccharides Released from Milk Glycoproteins Are Selective Growth Substrates for Infant-Associated Bifidobacteria. Applied and Environmental Microbiology, 2016, 82, 3622-3630.	1.4	124
63	Endo-Î²-N-acetylglucosaminidases from Infant Gut-associated Bifidobacteria Release Complex N-glycans from Human Milk Glycoproteins. Molecular and Cellular Proteomics, 2012, 11, 775-785.	2.5	121
64	Indole-3-lactic acid associated with Bifidobacterium-dominated microbiota significantly decreases inflammation in intestinal epithelial cells. BMC Microbiology, 2020, 20, 357.	1.3	117
65	A versatile and scalable strategy for glycoprofiling bifidobacterial consumption of human milk oligosaccharides. Microbial Biotechnology, 2009, 2, 333-342.	2.0	116
66	Next-generation approaches to the microbial ecology of food fermentations. BMB Reports, 2012, 45, 377-389.	1.1	113
67	Hepatic inflammation caused by dysregulated bile acid synthesis is reversible by butyrate supplementation. Journal of Pathology, 2017, 243, 431-441.	2.1	111
68	Phenolic metabolites and substantial microbiome changes in pig feces by ingesting grape seed proanthocyanidins. Food and Function, 2014, 5, 2298-2308.	2.1	109
69	(-)-Epicatechin protects the intestinal barrier from high fat diet-induced permeabilization: Implications for steatosis and insulin resistance. Redox Biology, 2018, 14, 588-599.	3.9	109
70	Real-Time PCR Assay for Detection and Enumeration of Dekkera bruxellensis in Wine. Applied and Environmental Microbiology, 2003, 69, 7430-7434.	1.4	107
71	A Comparison of Two Probiotic Strains of Bifidobacteria in Premature Infants. Journal of Pediatrics, 2013, 163, 1585-1591.e9.	0.9	107
72	SAMSA2: a standalone metatranscriptome analysis pipeline. BMC Bioinformatics, 2018, 19, 175.	1.2	107

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73	Development of Chemically Defined Media Supporting High-Cell-Density Growth of Lactococci, Enterococci, and Streptococci. Applied and Environmental Microbiology, 2009, 75, 1080-1087.	1.4	104
74	Peptidomic analysis reveals proteolytic activity of kefir microorganisms on bovine milk proteins. Food Chemistry, 2016, 197, 273-284.	4.2	103
75	Gender Differences in Bile Acids and Microbiota in Relationship with Gender Dissimilarity in Steatosis Induced by Diet and FXR Inactivation. Scientific Reports, 2017, 7, 1748.	1.6	103
76	Relaxed control of sugar utilization in Lactobacillus brevis. Microbiology (United Kingdom), 2009, 155, 1351-1359.	0.7	102
77	A new perspective on microbial landscapes within food production. Current Opinion in Biotechnology, 2016, 37, 182-189.	3.3	100
78	The fecal resistome of dairy cattle is associated with diet during nursing. Nature Communications, 2019, 10, 4406.	5.8	100
79	Bifidobacterium Abundance in Early Infancy and Vaccine Response at 2 Years of Age. Pediatrics, 2019, 143, .	1.0	99
80	Daily Variations in Oligosaccharides of Human Milk Determined by Microfluidic Chips and Mass Spectrometry. Journal of Agricultural and Food Chemistry, 2008, 56, 618-626.	2.4	98
81	Bifidobacterium longum subsp. infantis in experimental necrotizing enterocolitis: alterations in inflammation, innate immune response, and the microbiota. Pediatric Research, 2014, 76, 326-333.	1.1	95
82	Milk Glycans and Their Interaction with the Infant-Gut Microbiota. Annual Review of Food Science and Technology, 2018, 9, 429-450.	5.1	95
83	Utilization of galactooligosaccharides by Bifidobacterium longum subsp. infantis isolates. Food Microbiology, 2013, 33, 262-270.	2.1	94
84	Anthocyanins protect the gastrointestinal tract from high fat diet-induced alterations in redox signaling, barrier integrity and dysbiosis. Redox Biology, 2019, 26, 101269.	3.9	94
85	Western Dietâ€“Induced Dysbiosis in Farnesoid X Receptor Knockout Mice Causes Persistent Hepatic Inflammation after Antibiotic Treatment. American Journal of Pathology, 2017, 187, 1800-1813.	1.9	90
86	Release and utilization of N-acetyl-d-glucosamine from human milk oligosaccharides by Bifidobacterium longum subsp. infantis. Anaerobe, 2012, 18, 430-435.	1.0	88
87	A quantitative and comprehensive method to analyze human milk oligosaccharide structures in the urine and feces of infants. Analytical and Bioanalytical Chemistry, 2013, 405, 4089-4105.	1.9	86
88	Indigenous Bacteria and Fungi Drive Traditional Kimoto Sake Fermentations. Applied and Environmental Microbiology, 2014, 80, 5522-5529.	1.4	86
89	Bile acid dysregulation, gut dysbiosis, and gastrointestinal cancer. Experimental Biology and Medicine, 2014, 239, 1489-1504.	1.1	82
90	Homing of a group II intron from Lactococcus lactis subsp. lactis ML3. Journal of Bacteriology, 1997, 179, 6107-6111.	1.0	79

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91	Glycoprofiling Bifidobacterial Consumption of Galacto-Oligosaccharides by Mass Spectrometry Reveals Strain-Specific, Preferential Consumption of Glycans. Applied and Environmental Microbiology, 2009, 75, 7319-7325.	1.4	78
92	Identification of Oligosaccharides in Feces of Breast-fed Infants and Their Correlation with the Gut Microbial Community. Molecular and Cellular Proteomics, 2016, 15, 2987-3002.	2.5	77
93	Genetic Manipulation of Lactococcus lactis by Using Targeted Group II Introns: Generation of Stable Insertions without Selection. Applied and Environmental Microbiology, 2003, 69, 1121-1128.	1.4	74
94	Proteomic Analysis of Bifidobacterium longum subsp. infantis Reveals the Metabolic Insight on Consumption of Prebiotics and Host Glycans. PLoS ONE, 2013, 8, e57535.	1.1	74
95	Surface Microbes in the Neonatal Intensive Care Unit: Changes with Routine Cleaning and over Time. Journal of Clinical Microbiology, 2013, 51, 2617-2624.	1.8	73
96	Mapping microbial ecosystems and spoilage-gene flow in breweries highlights patterns of contamination and resistance. ELife, 2015, 4, .	2.8	71
97	Bifidobacterial Dominance of the Gut in Early Life and Acquisition of Antimicrobial Resistance. MSphere, 2018, 3, .	1.3	71
98	Role of Hypermutability in the Evolution of the GenusOenococcus. Journal of Bacteriology, 2008, 190, 564-570.	1.0	70
99	Buccal administration of human colostrum: impact on the oral microbiota of premature infants. Journal of Perinatology, 2016, 36, 106-111.	0.9	70
100	Methods for the quantitation of human milk oligosaccharides in bacterial fermentation by mass spectrometry. Analytical Biochemistry, 2007, 361, 15-23.	1.1	68
101	Bifidobacteria grown on human milk oligosaccharides downregulate the expression of inflammation-related genes in Caco-2 cells. BMC Microbiology, 2015, 15, 172.	1.3	67
102	Transposon Mutagenesis of Xylella fastidiosa by Electroporation of Tn5 Synaptic Complexes. Molecular Plant-Microbe Interactions, 2001, 14, 701-706.	1.4	66
103	Routine Habitat Change: A Source of Unrecognized Transient Alteration of Intestinal Microbiota in Laboratory Mice. PLoS ONE, 2012, 7, e47416.	1.1	65
104	Bovine milk oligosaccharides decrease gut permeability and improve inflammation and microbial dysbiosis in diet-induced obese mice. Journal of Dairy Science, 2017, 100, 2471-2481.	1.4	64
105	Effects of triclosan in breast milk on the infant fecal microbiome. Chemosphere, 2018, 203, 467-473.	4.2	64
106	Analysis of raw goat milk microbiota: Impact of stage of lactation and lysozyme on microbial diversity. Food Microbiology, 2015, 46, 121-131.	2.1	61
107	The one-pot multienzyme (OPME) synthesis of human blood group H antigens and a human milk oligosaccharide (HMOS) with highly active Thermosynechococcus elongatus Î±1â€“2-fucosyltransferase. Chemical Communications, 2016, 52, 3899-3902.	2.2	58
108	Prebiotic milk oligosaccharides prevent development of obese phenotype, impairment of gut permeability, and microbial dysbiosis in high fat-fed mice. American Journal of Physiology - Renal Physiology, 2017, 312, G474-G487.	1.6	58

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109	Sulfur Dioxide Treatment Alters Wine Microbial Diversity and Fermentation Progression in a Dose-Dependent Fashion. American Journal of Enology and Viticulture, 2015, 66, 73-79.	0.9	56
110	Characterization of porcine milk oligosaccharides during early lactation and their relation to the fecal microbiome. Journal of Dairy Science, 2016, 99, 7733-7743.	1.4	56
111	Lipopolysaccharideâ€induced maternal inflammation induces direct placental injury without alteration in placental blood flow and induces a secondary fetal intestinal injury that persists into adulthood. American Journal of Reproductive Immunology, 2018, 79, e12816.	1.2	55
112	Mechanisms by which sialylated milk oligosaccharides impact bone biology in a gnotobiotic mouse model of infant undernutrition. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11988-11996.	3.3	55
113	Differential Real-Time PCR Assay for Enumeration of Lactic Acid Bacteria in Wine. Applied and Environmental Microbiology, 2005, 71, 8954-8957.	1.4	53
114	Rapid Determination of the Bacterial Composition of Commercial Probiotic Products by Terminal Restriction Fragment Length Polymorphism Analysis. Journal of Pediatric Gastroenterology and Nutrition, 2008, 46, 608-611.	0.9	53
115	Loss of murine Paneth cell function alters the immature intestinal microbiome and mimics changes seen in neonatal necrotizing enterocolitis. PLoS ONE, 2018, 13, e0204967.	1.1	53
116	SAMSA: a comprehensive metatranscriptome analysis pipeline. BMC Bioinformatics, 2016, 17, 399.	1.2	49
117	A nonenzymatic method for cleaving polysaccharides to yield oligosaccharides for structural analysis. Nature Communications, 2020, 11, 3963.	5.8	49
118	Microbial biogeography of the transnational fermented milk matsoni. Food Microbiology, 2015, 50, 12-19.	2.1	47
119	Reservoirs of antimicrobial resistance genes in retail raw milk. Microbiome, 2020, 8, 99.	4.9	47
120	NMR assignments of the four histidines of staphylococcal nuclease in native and denatured states. Biochemistry, 1988, 27, 2158-2165.	1.2	46
121	Synbiotics Bifidobacterium infantis and milk oligosaccharides are effective in reversing cancer-prone nonalcoholic steatohepatitis using western diet-fed FXR knockout mouse models. Journal of Nutritional Biochemistry, 2018, 57, 246-254.	1.9	46
122	A dynamic, genome-scale flux model of Lactococcus lactis to increase specific recombinant protein expression. Metabolic Engineering, 2009, 11, 367-381.	3.6	45
123	Comparative Analyses of Prophage-Like Elements Present in Bifidobacterial Genomes. Applied and Environmental Microbiology, 2009, 75, 6929-6936.	1.4	45
124	Digestion of Human Milk Oligosaccharides by Bifidobacterium breve in the Premature Infant. Journal of Pediatric Gastroenterology and Nutrition, 2017, 65, 449-455.	0.9	45
125	Evaluation of PCR primers for denaturing gradient gel electrophoresis analysis of fungal communities in compost. Journal of Applied Microbiology, 2003, 95, 934-948.	1.4	44
126	Neonatal Vitamin A Supplementation and Vitamin A Status Are Associated with Gut Microbiome Composition in Bangladeshi Infants in Early Infancy and at 2 Years of Age. Journal of Nutrition, 2019, 149, 1075-1088.	1.3	42

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127	Sources and Assembly of Microbial Communities in Vineyards as a Functional Component of Winegrowing. Frontiers in Microbiology, 2021, 12, 673810.	1.5	39
128	Differentiation of mixed lactic acid bacteria communities in beverage fermentations using targeted terminal restriction fragment length polymorphism. Food Microbiology, 2012, 31, 126-132.	2.1	38
129	Differential Establishment of Bifidobacteria in the Breastfed Infant Gut. Nestle Nutrition Institute Workshop Series, 2017, 88, 149-160.	1.5	37
130	The developing gutâ€“lung axis: postnatal growth restriction, intestinal dysbiosis, and pulmonary hypertension in a rodent model. Pediatric Research, 2020, 87, 472-479.	1.1	37
131	The marriage of nutrigenomics with the microbiome: the case of infant-associated bifidobacteria and milk. American Journal of Clinical Nutrition, 2014, 99, 697S-703S.	2.2	36
132	Hydrolysis of milk gangliosides by infantâ€gut associated bifidobacteria determined by microfluidic chips and highâ€resolution mass spectrometry. Electrophoresis, 2014, 35, 1742-1750.	1.3	35
133	Prebiotic Oligosaccharides in Premature Infants. Journal of Pediatric Gastroenterology and Nutrition, 2014, 58, 352-360.	0.9	34
134	Influence of whole-wheat consumption on fecal microbial community structure of obese diabetic mice. PeerJ, 2016, 4, e1702.	0.9	34
135	Conversion of rice straw to bio-based chemicals: an integrated process using Lactobacillus brevis. Applied Microbiology and Biotechnology, 2010, 86, 1375-1385.	1.7	33
136	Kinetics ofLactococcus lactis growth and metabolite formation under aerobic and anaerobic conditions in the presence or absence of hemin. Biotechnology and Bioengineering, 2006, 95, 1070-1080.	1.7	32
137	Improvement of a nisin-inducible expression vector for use in lactic acid bacteria. Plasmid, 2007, 58, 275-283.	0.4	32
138	Complete Genome Sequence of Lactobacillus buchneri NRRL B-30929, a Novel Strain from a Commercial Ethanol Plant. Journal of Bacteriology, 2011, 193, 4019-4020.	1.0	31
139	Enterocyte glycosylation is responsive to changes in extracellular conditions: implications for membrane functions. Glycobiology, 2017, 27, 847-860.	1.3	31
140	Rapid discrimination of Bifidobacterium animalis subspecies by matrix-assisted laser desorption ionization-time of flight mass spectrometry. Food Microbiology, 2012, 30, 432-437.	2.1	30
141	Cervicovaginal Microbiome Composition Is Associated with Metabolic Profiles in Healthy Pregnancy. MBio, 2020, 11, .	1.8	30
142	Long-term effects of western diet consumption in male and female mice. Scientific Reports, 2020, 10, 14686.	1.6	30
143	Multicopy Integration of Heterologous Genes, Using the Lactococcal Group II Intron Targeted to Bacterial Insertion Sequences. Applied and Environmental Microbiology, 2006, 72, 6088-6093.	1.4	28
144	A Review of Molecular Methods for Microbial Community Profiling of Beer and Wine. Journal of the American Society of Brewing Chemists, 2012, 70, 150-162.	0.8	28

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145	Characterizing the release of bioactiveN-glycans from dairy products by a novel endo-Î²-N-acetylglucosaminidase. Biotechnology Progress, 2015, 31, 1331-1339.	1.3	28
146	The Fecal Microbial Community of Breast-fed Infants from Armenia and Georgia. Scientific Reports, 2017, 7, 40932.	1.6	28
147	Effect of barley supplementation on the fecal microbiota, caecal biochemistry, and key biomarkers of obesity and inflammation in obese db/db mice. European Journal of Nutrition, 2018, 57, 2513-2528.	1.8	28
148	Optimization of fed-batch production of the model recombinant protein GFP inLactococcus lactis. Biotechnology and Bioengineering, 2007, 96, 1127-1138.	1.7	26
149	Human microbiome science: vision for the future, Bethesda, MD, July 24 to 26, 2013. Microbiome, 2014, 2, .	4.9	25
150	Association of Diet and Antimicrobial Resistance in Healthy U.S. Adults. MBio, 2022, 13, e0010122.	1.8	25
151	Analysis and Quantitation of Fructooligosaccharides Using Matrix-Assisted Laser Desorption/Ionization Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. Analytical Chemistry, 2008, 80, 159-165.	3.2	24
152	Mutagenesis in the post genomics era: tools for generating insertional mutations in the lactic acid bacteria. Current Opinion in Biotechnology, 2001, 12, 503-509.	3.3	22
153	Identification and Accurate Quantitation of Biological Oligosaccharide Mixtures. Analytical Chemistry, 2012, 84, 7793-7801.	3.2	22
154	Fetal exposure to maternal inflammation interrupts murine intestinal development and increases susceptibility to neonatal intestinal injury. DMM Disease Models and Mechanisms, 2019, 12, .	1.2	22
155	Isomer-Specific Consumption of Galactooligosaccharides by Bifidobacterial Species. Journal of Agricultural and Food Chemistry, 2013, 61, 12612-12619.	2.4	21
156	Use of bifidobacterial specific terminal restriction fragment length polymorphisms to complement next generation sequence profiling of infant gut communities. Anaerobe, 2013, 19, 62-69.	1.0	20
157	A novel endo-Î²-N-acetylglucosaminidase releases specificN-glycans depending on different reaction conditions. Biotechnology Progress, 2015, 31, 1323-1330.	1.3	20
158	Kinetic characterization of a novel endo-Î²-N-acetylglucosaminidase on concentrated bovine colostrum whey to release bioactive glycans. Enzyme and Microbial Technology, 2015, 77, 46-53.	1.6	20
159	Human Milk Oligosaccharide Compositions Illustrate Global Variations in Early Nutrition. Journal of Nutrition, 2022, 152, 1239-1253.	1.3	19
160	Production of functional mimics of human milk oligosaccharides by enzymatic glycosylation of bovine milk oligosaccharides. International Dairy Journal, 2020, 102, 104583.	1.5	18
161	Bifidobacterium catabolism of human milk oligosaccharides overrides endogenous competitive exclusion driving colonization and protection. Gut Microbes, 2021, 13, 1986666.	4.3	18
162	Fucosylated Human Milk Oligosaccharide Foraging within the Species Bifidobacterium pseudocatenulatum Is Driven by Glycosyl Hydrolase Content and Specificity. Applied and Environmental Microbiology, 2022, 88, AEM0170721.	1.4	18

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163	Incorporation of nisI-mediated nisin immunity improves vector-based nisin-controlled gene expression in lactic acid bacteria. Plasmid, 2009, 61, 151-158.	0.4	17
164	Probiotic Administration in Infants With Gastroschisis. Journal of Pediatric Gastroenterology and Nutrition, 2016, 62, 852-857.	0.9	17
165	Tolerability and safety of the intake of bovine milk oligosaccharides extracted from cheese whey in healthy human adults. Journal of Nutritional Science, 2017, 6, e6.	0.7	17
166	Inulin Fermentation by Lactobacilli and Bifidobacteria from Dairy Calves. Applied and Environmental Microbiology, 2020, 87, .	1.4	17
167	Bifidobacterium Species Colonization in Infancy: A Global Cross-Sectional Comparison by Population History of Breastfeeding. Nutrients, 2022, 14, 1423.	1.7	17
168	Genomic analysis ofOenococcus oeniPSU-1 and its relevance to winemaking. FEMS Microbiology Reviews, 2005, 29, 465-475.	3.9	16
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