# Willem M De Vos

List of Publications by Year
in descending order

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| 725 | 114,049 | 135 | 250 |
| --- | --- | --- | --- |
| papers | citations | 159 h-index | 301 g-index |

| 749 | 749 | 749 | 68537 |
| --- | --- | --- | --- |
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Toxicological safety evaluation of live Anaerobutyricum soehngenii strain CH106. Journal of Applied Toxicology, 2022, 42, 244-257. | 2.8 | 7 |
| 2 | Comparative genomics and proteomics of Eubacterium maltosivorans: functional identification of trimethylamine methyltransferases and bacterial microcompartments in a human intestinal bacterium with a versatile lifestyle. Environmental Microbiology, 2022, 24, 517-534. | 3.8 | 8 |
| 3 | Gut microbiome and health: mechanistic insights. Gut, 2022, 71, 1020-1032. | 12.1 | 661 |
| 4 | Before the heart attack. Nature Medicine, 2022, 28, 237-238. | 30.7 | 1 |
| 5 | Camu-Camu Reduces Obesity and Improves Diabetic Profiles of Obese and Diabetic Mice: A Dose-Ranging Study. Metabolites, 2022, 12, 301. | 2.9 | 7 |
| 6 | Inter-species Metabolic Interactions in an In-vitro Minimal Human Gut Microbiome of Core Bacteria. Npj Biofilms and Microbiomes, 2022, 8, 21. | 6.4 | 26 |
| 7 | Peptidoglycan from Akkermansia muciniphila MucT: chemical structure and immunostimulatory properties of muropeptides. Glycobiology, 2022, 32, 712-719. | 2.5 | 2 |
| 8 | The gut fungal and bacterial microbiota in pediatric patients with inflammatory bowel disease introduced to treatment with anti-tumor necrosis factor-Î±. Scientific Reports, 2022, 12, 6654. | 3.3 | 5 |
| 9 | The Effect of Antibiotics on the Infant Gut Fungal Microbiota. Journal of Fungi (Basel, Switzerland), 2022, 8, 328. | 3.5 | 11 |
| 10 | Dried chicory root improves bowel function, benefits intestinal microbial trophic chains and increases faecal and circulating short chain fatty acids in subjects at risk for type 2 diabetes. Gut Microbiome, 2022, 3, . | 3.2 | 5 |
| 11 | A 4-Week Diet Low or High in Advanced Glycation Endproducts Has Limited Impact on Gut Microbial Composition in Abdominally Obese Individuals: The deAGEing Trial. International Journal of Molecular Sciences, 2022, 23, 5328. | 4.1 | 13 |
| 12 | Gut microbiota predicts body fat change following a low-energy diet: a PREVIEW intervention study. Genome Medicine, 2022, 14, . | 8.2 | 32 |
| 13 | Akkermansia muciniphila: paradigm for next-generation beneficial microorganisms. Nature Reviews Gastroenterology and Hepatology, 2022, 19, 625-637. | 17.8 | 239 |
| 14 | Dynamic metabolic interactions and trophic roles of human gut microbes identified using a minimal microbiome exhibiting ecological properties. ISME Journal, 2022, 16, 2144-2159. | 9.8 | 16 |
| 15 | Disruptions of Anaerobic Gut Bacteria Are Associated with Stroke and Post-stroke Infection: a Prospective Caseâ€“Control Study. Translational Stroke Research, 2021, 12, 581-592. | 4.2 | 75 |
| 16 | Toxicological safety evaluation of pasteurized Akkermansia muciniphila. Journal of Applied Toxicology, 2021, 41, 276-290. | 2.8 | 30 |
| 17 | Roadmap to functional characterization of the human intestinal microbiota in its interaction with the host. Journal of Pharmaceutical and Biomedical Analysis, 2021, 194, 113751. | 2.8 | 9 |
| 18 | Correlations between microbiota and metabolites after faecal microbiota transfer in irritable bowel syndrome. Beneficial Microbes, 2021, 12, 17-30. | 2.4 | 4 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Beneficial Effects of Akkermansia muciniphila Are Not Associated with Major Changes in the Circulating Endocannabinoidome but Linked to Higher Mono-Palmitoyl-Glycerol Levels as New PPARÎ± Agonists. Cells, 2021, 10, 185. | 4.1 | 43 |
| 20 | Gut bacteriophage dynamics during fecal microbial transplantation in subjects with metabolic syndrome. Gut Microbes, 2021, 13, 1-15. | 9.8 | 24 |
| 21 | Protocol for oral transplantation of maternal fecal microbiota to newborn infants born by cesarean section. STAR Protocols, 2021, 2, 100271. | 1.2 | 7 |
| 22 | Integrative Transkingdom Analysis of the Gut Microbiome in Antibiotic Perturbation and Critical Illness. MSystems, 2021, 6, . | 3.8 | 35 |
| 23 | Fecal Microbiota Transplantation from Overweight or Obese Donors in Cachectic Patients with Advanced Gastroesophageal Cancer: A Randomized, Double-blind, Placebo-Controlled, Phase II Study. Clinical Cancer Research, 2021, 27, 3784-3792. | 7.0 | 30 |
| 24 | Next-generation therapeutic bacteria for treatment of obesity, diabetes, and other endocrine diseases. Best Practice and Research in Clinical Endocrinology and Metabolism, 2021, 35, 101504. | 4.7 | 16 |
| 25 | DOP71 Fungal and bacterial gut microbiota in paediatric onset Inflammatory Bowel Disease introduced to infliximab. Journal of Crohn's and Colitis, 2021, 15, S105-S105. | 1.3 | 0 |
| 26 | A novel technique capable of taking â€˜protectedâ€™ biopsies for reliable assessment of the distribution of microbiota along the colonic mucosa. Journal of Microbiological Methods, 2021, 185, 106204. | 1.6 | 1 |
| 27 | Fecal microbiota transplantation in human metabolic diseases: From a murky past to a bright future?. Cell Metabolism, 2021, 33, 1098-1110. | 16.2 | 93 |
| 28 | A Continuous Battle for Host-Derived Glycans Between a Mucus Specialist and a Glycan Generalist in vitro and in vivo. Frontiers in Microbiology, 2021, 12, 632454. | 3.5 | 15 |
| 29 | Does Day-to-Day Variability in Stool Consistency Link to the Fecal Microbiota Composition?. Frontiers in Cellular and Infection Microbiology, 2021, 11, 639667. | 3.9 | 11 |
| 30 | Early-life gut microbiota and its connection to metabolic health in children: Perspective on ecological drivers and need for quantitative approach. EBioMedicine, 2021, 69, 103475. | 6.1 | 47 |
| 31 | Fecal Bacteria Implicated in Biofilm Production Are Enriched and Associate to Gastrointestinal Symptoms in Patients With APECED â€“ A Pilot Study. Frontiers in Immunology, 2021, 12, 668219. | 4.8 | 6 |
| 32 | Genomic diversity and ecology of human-associated Akkermansia species in the gut microbiome revealed by extensive metagenomic assembly. Genome Biology, 2021, 22, 209. | 8.8 | 65 |
| 33 | Conversion of dietary inositol into propionate and acetate by commensal Anaerostipes associates with host health. Nature Communications, 2021, 12, 4798. | 12.8 | 76 |
| 34 | Authors' Response: â€œ<scp>Akkermansia muciniphila</scp> reduces <scp>Porphyromonas gingivalis</scp> induced inflammation and periodontal bone destructionâ€• Journal of Clinical Periodontology, 2021, 48, 1493-1494. | 4.9 | 1 |
| 35 | The CRCbiome study: a large prospective cohort study examining the role of lifestyle and the gut microbiome in colorectal cancer screening participants. BMC Cancer, 2021, 21, 930. | 2.6 | 22 |
| 36 | Dietary advanced glycation endproducts (AGEs) increase their concentration in plasma and tissues, result in inflammation and modulate gut microbial composition in mice; evidence for reversibility. Food Research International, 2021, 147, 110547. | 6.2 | 41 |

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|---|---|---|---|
| 37 | Liraglutide and sitagliptin have no effect on intestinal microbiota composition: A 12-week randomized placebo-controlled trial in adults with type 2 diabetes. Diabetes and Metabolism, 2021, 47, 101223. | 2.9 | 25 |
| 38 | Remarkable Metabolic Versatility of the Commensal Bacteria Eubacterium hallii and Intestinimonas butyriciproducens: Potential Next-Generation Therapeutic Microbes. Microorganisms for Sustainability, 2021, , 139-151. | 0.7 | 5 |
| 39 | Selection and characterization of a SpaCBA pilus-secreting food-grade derivative of Lacticaseibacillus rhamnosus GG. Applied Microbiology and Biotechnology, 2021, 105, 1123-1131. | 3.6 | 4 |
| 40 | Duodenal Anaerobutyricum soehngenii infusion stimulates GLP-1 production, ameliorates glycaemic control and beneficially shapes the duodenal transcriptome in metabolic syndrome subjects: a randomised double-blind placebo-controlled cross-over study. Gut, 2021, , gutjnl-2020-323297. | 12.1 | 16 |
| 41 | Genomic convergence between Akkermansia muciniphila in different mammalian hosts. BMC Microbiology, 2021, 21, 298. | 3.3 | 10 |
| 42 | Effects of fecal microbiota transplant on DNA methylation in subjects with metabolic syndrome. Gut Microbes, 2021, 13, 1993513. | 9.8 | 25 |
| 43 | Implications of Gut Microbiota in Complex Human Diseases. International Journal of Molecular Sciences, 2021, 22, 12661. | 4.1 | 20 |
| 44 | Gut microbiota develop towards an adult profile in a sex-specific manner during puberty. Scientific Reports, 2021, 11, 23297. | 3.3 | 31 |
| 45 | Serum metabolite profiling yields insights into health promoting effect of A. muciniphila in human volunteers with a metabolic syndrome. Gut Microbes, 2021, 13, 1994270. | 9.8 | 24 |
| 46 | Molecular ecology of the yet uncultured bacterial Ct85-cluster in the mammalian gut. Anaerobe, 2020, 62, 102104. | 2.1 | 1 |
| 47 | Akkermansia muciniphila Exerts Lipidâ€Lowering and Immunomodulatory Effects without Affecting Neointima Formation in Hyperlipidemic APOE*3â€Leiden.CETP Mice. Molecular Nutrition and Food Research, 2020, 64, e1900732. | 3.3 | 39 |
| 48 | Akkermansia muciniphila reduces Porphyromonas gingivalisâ€induced inflammation and periodontal bone destruction. Journal of Clinical Periodontology, 2020, 47, 202-212. | 4.9 | 78 |
| 49 | Unravelling lactateâ€acetate and sugar conversion into butyrate by intestinal Anaerobutyricum and Anaerostipes species by comparative proteogenomics. Environmental Microbiology, 2020, 22, 4863-4875. | 3.8 | 36 |
| 50 | Characterization of Highly Mucus-Adherent Non-GMO Derivatives of Lacticaseibacillus rhamnosus GG. Frontiers in Bioengineering and Biotechnology, 2020, 8, 1024. | 4.1 | 9 |
| 51 | Maternal Fecal Microbiota Transplantation in Cesarean-Born Infants Rapidly Restores Normal Gut Microbial Development: A Proof-of-Concept Study. Cell, 2020, 183, 324-334.e5. | 28.9 | 188 |
| 52 | Does entry to center-based childcare affect gut microbial colonization in young infants?. Scientific Reports, 2020, 10, 10235. | 3.3 | 11 |
| 53 | Associations between Pro- and Anti-Inflammatory Gastro-Intestinal Microbiota, Diet, and Cognitive Functioning in Dutch Healthy Older Adults: The NU-AGE Study. Nutrients, 2020, 12, 3471. | 4.1 | 42 |
| 54 | Akkermansia muciniphila uses human milk oligosaccharides to thrive in the early life conditions in vitro. Scientific Reports, 2020, 10, 14330. | 3.3 | 96 |

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|---|---|---|---|
| 55 | Intestinimonas-like bacteria are important butyrate producers that utilize NÎµ-fructosyllysine and lysine in formula-fed infants and adults. Journal of Functional Foods, 2020, 70, 103974. | 3.4 | 47 |
| 56 | Bridging Bacteria and the Gut: Functional Aspects of Type IV Pili. Trends in Microbiology, 2020, 28, 340-348. | 7.7 | 50 |
| 57 | Back to the Roots: Revisiting the Use of the Fiber-Rich CichoriumÂintybusÂL. Taproots. Advances in Nutrition, 2020, 11, 878-890. | 6.4 | 22 |
| 58 | Pasteurized Akkermansia muciniphila increases whole-body energy expenditure and fecal energy excretion in diet-induced obese mice. Gut Microbes, 2020, 11, 1231-1245. | 9.8 | 134 |
| 59 | Mediterranean diet intervention alters the gut microbiome in older people reducing frailty and improving health status: the NU-AGE 1-year dietary intervention across five European countries. Gut, 2020, 69, 1218-1228. | 12.1 | 465 |
| 60 | Pasteurized Akkermansia muciniphila protects from fat mass gain but not from bone loss. American Journal of Physiology - Endocrinology and Metabolism, 2020, 318, E480-E491. | 3.5 | 27 |
| 61 | Effect of fructans, prebiotics and fibres on the human gut microbiome assessed by 16S rRNA-based approaches: a review. Beneficial Microbes, 2020, 11, 101-129. | 2.4 | 48 |
| 62 | Treatment with Anaerobutyricum soehngenii: a pilot study of safety and doseâ€“response effects on glucose metabolism in human subjects with metabolic syndrome. Npj Biofilms and Microbiomes, 2020, 6, 16. | 6.4 | 53 |
| 63 | Gut dysbacteriosis and intestinal disease: mechanism and treatment. Journal of Applied Microbiology, 2020, 129, 787-805. | 3.1 | 55 |
| 64 | Akkermansia and Microbial Degradation of Mucus in Cats and Dogs: Implications to the Growing Worldwide Epidemic of Pet Obesity. Veterinary Sciences, 2020, 7, 44. | 1.7 | 13 |
| 65 | Partial restoration of normal intestinal microbiota in morbidly obese women six months after bariatric surgery. PeerJ, 2020, 8, e10442. | 2.0 | 4 |
| 66 | Development of omicsâ€based protocols for the microbiological characterization of multiâ€strain formulations marketed as probiotics: the case of VSL#3. Microbial Biotechnology, 2019, 12, 1371-1386. | 4.2 | 30 |
| 67 | Universal membrane-labeling combined with expression of Katushka far-red fluorescent protein enables non-invasive dynamic and longitudinal quantitative 3D dual-color fluorescent imaging of multiple bacterial strains in mouse intestine. BMC Microbiology, 2019, 19, 167. | 3.3 | 5 |
| 68 | Supplementation with Akkermansia muciniphila in overweight and obese human volunteers: a proof-of-concept exploratory study. Nature Medicine, 2019, 25, 1096-1103. | 30.7 | 1,281 |
| 69 | Cohort profile: Finnish Health and Early Life Microbiota (HELMi) longitudinal birth cohort. BMJ Open, 2019, 9, e028500. | 1.9 | 25 |
| 70 | Allogenic Faecal Microbiota Transfer Induces Immune-Related Gene Sets in the Colon Mucosa of Patients with Irritable Bowel Syndrome. Biomolecules, 2019, 9, 586. | 4.0 | 5 |
| 71 | Mutual Metabolic Interactions in Co-cultures of the Intestinal Anaerostipes rhamnosivorans With an Acetogen, Methanogen, or Pectin-Degrader Affecting Butyrate Production. Frontiers in Microbiology, 2019, 10, 2449. | 3.5 | 43 |
| 72 | The Gut Microbiota in the First Decade of Life. Trends in Microbiology, 2019, 27, 997-1010. | 7.7 | 368 |

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|---|---|---|---|
| 73 | Intestinal epithelial N-acylphosphatidylethanolamine phospholipase D links dietary fat to metabolic adaptations in obesity and steatosis. Nature Communications, 2019, 10, 457. | 12.8 | 100 |
| 74 | The Effect of Psyllium Husk on Intestinal Microbiota in Constipated Patients and Healthy Controls. International Journal of Molecular Sciences, 2019, 20, 433. | 4.1 | 105 |
| 75 | Bicistronic Design-Based Continuous and High-Level Membrane Protein Production in Escherichia coli. ACS Synthetic Biology, 2019, 8, 1685-1690. | 3.8 | 23 |
| 76 | Enhanced nutrient supply and intestinal microbiota development in very low birth weight infants. Pediatric Research, 2019, 86, 323-332. | 2.3 | 5 |
| 77 | Anaerobic Degradation of N-Îµ-Carboxymethyllysine, a Major Glycation End-Product, by Human Intestinal Bacteria. Journal of Agricultural and Food Chemistry, 2019, 67, 6594-6602. | 5.2 | 40 |
| 78 | Gender-Specific Associations Between Saliva Microbiota and Body Size. Frontiers in Microbiology, 2019, 10, 767. | 3.5 | 51 |
| 79 | Akkermansia muciniphila ameliorates the age-related decline in colonic mucus thickness and attenuates immune activation in accelerated aging Ercc1â^'/Î”7 mice. Immunity and Ageing, 2019, 16, 6. | 4.2 | 130 |
| 80 | The Use of Defined Microbial Communities To Model Host-Microbe Interactions in the Human Gut. Microbiology and Molecular Biology Reviews, 2019, 83, . | 6.6 | 56 |
| 81 | Biotechnology of health-promoting bacteria. Biotechnology Advances, 2019, 37, 107369. | 11.7 | 53 |
| 82 | Reconstructing functional networks in the human intestinal tract using synthetic microbiomes. Current Opinion in Biotechnology, 2019, 58, 146-154. | 6.6 | 27 |
| 83 | Dynamics of the Gut Microbiota in Children Receiving Selective or Total Gut Decontamination Treatment during Hematopoietic Stem Cell Transplantation. Biology of Blood and Marrow Transplantation, 2019, 25, 1164-1171. | 2.0 | 18 |
| 84 | Metabolic improvement in obese patients after duodenalâ€“jejunal exclusion is associated with intestinal microbiota composition changes. International Journal of Obesity, 2019, 43, 2509-2517. | 3.4 | 19 |
| 85 | The Effect of Allogenic Versus Autologous Fecal Microbiota Transfer on Symptoms, Visceral Perception and Fecal and Mucosal Microbiota in Irritable Bowel Syndrome: A Randomized Controlled Study. Clinical and Translational Gastroenterology, 2019, 10, e00034. | 2.5 | 70 |
| 86 | Bowel Biofilms: Tipping Points between a Healthy and Compromised Gut?. Trends in Microbiology, 2019, 27, 17-25. | 7.7 | 97 |
| 87 | Long-term impact of oral vancomycin, ciprofloxacin and metronidazole on the gut microbiota in healthy humans. Journal of Antimicrobial Chemotherapy, 2019, 74, 782-786. | 3.0 | 78 |
| 88 | A Bifidobacterial pilusâ€associated protein promotes colonic epithelial proliferation. Molecular Microbiology, 2019, 111, 287-301. | 2.5 | 62 |
| 89 | Deciphering the trophic interaction between Akkermansia muciniphila and the butyrogenic gut commensal Anaerostipes caccae using a metatranscriptomic approach. Antonie Van Leeuwenhoek, 2018, 111, 859-873. | 1.7 | 90 |
| 90 | Modelâ€driven design of a minimal medium for Akkermansia muciniphila confirms mucus adaptation. Microbial Biotechnology, 2018, 11, 476-485. | 4.2 | 57 |

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|---|---|---|---|
| 91 | Enterotypes in the landscape of gut microbial community composition. Nature Microbiology, 2018, 3, 8-16. | 13.3 | 717 |
| 92 | Akkermansia muciniphila induces gut microbiota remodelling and controls islet autoimmunity in NOD mice. Gut, 2018, 67, 1445-1453. | 12.1 | 270 |
| 93 | Effect of Vegan Fecal Microbiota Transplantation on Carnitineâ€•and Cholineâ€Derived Trimethylamineâ€Nâ€Oxide Production and Vascular Inflammation in Patients With Metabolic Syndrome. Journal of the American Heart Association, 2018, 7, . | 3.7 | 164 |
| 94 | Reproducibility and repeatability of six high-throughput 16S rDNA sequencing protocols for microbiota profiling. Journal of Microbiological Methods, 2018, 147, 76-86. | 1.6 | 30 |
| 95 | Selected aspects of the human gut microbiota. Cellular and Molecular Life Sciences, 2018, 75, 81-82. | 5.4 | 19 |
| 96 | Rotavirus vaccine response correlates with the infant gut microbiota composition in Pakistan. Gut Microbes, 2018, 9, 93-101. | 9.8 | 142 |
| 97 | Mouse models for human intestinal microbiota research: a critical evaluation. Cellular and Molecular Life Sciences, 2018, 75, 149-160. | 5.4 | 380 |
| 98 | Probiotic supplementation restores normal microbiota composition and function in antibiotic-treated and in caesarean-born infants. Microbiome, 2018, 6, 182. | 11.1 | 160 |
| 99 | Fucosylated oligosaccharides in motherâ€™s milk alleviate the effects of caesarean birth on infant gut microbiota. Scientific Reports, 2018, 8, 13757. | 3.3 | 86 |
| 100 | A low FODMAP diet is associated with changes in the microbiota and reduction in breath hydrogen but not colonic volume in healthy subjects. PLoS ONE, 2018, 13, e0201410. | 2.5 | 74 |
| 101 | Flux, Impact, and Fate of Halogenated Xenobiotic Compounds in the Gut. Frontiers in Physiology, 2018, 9, 888. | 2.8 | 44 |
| 102 | Akkermansia muciniphila in the Human Gastrointestinal Tract: When, Where, and How?. Microorganisms, 2018, 6, 75. | 3.6 | 286 |
| 103 | Organic acid production from potato starch waste fermentation by rumen microbial communities from Dutch and Thai dairy cows. Biotechnology for Biofuels, 2018, 11, 13. | 6.2 | 30 |
| 104 | Fecal microbiota transplantation against intestinal colonization by extended spectrum beta-lactamase producing Enterobacteriaceae: a proof of principle study. BMC Research Notes, 2018, 11, 190. | 1.4 | 76 |
| 105 | Transcriptome analysis in whole blood reveals increased microbial diversity in schizophrenia. Translational Psychiatry, 2018, 8, 96. | 4.8 | 92 |
| 106 | Early life colonization of the human gut: microbes matter everywhere. Current Opinion in Microbiology, 2018, 44, 70-78. | 5.1 | 141 |
| 107 | Comparative genomic analysis of the multispecies probiotic-marketed product VSL#3. PLoS ONE, 2018, 13, e0192452. | 2.5 | 33 |
| 108 | Romboutsia hominis sp. nov., the first human gut-derived representative of the genus Romboutsia, isolated from ileostoma effluent. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3479-3486. | 1.7 | 37 |

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|---|---|---|---|
| 109 | Eubacterium maltosivorans sp. nov., a novel human intestinal acetogenic and butyrogenic bacterium with a versatile metabolism. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3546-3550. | 1.7 | 11 |
| 110 | Reclassification of Eubacterium hallii as Anaerobutyricum hallii gen. nov., comb. nov., and description of Anaerobutyricum soehngenii sp. nov., a butyrate and propionate-producing bacterium from infant faeces. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3741-3746. | 1.7 | 77 |
| 111 | Faecal and serum metabolomics in paediatric inflammatory bowel disease. Journal of Crohn's and Colitis, 2017, 11, jjw158. | 1.3 | 104 |
| 112 | Intestinal Microbiota Signatures Associated With Histological Liver Steatosis in Pediatricâ€Onset Intestinal Failure. Journal of Parenteral and Enteral Nutrition, 2017, 41, 238-248. | 2.6 | 75 |
| 113 | Akkermansia muciniphila and its role in regulating host functions. Microbial Pathogenesis, 2017, 106, 171-181. | 2.9 | 775 |
| 114 | Effects of plant stanol ester consumption on fasting plasma oxy(phyto)sterol concentrations as related to fecal microbiota characteristics. Journal of Steroid Biochemistry and Molecular Biology, 2017, 169, 46-53. | 2.5 | 27 |
| 115 | Complete Genome Sequence of Akkermansia glycaniphila Strain Pyt <sup>T</sup> , a Mucin-Degrading Specialist of the Reticulated Python Gut. Genome Announcements, 2017, 5, . | 0.8 | 16 |
| 116 | Homeostasis of the gut barrier and potential biomarkers. American Journal of Physiology - Renal Physiology, 2017, 312, G171-G193. | 3.4 | 408 |
| 117 | European consensus conference on faecal microbiota transplantation in clinical practice. Gut, 2017, 66, 569-580. | 12.1 | 793 |
| 118 | Childhood BMI in relation to microbiota in infancy and lifetime antibiotic use. Microbiome, 2017, 5, 26. | 11.1 | 99 |
| 119 | Microbiome yarns: microbiomology of curly and straight hair. Microbial Biotechnology, 2017, 10, 231-237. | 4.2 | 1 |
| 120 | Microbial shifts and signatures of long-term remission in ulcerative colitis after faecal microbiota transplantation. ISME Journal, 2017, 11, 1877-1889. | 9.8 | 157 |
| 121 | Enrichment of sulfidogenic bacteria from the human intestinal tract. FEMS Microbiology Letters, 2017, 364, . | 1.8 | 25 |
| 122 | Antibiotic-induced gut microbiota disruption during human endotoxemia: a randomised controlled study. Gut, 2017, 66, 1623-1630. | 12.1 | 69 |
| 123 | Complete Genome Sequence of Eubacterium hallii Strain L2-7. Genome Announcements, 2017, 5, . | 0.8 | 17 |
| 124 | Towards standards for human fecal sample processing in metagenomic studies. Nature Biotechnology, 2017, 35, 1069-1076. | 17.5 | 581 |
| 125 | Improvement of Insulin Sensitivity after Lean Donor Feces in Metabolic Syndrome Is Driven by Baseline Intestinal Microbiota Composition. Cell Metabolism, 2017, 26, 611-619.e6. | 16.2 | 689 |
| 126 | Preparation and preservation of viable Akkermansia muciniphila cells for therapeutic interventions. Beneficial Microbes, 2017, 8, 163-169. | 2.4 | 28 |

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|---|---|---|---|
| 127 | Action and function of Akkermansia muciniphila in microbiome ecology, health and disease. Bailliere's Best Practice and Research in Clinical Gastroenterology, 2017, 31, 637-642. | 2.4 | 191 |
| 128 | Anti-Infective Effect of Adhesive Probiotic Lactobacillus in Fish is Correlated With Their Spatial Distribution in the Intestinal Tissue. Scientific Reports, 2017, 7, 13195. | 3.3 | 53 |
| 129 | C4Bgene influences intestinal microbiota through complement activation in patients with paediatric-onset inflammatory bowel disease. Clinical and Experimental Immunology, 2017, 190, 394-405. | 2.6 | 20 |
| 130 | The contribution of microbial biotechnology to sustainable development goals. Microbial Biotechnology, 2017, 10, 984-987. | 4.2 | 73 |
| 131 | Encapsulation of the therapeutic microbe Akkermansia muciniphila in a double emulsion enhances survival in simulated gastric conditions. Food Research International, 2017, 102, 372-379. | 6.2 | 56 |
| 132 | Variation of mucin adhesion, cell surface characteristics, and molecular mechanisms among Lactobacillus plantarum isolated from different habitats. Applied Microbiology and Biotechnology, 2017, 101, 7663-7674. | 3.6 | 34 |
| 133 | Microbial Metabolic Networks at the Mucus Layer Lead to Diet-Independent Butyrate and Vitamin B <sub>12</sub> Production by Intestinal Symbionts. MBio, 2017, 8, . | 4.1 | 269 |
| 134 | In vitro colonisation of the distal colon by Akkermansia muciniphila is largely mucin and pH dependent. Beneficial Microbes, 2017, 8, 81-96. | 2.4 | 80 |
| 135 | More than just a gut feeling: constraint-based genome-scale metabolic models for predicting functions of human intestinal microbes. Microbiome, 2017, 5, 78. | 11.1 | 54 |
| 136 | Genome-Scale Model and Omics Analysis of Metabolic Capacities of Akkermansia muciniphila Reveal a Preferential Mucin-Degrading Lifestyle. Applied and Environmental Microbiology, 2017, 83, . | 3.1 | 170 |
| 137 | Biochemical characterization of the xylan hydrolysis profile of the extracellular endo-xylanase from Geobacillus thermodenitrificans T12. BMC Biotechnology, 2017, 17, 44. | 3.3 | 15 |
| 138 | An Inducible Operon Is Involved in Inulin Utilization in Lactobacillus plantarum Strains, as Revealed by Comparative Proteogenomics and Metabolic Profiling. Applied and Environmental Microbiology, 2017, 83, . | 3.1 | 43 |
| 139 | Critically ill patients demonstrate large interpersonal variation in intestinal microbiota dysregulation: a pilot study. Intensive Care Medicine, 2017, 43, 59-68. | 8.2 | 183 |
| 140 | Significant Correlation Between the Infant Gut Microbiome and Rotavirus Vaccine Response in Rural Ghana. Journal of Infectious Diseases, 2017, 215, 34-41. | 4.0 | 227 |
| 141 | A purified membrane protein from Akkermansia muciniphila or the pasteurized bacterium improves metabolism in obese and diabetic mice. Nature Medicine, 2017, 23, 107-113. | 30.7 | 1,451 |
| 142 | Intestinal microbiome landscaping: insight in community assemblage and implications for microbial modulation strategies. FEMS Microbiology Reviews, 2017, 41, 182-199. | 8.6 | 182 |
| 143 | Bacteriological and Immunological Profiling of Meconium and Fecal Samples from Preterm Infants: A Two-Year Follow-Up Study. Nutrients, 2017, 9, 1293. | 4.1 | 18 |
| 144 | Effects of Soluble Corn Fiber Alone or in Synbiotic Combination with Lactobacillus rhamnosus GG and the Pilus-Deficient Derivative GG-PB12 on Fecal Microbiota, Metabolism, and Markers of Immune Function: A Randomized, Double-Blind, Placebo-Controlled, Crossover Study in Healthy Elderly (Saimes Study). Frontiers in Immunology, 2017, 8, 1443. | 4.8 | 67 |

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|---|---|---|---|
| 145 | Safety of Novel Microbes for Human Consumption: Practical Examples of Assessment in the European Union. Frontiers in Microbiology, 2017, 8, 1725. | 3.5 | 125 |
| 146 | Next-Generation Beneficial Microbes: The Case of Akkermansia muciniphila. Frontiers in Microbiology, 2017, 8, 1765. | 3.5 | 713 |
| 147 | Feasibility of Metatranscriptome Analysis from Infant Gut Microbiota: Adaptation to Solid Foods Results in Increased Activity of Firmicutes at Six Months. International Journal of Microbiology, 2017, 2017, 1-9. | 2.3 | 11 |
| 148 | Distinct fecal and oral microbiota composition in human type 1 diabetes, an observational study. PLoS ONE, 2017, 12, e0188475. | 2.5 | 163 |
| 149 | Pili-like proteins of Akkermansia muciniphila modulate host immune responses and gut barrier function. PLoS ONE, 2017, 12, e0173004. | 2.5 | 340 |
| 150 | Draft Genome Sequences of the Aerobic Strains Lactobacillus gasseri AL3 and AL5. Genome Announcements, 2017, 5, . | 0.8 | 5 |
| 151 | Streptococcus caviae sp. nov., isolated from guinea pig faecal samples. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1551-1556. | 1.7 | 10 |
| 152 | Microbe Profile: Akkermansia muciniphila: a conserved intestinal symbiont that acts as the gatekeeper of our mucosa. Microbiology (United Kingdom), 2017, 163, 646-648. | 1.8 | 107 |
| 153 | Genotypic and phenotypic diversity of Lactobacillus rhamnosus clinical isolates, their comparison with strain GG and their recognition by complement system. PLoS ONE, 2017, 12, e0176739. | 2.5 | 21 |
| 154 | Intestinal Ralstonia pickettii augments glucose intolerance in obesity. PLoS ONE, 2017, 12, e0181693. | 2.5 | 53 |
| 155 | Genomic and functional analysis ofRomboutsia ilealisCRIB<sup>T</sup>reveals adaptation to the small intestine. PeerJ, 2017, 5, e3698. | 2.0 | 88 |
| 156 | Antibiotic use in childhood alters the gut microbiota and predisposes to overweight. Microbial Cell, 2016, 3, 296-298. | 3.2 | 58 |
| 157 | Characterization of Outer Membrane Proteome of Akkermansia muciniphila Reveals Sets of Novel Proteins Exposed to the Human Intestine. Frontiers in Microbiology, 2016, 7, 1157. | 3.5 | 106 |
| 158 | Lactobacillus rhamnosus GG Intake Modifies Preschool Childrenâ€™s Intestinal Microbiota, Alleviates Penicillin-Associated Changes, and Reduces Antibiotic Use. PLoS ONE, 2016, 11, e0154012. | 2.5 | 62 |
| 159 | Faecal Metaproteomic Analysis Reveals a Personalized and Stable Functional Microbiome and Limited Effects of a Probiotic Intervention in Adults. PLoS ONE, 2016, 11, e0153294. | 2.5 | 70 |
| 160 | Integrated In Silico Analysis of Pathway Designs for Synthetic Photo-Electro-Autotrophy. PLoS ONE, 2016, 11, e0157851. | 2.5 | 9 |
| 161 | Lactobacillus plantarum <scp>WCFS</scp>1 and its host interaction: a dozen years after the genome. Microbial Biotechnology, 2016, 9, 452-465. | 4.2 | 115 |
| 162 | The Variable Regions ofLactobacillus rhamnosusGenomes Reveal the Dynamic Evolution of Metabolic and Host-Adaptation Repertoires. Genome Biology and Evolution, 2016, 8, 1889-1905. | 2.5 | 53 |

| # | Article | IF | Citations |
|---|---|---|---|
| 163 | Genome and proteome analysis of <scp>P</scp>seudomonas chloritidismutansâ€...<scp>AW</scp>â€¡<scp><sup>T</sup></scp> that grows on nâ€decane with chlorate or oxygen as electron acceptor. Environmental Microbiology, 2016, 18, 3247-3257. | 3.8 | 21 |
| 164 | Complete Genome Sequence of Enterococcus faecium Commensal Isolate E1002. Genome Announcements, 2016, 4, . | 0.8 | 2 |
| 165 | Sugar Coating the Envelope: Glycoconjugates for Microbeâ€“Host Crosstalk. Trends in Microbiology, 2016, 24, 853-861. | 7.7 | 44 |
| 166 | Oral treatment with Eubacterium hallii improves insulin sensitivity in db/db mice. Npj Biofilms and Microbiomes, 2016, 2, 16009. | 6.4 | 159 |
| 167 | Polymorphisms, Chromosomal Rearrangements, and Mutator Phenotype Development during Experimental Evolution of Lactobacillus rhamnosus GG. Applied and Environmental Microbiology, 2016, 82, 3783-3792. | 3.1 | 27 |
| 168 | Durable coexistence of donor and recipient strains after fecal microbiota transplantation. Science, 2016, 352, 586-589. | 12.6 | 461 |
| 169 | How to Manipulate the Microbiota: Fecal Microbiota Transplantation. Advances in Experimental Medicine and Biology, 2016, 902, 143-153. | 1.6 | 25 |
| 170 | Adaptation of Akkermansia muciniphila to the Oxic-Anoxic Interface of the Mucus Layer. Applied and Environmental Microbiology, 2016, 82, 6983-6993. | 3.1 | 101 |
| 171 | Lactobacillus rhamnosus GG Outcompetes Enterococcus faecium via Mucus-Binding Pili: Evidence for a Novel and Heterospecific Probiotic Mechanism. Applied and Environmental Microbiology, 2016, 82, 5756-5762. | 3.1 | 93 |
| 172 | Long-term effects on luminal and mucosal microbiota and commonly acquired taxa in faecal microbiota transplantation for recurrent Clostridium difficile infection. BMC Medicine, 2016, 14, 155. | 5.5 | 86 |
| 173 | Harnessing the power of microbial autotrophy. Nature Reviews Microbiology, 2016, 14, 692-706. | 28.6 | 189 |
| 174 | Causality of small and large intestinal microbiota in weight regulation and insulin resistance. Molecular Metabolism, 2016, 5, 759-770. | 6.5 | 142 |
| 175 | Healthy human gut phageome. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10400-10405. | 7.1 | 439 |
| 176 | Antibiotic-Induced Gut Microbiota Disruption Decreases TNF-Î± Release by Mononuclear Cells in Healthy Adults. Clinical and Translational Gastroenterology, 2016, 7, e186. | 2.5 | 18 |
| 177 | Comparative genomics and physiology of the butyrateâ€producing bacterium Intestinimonas butyriciproducens. Environmental Microbiology Reports, 2016, 8, 1024-1037. | 2.4 | 104 |
| 178 | Isolation of a genetically accessible thermophilic xylan degrading bacterium from compost. Biotechnology for Biofuels, 2016, 9, 210. | 6.2 | 20 |
| 179 | Interaction of mouse splenocytes and macrophages with bacterial strains in vitro: the effect of age in the immune response. Beneficial Microbes, 2016, 7, 275-287. | 2.4 | 10 |
| 180 | Complete genome sequence of thermophilic Bacillus smithii type strain DSM 4216T. Standards in Genomic Sciences, 2016, 11, 52. | 1.5 | 13 |

| # | Article | IF | Citations |
|---|---|---|---|
| 181 | Akkermansia muciniphila: a novel functional microbe with probiotic properties. Beneficial Microbes, 2016, 7, 571-584. | 2.4 | 104 |
| 182 | Association of Early-Life Antibiotic Use and Protective Effects of Breastfeeding. JAMA Pediatrics, 2016, 170, 750. | 6.2 | 76 |
| 183 | Unravelling the oneâ€carbon metabolism of the acetogen <scp>S</scp>poromusa strain <scp>A</scp>n4 by genome and proteome analysis. Environmental Microbiology, 2016, 18, 2843-2855. | 3.8 | 25 |
| 184 | Intestinal microbiome is related to lifetime antibiotic use in Finnish pre-school children. Nature Communications, 2016, 7, 10410. | 12.8 | 557 |
| 185 | Next Generation Prokaryotic Engineering: The CRISPR-Cas Toolkit. Trends in Biotechnology, 2016, 34, 575-587. | 9.3 | 113 |
| 186 | Isolation and whole genome sequencing of a Ruminococcus-like bacterium, associated with irritable bowel syndrome. Anaerobe, 2016, 39, 60-67. | 2.1 | 24 |
| 187 | Discordant temporal development of bacterial phyla and the emergence of core in the fecal microbiota of young children. ISME Journal, 2016, 10, 1002-1014. | 9.8 | 104 |
| 188 | The gut microbiota plays a protective role in the host defence against pneumococcal pneumonia. Gut, 2016, 65, 575-583. | 12.1 | 601 |
| 189 | Akkermansia glycaniphila sp. nov., an anaerobic mucin-degrading bacterium isolated from reticulated python faeces. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4614-4620. | 1.7 | 68 |
| 190 | Probiotic Gut Microbiota Isolate Interacts with Dendritic Cells via Glycosylated Heterotrimeric Pili. PLoS ONE, 2016, 11, e0151824. | 2.5 | 62 |
| 191 | The N-Terminal GYPSY Motif Is Required for Pilin-Specific Sortase SrtC1 Functionality in Lactobacillus rhamnosus Strain GG. PLoS ONE, 2016, 11, e0153373. | 2.5 | 8 |
| 192 | In tribute to Bernard Witholt. Microbial Biotechnology, 2015, 8, 621-621. | 4.2 | 0 |
| 193 | Production of butyrate from lysine and the Amadori product fructoselysine by a human gut commensal. Nature Communications, 2015, 6, 10062. | 12.8 | 199 |
| 194 | Microbial biofilms and the human intestinal microbiome. Npj Biofilms and Microbiomes, 2015, 1, 15005. | 6.4 | 127 |
| 195 | Application of the Human Intestinal Tract Chip to the non-human primate gut microbiota. Beneficial Microbes, 2015, 6, 271-276. | 2.4 | 3 |
| 196 | Improved taxonomic assignment of human intestinal 16S rRNA sequences by a dedicated reference database. BMC Genomics, 2015, 16, 1056. | 2.8 | 127 |
| 197 | Establishment of markerless gene deletion tools in thermophilic Bacillus smithii and construction of multiple mutant strains. Microbial Cell Factories, 2015, 14, 99. | 4.0 | 18 |
| 198 | The relationship between faecal-associated and mucosal-associated microbiota in irritable bowel syndrome patients and healthy subjects. Alimentary Pharmacology and Therapeutics, 2015, 42, 1211-1221. | 3.7 | 117 |

| # | Article | IF | Citations |
|---|---|---|---|
| 199 | Colonic metaproteomic signatures of active bacteria and the host in obesity. Proteomics, 2015, 15, 3544-3552. | 2.2 | 70 |
| 200 | Fecal microbiota transplantation as novel therapy in gastroenterology: A systematic review. World Journal of Gastroenterology, 2015, 21, 5359. | 3.3 | 204 |
| 201 | Phylogenetic and Metabolic Tracking of Gut Microbiota during Perinatal Development. PLoS ONE, 2015, 10, e0137347. | 2.5 | 84 |
| 202 | Metagenomics meets time series analysis: unraveling microbial community dynamics. Current Opinion in Microbiology, 2015, 25, 56-66. | 5.1 | 345 |
| 203 | Fecal Microbiota in Pediatric Inflammatory Bowel Disease and Its Relation to Inflammation. American Journal of Gastroenterology, 2015, 110, 921-930. | 0.4 | 193 |
| 204 | A novel consortium of Lactobacillus rhamnosus and Streptococcus thermophilus for increased access to functional fermented foods. Microbial Cell Factories, 2015, 14, 195. | 4.0 | 58 |
| 205 | Isolation and Screening of Thermophilic Bacilli from Compost for Electrotransformation and Fermentation: Characterization of Bacillus smithii ET 138 as a New Biocatalyst. Applied and Environmental Microbiology, 2015, 81, 1874-1883. | 3.1 | 42 |
| 206 | Altered faecal and mucosal microbial composition in postâ€infectious irritable bowel syndrome patients correlates with mucosal lymphocyte phenotypes and psychological distress. Alimentary Pharmacology and Therapeutics, 2015, 41, 342-351. | 3.7 | 125 |
| 207 | Intestinal Microbiota And Diet in IBS: Causes, Consequences, or Epiphenomena?. American Journal of Gastroenterology, 2015, 110, 278-287. | 0.4 | 283 |
| 208 | Severity of atopic disease inversely correlates with intestinal microbiota diversity and butyrate-producing bacteria. Allergy: European Journal of Allergy and Clinical Immunology, 2015, 70, 241-244. | 5.7 | 194 |
| 209 | Maternal prenatal stress is associated with the infant intestinal microbiota. Psychoneuroendocrinology, 2015, 53, 233-245. | 2.7 | 359 |
| 210 | Genomic, Proteomic, and Biochemical Analysis of the Organohalide Respiratory Pathway in Desulfitobacterium dehalogenans. Journal of Bacteriology, 2015, 197, 893-904. | 2.2 | 43 |
| 211 | Lactobacillus rhamnosus GG and its SpaC pilus adhesin modulate inflammatory responsiveness and TLR-related gene expression in the fetal human gut. Pediatric Research, 2015, 77, 528-535. | 2.3 | 52 |
| 212 | The Mucosa-associated Microbiota of PSC Patients is Characterized by Low Diversity and Low Abundance of Uncultured Clostridiales II. Journal of Crohn's and Colitis, 2015, 9, 342-348. | 1.3 | 106 |
| 213 | Mining microbial metatranscriptomes for expression of antibiotic resistance genes under natural conditions. Scientific Reports, 2015, 5, 11981. | 3.3 | 50 |
| 214 | Fat, fibre and cancer risk in African Americans and rural Africans. Nature Communications, 2015, 6, 6342. | 12.8 | 761 |
| 215 | Versatile (Bio)Functionalization of Bromo-Terminated Phosphonate-Modified Porous Aluminum Oxide. Langmuir, 2015, 31, 5633-5644. | 3.5 | 10 |
| 216 | Helsinki alert of biodiversity and health. Annals of Medicine, 2015, 47, 218-225. | 3.8 | 95 |

| # | Article | IF | Citations |
|---|---|---|---|
| 217 | Findings From a Randomized Controlled Trial of Fecal Transplantation for Patients With Ulcerative Colitis. Gastroenterology, 2015, 149, 110-118.e4. | 1.3 | 769 |
| 218 | Akkermansia muciniphila Adheres to Enterocytes and Strengthens the Integrity of the Epithelial Cell Layer. Applied and Environmental Microbiology, 2015, 81, 3655-3662. | 3.1 | 437 |
| 219 | Navigating through metaproteomics data: A logbook of database searching. Proteomics, 2015, 15, 3439-3453. | 2.2 | 128 |
| 220 | Protein costs do not explain evolution of metabolic strategies and regulation of ribosomal content: does protein investment explain an anaerobic bacterial <scp>C</scp>rabtree effect?. Molecular Microbiology, 2015, 97, 77-92. | 2.5 | 57 |
| 221 | Microbial signatures in post-infectious irritable bowel syndrome â€“ toward patient stratification for improved diagnostics and treatment. Gut Microbes, 2015, 6, 364-369. | 9.8 | 51 |
| 222 | Akkermansia muciniphilaandHelicobacter typhloniusmodulate intestinal tumor development in mice. Carcinogenesis, 2015, 36, 1388-1396. | 2.8 | 87 |
| 223 | Expanding the biotechnology potential of lactobacilli through comparative genomics of 213 strains and associated genera. Nature Communications, 2015, 6, 8322. | 12.8 | 488 |
| 224 | Discovery of intramolecular trans-sialidases in human gut microbiota suggests novel mechanisms of mucosal adaptation. Nature Communications, 2015, 6, 7624. | 12.8 | 143 |
| 225 | Effects of bowel cleansing on the intestinal microbiota. Gut, 2015, 64, 1562-1568. | 12.1 | 201 |
| 226 | Simulating distal gut mucosal and luminal communities using packed-column biofilm reactors and an in vitro chemostat model. Journal of Microbiological Methods, 2015, 108, 36-44. | 1.6 | 47 |
| 227 | Inulin-type fructans modulate intestinal Bifidobacterium species populations and decrease fecal short-chain fatty acids in obese women. Clinical Nutrition, 2015, 34, 501-507. | 5.0 | 220 |
| 228 | The gut microbiota in internal medicine: implications for health and disease. Netherlands Journal of Medicine, 2015, 73, 61-8. | 0.5 | 46 |
| 229 | Gut Microbiota Signatures Predict Host and Microbiota Responses to Dietary Interventions in Obese Individuals. PLoS ONE, 2014, 9, e90702. | 2.5 | 163 |
| 230 | Tipping elements in the human intestinal ecosystem. Nature Communications, 2014, 5, 4344. | 12.8 | 217 |
| 231 | Anaerostipes rhamnosivorans sp. nov., a human intestinal, butyrate-forming bacterium. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 787-793. | 1.7 | 62 |
| 232 | The Salivary Scavenger and Agglutinin in Early Life: Diverse Roles in Amniotic Fluid and in the Infant Intestine. Journal of Immunology, 2014, 193, 5240-5248. | 0.8 | 21 |
| 233 | Functional Identification of Conserved Residues Involved in Lactobacillus rhamnosus Strain GG Sortase Specificity and Pilus Biogenesis. Journal of Biological Chemistry, 2014, 289, 15764-15775. | 3.4 | 25 |
| 234 | Fecal Transplantation Treatment of Antibiotic-Induced, Noninfectious Colitis and Long-Term Microbiota Follow-Up. Case Reports in Medicine, 2014, 2014, 1-7. | 0.7 | 37 |

| # | Article | IF | Citations |
|---|---|---|---|
| 235 | Stimulation of colonic motility by oral <scp>PEG</scp> electrolyte bowel preparation assessed by <scp>MRI</scp>: comparison of split vs single dose. Neurogastroenterology and Motility, 2014, 26, 1426-1436. | 3.0 | 44 |
| 236 | Use of non-growing Lactococcus lactis cell suspensions for production of volatile metabolites with direct relevance for flavour formation during dairy fermentations. Microbial Cell Factories, 2014, 13, 176. | 4.0 | 25 |
| 237 | Effect of diet on the intestinal microbiota and its activity. Current Opinion in Gastroenterology, 2014, 30, 189-195. | 2.3 | 74 |
| 238 | Intestinal microbiota during early life â€“ impact on health and disease. Proceedings of the Nutrition Society, 2014, 73, 457-469. | 1.0 | 54 |
| 239 | Differential Modulation by Akkermansia muciniphila and Faecalibacterium prausnitzii of Host Peripheral Lipid Metabolism and Histone Acetylation in Mouse Gut Organoids. MBio, 2014, 5, . | 4.1 | 376 |
| 240 | Metaproteomics of our microbiome â€" Developing insight in function and activity in man and model systems. Journal of Proteomics, 2014, 97, 3-16. | 2.4 | 97 |
| 241 | The first 1000 cultured species of the human gastrointestinal microbiota. FEMS Microbiology Reviews, 2014, 38, 996-1047. | 8.6 | 923 |
| 242 | Impact of oral vancomycin on gut microbiota, bile acid metabolism, and insulin sensitivity. Journal of Hepatology, 2014, 60, 824-831. | 3.7 | 475 |
| 243 | Maintenance of a healthy trajectory of the intestinal microbiome during aging: A dietary approach. Mechanisms of Ageing and Development, 2014, 136-137, 70-75. | 4.6 | 72 |
| 244 | Impact of Diet on Human Intestinal Microbiota and Health. Annual Review of Food Science and Technology, 2014, 5, 239-262. | 9.9 | 173 |
| 245 | Faecal microbiota composition and hostâ€“microbe cross-talk following gastroenteritis and in postinfectious irritable bowel syndrome. Gut, 2014, 63, 1737-1745. | 12.1 | 282 |
| 246 | Stability of (Bio)Functionalized Porous Aluminum Oxide. Langmuir, 2014, 30, 1311-1320. | 3.5 | 38 |
| 247 | Immunostimulatory CpG motifs in the genomes of gut bacteria and their role in human health and disease. Journal of Medical Microbiology, 2014, 63, 293-308. | 1.8 | 54 |
| 248 | Genomic Characterization of Non-Mucus-Adherent Derivatives of Lactobacillus rhamnosus GG Reveals Genes Affecting Pilus Biogenesis. Applied and Environmental Microbiology, 2014, 80, 7001-7009. | 3.1 | 22 |
| 249 | The microbial eukaryoteBlastocystisis a prevalent and diverse member of the healthy human gut microbiota. FEMS Microbiology Ecology, 2014, 90, 326-330. | 2.7 | 208 |
| 250 | Reset of a critically disturbed microbial ecosystem: faecal transplant in recurrent Clostridium difficile infection. ISME Journal, 2014, 8, 1621-1633. | 9.8 | 172 |
| 251 | Aberrant gut microbiota composition at the onset of type 1 diabetes in young children. Diabetologia, 2014, 57, 1569-1577. | 6.3 | 274 |
| 252 | Impact of diet and individual variation on intestinal microbiota composition and fermentation products in obese men. ISME Journal, 2014, 8, 2218-2230. | 9.8 | 489 |

| # | Article | IF | Citations |
|---|---|---|---|
| 253 | Functional genomics of lactic acid bacteria: from food to health. Microbial Cell Factories, 2014, 13, S8. | 4.0 | 132 |
| 254 | Faecal Microbiota Composition in Adults Is Associated with the FUT2 Gene Determining the Secretor Status. PLoS ONE, 2014, 9, e94863. | 2.5 | 129 |
| 255 | Human intestinal metagenomics: state of the art and future. Current Opinion in Microbiology, 2013, 16, 232-239. | 5.1 | 62 |
| 256 | Microarray analysis reveals marked intestinal microbiota aberrancy in infants having eczema compared to healthy children in at-risk for atopic disease. BMC Microbiology, 2013, 13, 12. | 3.3 | 127 |
| 257 | Duodenal microbiota composition and mucosal homeostasis in pediatric celiac disease. BMC Gastroenterology, 2013, 13, 113. | 2.0 | 124 |
| 258 | Glycobiome: Bacteria and mucus at the epithelial interface. Bailliere's Best Practice and Research in Clinical Gastroenterology, 2013, 27, 25-38. | 2.4 | 171 |
| 259 | Evaluation of microbial community reproducibility, stability and composition in a human distal gut chemostat model. Journal of Microbiological Methods, 2013, 95, 167-174. | 1.6 | 144 |
| 260 | Richness of human gut microbiome correlates with metabolic markers. Nature, 2013, 500, 541-546. | 27.8 | 3,641 |
| 261 | Metagenomic species profiling using universal phylogenetic marker genes. Nature Methods, 2013, 10, 1196-1199. | 19.0 | 442 |
| 262 | Potential of proton-pumping rhodopsins: engineering photosystems into microorganisms. Trends in Biotechnology, 2013, 31, 633-642. | 9.3 | 23 |
| 263 | Towards metagenome-scale models for industrial applicationsâ€"the case of Lactic Acid Bacteria. Current Opinion in Biotechnology, 2013, 24, 200-206. | 6.6 | 43 |
| 264 | Genome-scale metabolic model for Lactococcus lactis MG1363 and its application to the analysis of flavor formation. Applied Microbiology and Biotechnology, 2013, 97, 8729-8739. | 3.6 | 109 |
| 265 | Duodenal Infusion of Donor Feces for RecurrentClostridium difficile. New England Journal of Medicine, 2013, 368, 407-415. | 27.0 | 3,157 |
| 266 | The intestinal microbiota and host immune interactions in the critically ill. Trends in Microbiology, 2013, 21, 221-229. | 7.7 | 105 |
| 267 | Adhesion and Nanomechanics of Pili from the Probiotic Lactobacillus rhamnosus GG. ACS Nano, 2013, 7, 3685-3697. | 14.6 | 148 |
| 268 | Translating the human microbiome. Nature Biotechnology, 2013, 31, 304-308. | 17.5 | 30 |
| 269 | Human intestinal microbiota composition is associated with local and systemic inflammation in obesity. Obesity, 2013, 21, E607-15. | 3.0 | 469 |
| 270 | Obesity, non-alcoholic fatty liver disease, and atherothrombosis: a role for the intestinal microbiota?. Clinical Microbiology and Infection, 2013, 19, 331-337. | 6.0 | 19 |

| # | Article | IF | Citations |
|---|---|---|---|
| 271 | Butyrate-producing Clostridium cluster XIVa species specifically colonize mucins in an in vitro gut model. ISME Journal, 2013, 7, 949-961. | 9.8 | 501 |
| 272 | A gut prediction. Nature, 2013, 498, 48-49. | 27.8 | 66 |
| 273 | Longâ€term monitoring of the human intestinal microbiota composition. Environmental Microbiology, 2013, 15, 1146-1159. | 3.8 | 195 |
| 274 | Insight into the prebiotic concept: lessons from an exploratory, double blind intervention study with inulin-type fructans in obese women. Gut, 2013, 62, 1112-1121. | 12.1 | 632 |
| 275 | Cross-talk between Akkermansia muciniphila and intestinal epithelium controls diet-induced obesity. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 9066-9071. | 7.1 | 3,474 |
| 276 | Phylogenetic Analysis of Dysbiosis in Ulcerative Colitis During Remission. Inflammatory Bowel Diseases, 2013, 19, 481-488. | 1.9 | 285 |
| 277 | Microbiota conservation and BMI signatures in adult monozygotic twins. ISME Journal, 2013, 7, 707-717. | 9.8 | 311 |
| 278 | Comparative Genomic and Functional Analysis of 100 Lactobacillus rhamnosus Strains and Their Comparison with Strain GG. PLoS Genetics, 2013, 9, e1003683. | 3.5 | 180 |
| 279 | Intake of Whole-Grain and Fiber-Rich Rye Bread Versus Refined Wheat Bread Does Not Differentiate Intestinal Microbiota Composition in Finnish Adults with Metabolic Syndrome. Journal of Nutrition, 2013, 143, 648-655. | 2.9 | 85 |
| 280 | Intestinal Microbiota of Infants With Colic: Development and Specific Signatures. Pediatrics, 2013, 131, e550-e558. | 2.1 | 213 |
| 281 | Comparative Genomic and Functional Analysis of Lactobacillus casei and Lactobacillus rhamnosus Strains Marketed as Probiotics. Applied and Environmental Microbiology, 2013, 79, 1923-1933. | 3.1 | 108 |
| 282 | Comparative genome analysis of <scp>L</scp>actobacillus casei strains isolated from <scp>A</scp>ctimel and <scp>Y</scp>akult products reveals marked similarities and points to a common origin. Microbial Biotechnology, 2013, 6, 576-587. | 4.2 | 27 |
| 283 | Fame and future of faecal transplantations â€“ developing nextâ€generation therapies with synthetic microbiomes. Microbial Biotechnology, 2013, 6, 316-325. | 4.2 | 57 |
| 284 | Crying in infants. Gut Microbes, 2013, 4, 416-421. | 9.8 | 78 |
| 285 | Intestinal Microbiota in Healthy U.S. Young Children and Adultsâ€”A High Throughput Microarray Analysis. PLoS ONE, 2013, 8, e64315. | 2.5 | 196 |
| 286 | Using Recombinant Lactococci as an Approach to Dissect the Immunomodulating Capacity of Surface Piliation in Probiotic Lactobacillus rhamnosus GG. PLoS ONE, 2013, 8, e64416. | 2.5 | 55 |
| 287 | Novel Polyfermentor Intestinal Model (PolyFermS) for Controlled Ecological Studies: Validation and Effect of pH. PLoS ONE, 2013, 8, e77772. | 2.5 | 82 |
| 288 | Associations between the human intestinal microbiota,Lactobacillus rhamnosusGG and serum lipids indicated by integrated analysis of high-throughput profiling data. PeerJ, 2013, 1, e32. | 2.0 | 166 |

| # | Article | IF | Citations |
|---|---|---|---|
| 289 | Characterization of the SpaCBA Pilus Fibers in the Probiotic Lactobacillus rhamnosus GG. Applied and Environmental Microbiology, 2012, 78, 2337-2344. | 3.1 | 130 |
| 290 | Standardized Assay Medium To Measure Lactococcus lactis Enzyme Activities while Mimicking Intracellular Conditions. Applied and Environmental Microbiology, 2012, 78, 134-143. | 3.1 | 66 |
| 291 | PS14 - 68. Differential effects of antibiotics on bile acid metabolism, intestinal microbiota composition and insulin resistance in obese humans; a randomised controlled trial. Nederlands Tijdschrift Voor Diabetologie, 2012, 10, 147-147. | 0.0 | 0 |
| 292 | PS14 - 70. Intestinal microbiota translocation is associated with inflamed visceral adipose tissue. Nederlands Tijdschrift Voor Diabetologie, 2012, 10, 148-148. | 0.0 | 0 |
| 293 | Functional Analysis of Lactobacillus rhamnosus GG Pili in Relation to Adhesion and Immunomodulatory Interactions with Intestinal Epithelial Cells. Applied and Environmental Microbiology, 2012, 78, 185-193. | 3.1 | 274 |
| 294 | Adhesion of microbes to the intestinal surface: lessons from the paradigm probiotic Lactobacillus rhamnosus GG. Japanese Journal of Lactic Acid Bacteria, 2012, 23, 7-13. | 0.1 | 0 |
| 295 | The human small intestinal microbiota is driven by rapid uptake and conversion of simple carbohydrates. ISME Journal, 2012, 6, 1415-1426. | 9.8 | 544 |
| 296 | Role of the intestinal microbiome in health and disease: from correlation to causation. Nutrition Reviews, 2012, 70, S45-S56. | 5.8 | 333 |
| 297 | Metagenome analysis reveals yet unexplored reductive dechlorinating potential of <scp>D</scp>ehalobacter sp. <scp>E</scp>1 growing in coâ€culture with <scp>S</scp>edimentibacter sp.. Environmental Microbiology Reports, 2012, 4, 604-616. | 2.4 | 57 |
| 298 | Where bio meets nano: The many uses for nanoporous aluminum oxide in biotechnology. Biotechnology Advances, 2012, 30, 1089-1099. | 11.7 | 99 |
| 299 | The adult intestinal core microbiota is determined by analysis depth and health status. Clinical Microbiology and Infection, 2012, 18, 16-20. | 6.0 | 95 |
| 300 | The function of our microbiota: who is out there and what do they do?. Frontiers in Cellular and Infection Microbiology, 2012, 2, 104. | 3.9 | 352 |
| 301 | CRISPR Immunity Relies on the Consecutive Binding and Degradation of Negatively Supercoiled Invader DNA by Cascade and Cas3. Molecular Cell, 2012, 46, 595-605. | 9.7 | 475 |
| 302 | Genetic and Biochemical Characterization of the Cell Wall Hydrolase Activity of the Major Secreted Protein of Lactobacillus rhamnosus GG. PLoS ONE, 2012, 7, e31588. | 2.5 | 77 |
| 303 | Transfer of Intestinal Microbiota From Lean Donors Increases Insulin Sensitivity in Individuals With Metabolic Syndrome. Gastroenterology, 2012, 143, 913-916.e7. | 1.3 | 2,287 |
| 304 | Thermal Stabilization of an Endoglucanase by Cyclization. Applied Biochemistry and Biotechnology, 2012, 167, 2039-2053. | 2.9 | 16 |
| 305 | Comparative Metaproteomics and Diversity Analysis of Human Intestinal Microbiota Testifies for Its Temporal Stability and Expression of Core Functions. PLoS ONE, 2012, 7, e29913. | 2.5 | 183 |
| 306 | The major secreted protein Msp1/p75 is O-glycosylated in Lactobacillus rhamnosus GG. Microbial Cell Factories, 2012, 11, 15. | 4.0 | 72 |

| # | Article | IF | Citations |
|---|---|---|---|
| 307 | Microbes insideâ€"from diversity to function: the case of Akkermansia. ISME Journal, 2012, 6, 1449-1458. | 9.8 | 551 |
| 308 | The therapeutic potential of manipulating gut microbiota in obesity and type 2 diabetes mellitus. Diabetes, Obesity and Metabolism, 2012, 14, 112-120. | 4.4 | 283 |
| 309 | Role of phosphate in the central metabolism of two lactic acid bacteria â€“ a comparative systems biology approach. FEBS Journal, 2012, 279, 1274-1290. | 4.7 | 52 |
| 310 | Effect of acid stress on protein expression and phosphorylation in Lactobacillus rhamnosus GG. Journal of Proteomics, 2012, 75, 1357-1374. | 2.4 | 130 |
| 311 | Anaerobic benzene degradation under denitrifying conditions: Peptococcaceae as dominant benzene degraders and evidence for a syntrophic process. Environmental Microbiology, 2012, 14, 1171-1181. | 3.8 | 100 |
| 312 | Global and Deep Molecular Analysis of Microbiota Signatures in Fecal Samples From Patients With Irritable Bowel Syndrome. Gastroenterology, 2011, 141, 1792-1801. | 1.3 | 885 |
| 313 | Organic Modification and Subsequent Biofunctionalization of Porous Anodic Alumina Using Terminal Alkynes. Langmuir, 2011, 27, 13606-13617. | 3.5 | 27 |
| 314 | Analysis of infant isolates of Bifidobacterium breve by comparative genome hybridization indicates the existence of new subspecies with marked infant specificity. Research in Microbiology, 2011, 162, 664-670. | 2.1 | 2 |
| 315 | Intestinal Microbiota in Healthy Adults: Temporal Analysis Reveals Individual and Common Core and Relation to Intestinal Symptoms. PLoS ONE, 2011, 6, e23035. | 2.5 | 302 |
| 316 | Bifidobacterium breve â€“ HT-29 cell line interaction: modulation of TNF-Î± induced gene expression. Beneficial Microbes, 2011, 2, 115-128. | 2.4 | 18 |
| 317 | Do nutrientâ€"gutâ€"microbiota interactions play a role in human obesity, insulin resistance and type 2 diabetes?. Obesity Reviews, 2011, 12, 272-281. | 6.5 | 248 |
| 318 | Enterotypes of the human gut microbiome. Nature, 2011, 473, 174-180. | 27.8 | 5,800 |
| 319 | Comparative genomics of Lactobacillus. Microbial Biotechnology, 2011, 4, 323-332. | 4.2 | 112 |
| 320 | Responses of Gut Microbiota and Glucose and Lipid Metabolism to Prebiotics in Genetic Obese and Diet-Induced Leptin-Resistant Mice. Diabetes, 2011, 60, 2775-2786. | 0.6 | 881 |
| 321 | Intestinal microbiota in human health and disease: the impact of probiotics. Genes and Nutrition, 2011, 6, 209-240. | 2.5 | 557 |
| 322 | Systems solutions by lactic acid bacteria: from paradigms to practice. Microbial Cell Factories, 2011, 10, S2. | 4.0 | 108 |
| 323 | Genome Sequence of the Verrucomicrobium Opitutus terrae PB90-1, an Abundant Inhabitant of Rice Paddy Soil Ecosystems. Journal of Bacteriology, 2011, 193, 2367-2368. | 2.2 | 44 |
| 324 | Genome Sequence of Victivallis vadensis ATCC BAA-548, an Anaerobic Bacterium from the Phylum Lentisphaerae, Isolated from the Human Gastrointestinal Tract. Journal of Bacteriology, 2011, 193, 2373-2374. | 2.2 | 14 |

| # | Article | IF | Citations |
|---|---|---|---|
| 325 | Modulation of Mucosal Immune Response, Tolerance, and Proliferation in Mice Colonized by the Mucin-Degrader Akkermansia muciniphila. Frontiers in Microbiology, 2011, 2, 166. | 3.5 | 438 |
| 326 | Microarray Analysis and Barcoded Pyrosequencing Provide Consistent Microbial Profiles Depending on the Source of Human Intestinal Samples. Applied and Environmental Microbiology, 2011, 77, 2071-2080. | 3.1 | 141 |
| 327 | Genome Sequence of Chthoniobacter flavus Ellin428, an Aerobic Heterotrophic Soil Bacterium. Journal of Bacteriology, 2011, 193, 2902-2903. | 2.2 | 52 |
| 328 | Genome Sequence of â€œPedosphaera parvulaâ€•Ellin514, an Aerobic Verrucomicrobial Isolate from Pasture Soil. Journal of Bacteriology, 2011, 193, 2900-2901. | 2.2 | 28 |
| 329 | Genome Sequence of Lactobacillus amylovorus GRL1118, Isolated from Pig Ileum. Journal of Bacteriology, 2011, 193, 3147-3148. | 2.2 | 20 |
| 330 | Altered Gut Microbiota and Endocannabinoid System Tone in Obese and Diabetic Leptin-Resistant Mice: Impact on Apelin Regulation in Adipose Tissue. Frontiers in Microbiology, 2011, 2, 149. | 3.5 | 267 |
| 331 | Functional Characterization of a Mucus-Specific LPXTG Surface Adhesin from Probiotic Lactobacillus rhamnosus GG. Applied and Environmental Microbiology, 2011, 77, 4465-4472. | 3.1 | 90 |
| 332 | Health benefits and health claims of probiotics: bridging science and marketing. British Journal of Nutrition, 2011, 106, 1291-1296. | 2.3 | 176 |
| 333 | Role of â€œDehalococcoidesâ€•spp. in the Anaerobic Transformation of Hexachlorobenzene in European Rivers. Applied and Environmental Microbiology, 2011, 77, 4437-4445. | 3.1 | 20 |
| 334 | Functional genome analysis of Bifidobacterium breve UCC2003 reveals type IVb tight adherence (Tad) pili as an essential and conserved host-colonization factor. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11217-11222. | 7.1 | 328 |
| 335 | Genome Sequence of Lactobacillus amylovorus GRL1112. Journal of Bacteriology, 2011, 193, 789-790. | 2.2 | 15 |
| 336 | The Genome of Akkermansia muciniphila, a Dedicated Intestinal Mucin Degrader, and Its Use in Exploring Intestinal Metagenomes. PLoS ONE, 2011, 6, e16876. | 2.5 | 328 |
| 337 | The environment within: how gut microbiota may influence metabolism and body composition. Diabetologia, 2010, 53, 606-613. | 6.3 | 270 |
| 338 | Systems biology of the gut: the interplay of food, microbiota and host at the mucosal interface. Current Opinion in Biotechnology, 2010, 21, 539-550. | 6.6 | 62 |
| 339 | Supplementation with engineered Lactococcus lactis improves the folate status in deficient rats. Nutrition, 2010, 26, 835-841. | 2.4 | 33 |
| 340 | Exploiting the ecogenomics toolbox for environmental diagnostics of organohalide-respiring bacteria. Trends in Biotechnology, 2010, 28, 308-316. | 9.3 | 145 |
| 341 | Development of a minimal growth medium for Lactobacillus plantarum. Letters in Applied Microbiology, 2010, 50, 57-64. | 2.2 | 105 |
| 342 | Stability of the total and functional microbial communities in river sediment mesocosms exposed to anthropogenic disturbances. FEMS Microbiology Ecology, 2010, 74, 72-82. | 2.7 | 13 |

| # | Article | IF | Citations |
|---|---|---|---|
| 343 | Concurrent hexachlorobenzene and chloroethene transformation by endogenous dechlorinating microorganisms in the Ebro River sediment. FEMS Microbiology Ecology, 2010, 74, 682-692. | 2.7 | 7 |
| 344 | Convergence in probiotic Lactobacillus gut-adaptive responses in humans and mice. ISME Journal, 2010, 4, 1481-1484. | 9.8 | 95 |
| 345 | High temporal and interâ€individual variation detected in the human ileal microbiota. Environmental Microbiology, 2010, 12, 3213-3227. | 3.8 | 254 |
| 346 | Evaluating the microbial diversity of an in vitro model of the human large intestine by phylogenetic microarray analysis. Microbiology (United Kingdom), 2010, 156, 3270-3281. | 1.8 | 84 |
| 347 | Mucin-bacterial interactions in the human oral cavity and digestive tract. Gut Microbes, 2010, 1, 254-268. | 9.8 | 421 |
| 348 | Correlation of Dehalococcoides 16S rRNA and Chloroethene-Reductive Dehalogenase Genes with Geochemical Conditions in Chloroethene-Contaminated Groundwater. Applied and Environmental Microbiology, 2010, 76, 843-850. | 3.1 | 92 |
| 349 | Mucosal Adhesion Properties of the ProbioticLactobacillus rhamnosusGG SpaCBA and SpaFED Pilin Subunits. Applied and Environmental Microbiology, 2010, 76, 2049-2057. | 3.1 | 189 |
| 350 | Molecular characterization of the glucose isomerase from the thermophilic bacteriumFervidobacterium gondwanense. Environmental Technology (United Kingdom), 2010, 31, 1083-1090. | 2.2 | 18 |
| 351 | Metatranscriptome Analysis of the Human Fecal Microbiota Reveals Subject-Specific Expression Profiles, with Genes Encoding Proteins Involved in Carbohydrate Metabolism Being Dominantly Expressed. Applied and Environmental Microbiology, 2010, 76, 5533-5540. | 3.1 | 76 |
| 352 | Ïƒ 54-mediated control of the mannose phosphotransferase sytem in Lactobacillus plantarum impacts on carbohydrate metabolism. Microbiology (United Kingdom), 2010, 156, 695-707. | 1.8 | 24 |
| 353 | Involvement of the Mannose Phosphotransferase System of Lactobacillus plantarum WCFS1 in Peroxide Stress Tolerance. Applied and Environmental Microbiology, 2010, 76, 3748-3752. | 3.1 | 37 |
| 354 | Microbial Community- And Metabolite Dynamics of an Anoxic Dechlorinating Bioreactor. Environmental Science & Technology, 2010, 44, 4884-4890. | 10.0 | 28 |
| 355 | Mixed-Culture Transcriptome Analysis Reveals the Molecular Basis of Mixed-Culture Growth in Streptococcus thermophilus and Lactobacillus bulgaricus. Applied and Environmental Microbiology, 2010, 76, 7775-7784. | 3.1 | 194 |
| 356 | Comparative analysis of fecal DNA extraction methods with phylogenetic microarray: Effective recovery of bacterial and archaeal DNA using mechanical cell lysis. Journal of Microbiological Methods, 2010, 81, 127-134. | 1.6 | 480 |
| 357 | Semi-automated extraction of microbial DNA from feces for qPCR and phylogenetic microarray analysis. Journal of Microbiological Methods, 2010, 83, 231-235. | 1.6 | 41 |
| 358 | Gastrointestinal microbiota in irritable bowel syndrome: present state and perspectives. Microbiology (United Kingdom), 2010, 156, 3205-3215. | 1.8 | 231 |
| 359 | Microbial functionality in the human intestinal tract. Frontiers in Bioscience - Landmark, 2009, Volume, 3074. | 3.0 | 17 |
| 360 | Differential NF-Îºß pathways induction by Lactobacillus plantarum in the duodenum of healthy humans correlating with immune tolerance. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2371-2376. | 7.1 | 363 |

| # | Article | IF | Citations |
|---|---|---|---|
| 361 | Genome-Scale Model of Streptococcus thermophilus LMG18311 for Metabolic Comparison of Lactic Acid Bacteria. Applied and Environmental Microbiology, 2009, 75, 3627-3633. | 3.1 | 148 |
| 362 | Large Intergenic Cruciform-Like Supermotifs in the Lactobacillus plantarum Genome. Journal of Bacteriology, 2009, 191, 3420-3423. | 2.2 | 4 |
| 363 | Tracking Functional Guilds: â€œDehalococcoidesâ€•spp. in European River Basins Contaminated with Hexachlorobenzene. Applied and Environmental Microbiology, 2009, 75, 4696-4704. | 3.1 | 41 |
| 364 | Effect of Amino Acid Availability on Vitamin B 12 Production in Lactobacillus reuteri. Applied and Environmental Microbiology, 2009, 75, 3930-3936. | 3.1 | 26 |
| 365 | Review: Tools for the tract: understanding the functionality of the gastrointestinal tract. Therapeutic Advances in Gastroenterology, 2009, 2, S9-S22. | 3.2 | 31 |
| 366 | Mixed-Species Genomic Microarray Analysis of Fecal Samples Reveals Differential Transcriptional Responses of Bifidobacteria in Breast- and Formula-Fed Infants. Applied and Environmental Microbiology, 2009, 75, 2668-2676. | 3.1 | 100 |
| 367 | Lactobacillus plantarum WCFS1 Electron Transport Chains. Applied and Environmental Microbiology, 2009, 75, 3580-3585. | 3.1 | 86 |
| 368 | Isolation and characterization of a new CO-utilizing strain, Thermoanaerobacter thermohydrosulfuricus subsp. carboxydovorans, isolated from a geothermal spring in Turkey. Extremophiles, 2009, 13, 885-894. | 2.3 | 30 |
| 369 | Genome-wide screen forListeria monocytogenesgenes important for growth at high temperatures. FEMS Microbiology Letters, 2009, 295, 195-203. | 1.8 | 8 |
| 370 | Folate overproduction inLactobacillus plantarumWCFS1 causes methotrexate resistance. FEMS Microbiology Letters, 2009, 297, 261-265. | 1.8 | 15 |
| 371 | Linking phylogenetic identities of bacteria to starch fermentation in an in vitro model of the large intestine by RNAâ€based stable isotope probing. Environmental Microbiology, 2009, 11, 914-926. | 3.8 | 157 |
| 372 | Development and application of the human intestinal tract chip, a phylogenetic microarray: analysis of universally conserved phylotypes in the abundant microbiota of young and elderly adults. Environmental Microbiology, 2009, 11, 1736-1751. | 3.8 | 420 |
| 373 | Proteome Analysis of Lactobacillus rhamnosus GG Using 2-D DIGE and Mass Spectrometry Shows Differential Protein Production in Laboratory and Industrial-Type Growth Media. Journal of Proteome Research, 2009, 8, 4993-5007. | 3.7 | 56 |
| 374 | Effect of soil sample preservation, compared to the effect of other environmental variables, on bacterial and eukaryotic diversity. Research in Microbiology, 2009, 160, 89-98. | 2.1 | 59 |
| 375 | Degradation of 1,2-dichloroethane by microbial communities from river sediment at various redox conditions. Water Research, 2009, 43, 3207-3216. | 11.3 | 46 |
| 376 | A Bifidobacterium mixed-species microarray for high resolution discrimination between intestinal bifidobacteria. Journal of Microbiological Methods, 2009, 76, 269-277. | 1.6 | 26 |
| 377 | Comparative genomic analysis of Lactobacillus rhamnosus GG reveals pili containing a human-mucus binding protein. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 17193-17198. | 7.1 | 654 |
| 378 | Comparative Analysis of Pyrosequencing and a Phylogenetic Microarray for Exploring Microbial Community Structures in the Human Distal Intestine. PLoS ONE, 2009, 4, e6669. | 2.5 | 719 |

| # | Article | IF | Citations |
|---|---|---|---|
| 379 | Clinical trial: multispecies probiotic supplementation alleviates the symptoms of irritable bowel syndrome and stabilizes intestinal microbiota. Alimentary Pharmacology and Therapeutics, 2008, 27, 48-57. | 3.7 | 309 |
| 380 | A simple and fast method for determining colony forming units. Letters in Applied Microbiology, 2008, 47, 275-278. | 2.2 | 150 |
| 381 | Identification of the transcriptional response of human intestinal mucosa to Lactobacillus plantarum WCFS1 in vivo. BMC Genomics, 2008, 9, 374. | 2.8 | 69 |
| 382 | Feeding of Lactobacillus sobrius reduces Escherichia coli F4 levels in the gut and promotes growth of infected piglets. FEMS Microbiology Ecology, 2008, 66, 599-607. | 2.7 | 115 |
| 383 | High-throughput diversity and functionality analysis of the gastrointestinal tract microbiota. Gut, 2008, 57, 1605-1615. | 12.1 | 528 |
| 384 | High-Level Folate Production in Fermented Foods by the B <sub>12</sub> Producer Lactobacillus reuteri JCM1112. Applied and Environmental Microbiology, 2008, 74, 3291-3294. | 3.1 | 131 |
| 385 | Improved annotation of conjugated bile acid hydrolase superfamily members in Gram-positive bacteria. Microbiology (United Kingdom), 2008, 154, 2492-2500. | 1.8 | 39 |
| 386 | Divergent roles of CprK paralogues from Desulfitobacterium hafniense in activating gene expression. Microbiology (United Kingdom), 2008, 154, 3686-3696. | 1.8 | 22 |
| 387 | Hydrogenomics of the Extremely Thermophilic Bacterium Caldicellulosiruptor saccharolyticus. Applied and Environmental Microbiology, 2008, 74, 6720-6729. | 3.1 | 142 |
| 388 | S layer protein A of Lactobacillus acidophilus NCFM regulates immature dendritic cell and T cell functions. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 19474-19479. | 7.1 | 515 |
| 389 | The Mucin Degrader Akkermansia muciniphila Is an Abundant Resident of the Human Intestinal Tract. Applied and Environmental Microbiology, 2008, 74, 1646-1648. | 3.1 | 517 |
| 390 | Functional Analysis of Four Bile Salt Hydrolase and Penicillin Acylase Family Members in Lactobacillus plantarum WCFS1. Applied and Environmental Microbiology, 2008, 74, 4719-4726. | 3.1 | 173 |
| 391 | Improvement of Lactobacillus plantarum Aerobic Growth as Directed by Comprehensive Transcriptome Analysis. Applied and Environmental Microbiology, 2008, 74, 4776-4778. | 3.1 | 49 |
| 392 | Differential Transcriptional Response of Bifidobacterium longum to Human Milk, Formula Milk, and Galactooligosaccharide. Applied and Environmental Microbiology, 2008, 74, 4686-4694. | 3.1 | 82 |
| 393 | Interactomics in the Human Intestine. Journal of Clinical Gastroenterology, 2008, 42, S163-S167. | 2.2 | 63 |
| 394 | Identification of the Ïƒ B Regulon of Bacillus cereus and Conservation of Ïƒ B -Regulated Genes in Low-GC-Content Gram-Positive Bacteria. Journal of Bacteriology, 2007, 189, 4384-4390. | 2.2 | 53 |
| 395 | The micro-Petri dish, a million-well growth chip for the culture and high-throughput screening of microorganisms. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18217-18222. | 7.1 | 255 |
| 396 | Intestinal Integrity and Akkermansia muciniphila , a Mucin-Degrading Member of the Intestinal Microbiota Present in Infants, Adults, and the Elderly. Applied and Environmental Microbiology, 2007, 73, 7767-7770. | 3.1 | 540 |

| # | Article | IF | Citations |
|---|---|---|---|
| 397 | Identification of Prebiotic Fructooligosaccharide Metabolism in Lactobacillus plantarum WCFS1 through Microarrays. Applied and Environmental Microbiology, 2007, 73, 1753-1765. | 3.1 | 210 |
| 398 | Generation of a Membrane Potential by Lactococcus lactis through Aerobic Electron Transport. Journal of Bacteriology, 2007, 189, 5203-5209. | 2.2 | 65 |
| 399 | Spatial and Temporal Expression of Lactobacillus plantarum Genes in the Gastrointestinal Tracts of Mice. Applied and Environmental Microbiology, 2007, 73, 124-132. | 3.1 | 107 |
| 400 | Metaproteomics Approach To Study the Functionality of the Microbiota in the Human Infant Gastrointestinal Tract. Applied and Environmental Microbiology, 2007, 73, 1388-1392. | 3.1 | 149 |
| 401 | The Novel Porcine Lactobacillus sobrius Strain Protects Intestinal Cells from Enterotoxigenic Escherichia coli K88 Infection and Prevents Membrane Barrier Damage ,. Journal of Nutrition, 2007, 137, 2709-2716. | 2.9 | 143 |
| 402 | Advanced Molecular Tools for the Identification of Lactic Acid Bacteria1, ,. Journal of Nutrition, 2007, 137, 741S-747S. | 2.9 | 113 |
| 403 | Pseudovitamin is the corrinoid produced by Lactobacillus reuteri CRL1098 under anaerobic conditions. FEBS Letters, 2007, 581, 4865-4870. | 2.8 | 72 |
| 404 | Characterization of the Role of para-Aminobenzoic Acid Biosynthesis in Folate Production by Lactococcus lactis. Applied and Environmental Microbiology, 2007, 73, 2673-2681. | 3.1 | 110 |
| 405 | Making sense of quorum sensing in lactobacilli: a special focus on Lactobacillus plantarum WCFS1. Microbiology (United Kingdom), 2007, 153, 3939-3947. | 1.8 | 74 |
| 406 | Thioredoxin reductase is a key factor in the oxidative stress response of Lactobacillus plantarum WCFS1. Microbial Cell Factories, 2007, 6, 29. | 4.0 | 110 |
| 407 | Microbial communities in the human small intestine: coupling diversity to metagenomics. Future Microbiology, 2007, 2, 285-295. | 2.0 | 117 |
| 408 | Diversity of the human gastrointestinal tract microbiota revisited. Environmental Microbiology, 2007, 9, 2125-2136. | 3.8 | 485 |
| 409 | Dynamics of competitive population abundance of Lactobacillus plantarum ivi gene mutants in faecal samples after passage through the gastrointestinal tract of mice. Journal of Applied Microbiology, 2007, 103, 1424-1434. | 3.1 | 36 |
| 410 | Identification of glucose-fermenting bacteria present in an in vitro model of the human intestine by RNA-stable isotope probing. FEMS Microbiology Ecology, 2007, 60, 126-135. | 2.7 | 74 |
| 411 | Germination of Bacillus cereus spores adhered to stainless steel. International Journal of Food Microbiology, 2007, 116, 367-371. | 4.7 | 50 |
| 412 | Identification of a Novel Î±-Galactosidase from the Hyperthermophilic Archaeon Sulfolobus solfataricus. Journal of Bacteriology, 2006, 188, 2392-2399. | 2.2 | 51 |
| 413 | Identification of the Missing Links in Prokaryotic Pentose Oxidation Pathways. Journal of Biological Chemistry, 2006, 281, 27378-27388. | 3.4 | 102 |
| 414 | Lactobacillus plantarumâ€"survival, functional and potential probiotic properties in the human intestinal tract. International Dairy Journal, 2006, 16, 1018-1028. | 3.0 | 410 |

| # | Article | IF | Citations |
|---|---|---|---|
| 415 | Beyond diversity: functional microbiomics of the human colon. Trends in Microbiology, 2006, 14, 86-91. | 7.7 | 187 |
| 416 | 9 Functional Genomics of the Thermo-Acidophilic Archaeon Sulfolobus solfataricus. Methods in Microbiology, 2006, 35, 201-231. | 0.8 | 0 |
| 417 | Proteomic analysis of log to stationary growth phaseLactobacillus plantarum cells and a 2-DE database. Proteomics, 2006, 6, 6485-6493. | 2.2 | 95 |
| 418 | Post-natal development of the porcine microbiota composition and activities. Environmental Microbiology, 2006, 8, 1191-1199. | 3.8 | 253 |
| 419 | Identification of a glycolytic regulon in the archaeaPyrococcusandThermococcus. FEMS Microbiology Letters, 2006, 260, 69-76. | 1.8 | 39 |
| 420 | Eukaryotic diversity in historical soil samples. FEMS Microbiology Ecology, 2006, 57, 420-428. | 2.7 | 64 |
| 421 | DNA micro-array-based identification of bile-responsive genes in Lactobacillus plantarum. Journal of Applied Microbiology, 2006, 100, 728-738. | 3.1 | 139 |
| 422 | A microbial world within us. Molecular Microbiology, 2006, 59, 1639-1650. | 2.5 | 335 |
| 423 | Isolation of DNA from bacterial samples of the human gastrointestinal tract. Nature Protocols, 2006, 1, 870-873. | 12.0 | 171 |
| 424 | Isolation of RNA from bacterial samples of the human gastrointestinal tract. Nature Protocols, 2006, 1, 954-959. | 12.0 | 82 |
| 425 | Nutridynamics â€“ studying the dynamics of food components in products and in the consumer. Current Opinion in Biotechnology, 2006, 17, 217-225. | 6.6 | 27 |
| 426 | Characterization of CprK1, a CRP/FNR-Type Transcriptional Regulator of Halorespiration from Desulfitobacterium hafniense. Journal of Bacteriology, 2006, 188, 2604-2613. | 2.2 | 40 |
| 427 | Lactobacillus sobrius sp. nov., abundant in the intestine of weaning piglets. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 29-32. | 1.7 | 52 |
| 428 | Characterization of Germination Receptors of Bacillus cereus ATCC 14579. Applied and Environmental Microbiology, 2006, 72, 44-53. | 3.1 | 79 |
| 429 | Influence of Sporulation Medium Composition on Transcription of ger Operons and the Germination Response of Spores of Bacillus cereus ATCC 14579. Applied and Environmental Microbiology, 2006, 72, 3746-3749. | 3.1 | 63 |
| 430 | Analysis of Growth of Lactobacillus plantarum WCFS1 on a Complex Medium Using a Genome-scale Metabolic Model. Journal of Biological Chemistry, 2006, 281, 40041-40048. | 3.4 | 261 |
| 431 | Safe use of genetically modified lactic acid bacteria in food. Bridging the gap between consumers, green groups, and industry. Electronic Journal of Biotechnology, 2006, 9, 0-0. | 2.2 | 49 |
| 432 | Molecular characterization of a conserved archaeal copper resistance (cop) gene cluster and its copper-responsive regulator in Sulfolobus solfataricus P2. Microbiology (United Kingdom), 2006, 152, 1969-1979. | 1.8 | 49 |

| # | Article | IF | Citations |
|---|---|---|---|
| 433 | Diversity, vitality and activities of intestinal lactic acid bacteria and bifidobacteria assessed by molecular approaches. FEMS Microbiology Reviews, 2005, 29, 477-490. | 8.6 | 122 |
| 434 | Probiotic and other functional microbes: from markets to mechanisms. Current Opinion in Biotechnology, 2005, 16, 204-211. | 6.6 | 344 |
| 435 | Functional ingredient production: application of global metabolic models. Current Opinion in Biotechnology, 2005, 16, 190-197. | 6.6 | 35 |
| 436 | Discovering novel biology by in silico archaeology. Nature Reviews Microbiology, 2005, 3, 859-869. | 28.6 | 21 |
| 437 | Characterization and mode of action of an exopolygalacturonase from the hyperthermophilic bacterium Thermotoga maritima. FEBS Journal, 2005, 272, 5464-5473. | 4.7 | 46 |
| 438 | Lactic acid bacteria â€“ Genetics, metabolism and application. FEMS Microbiology Reviews, 2005, 29, 391-391. | 8.6 | 11 |
| 439 | Unity in organisation and regulation of catabolic operons in Lactobacillus plantarum, Lactococcus lactis and Listeria monocytogenes. Systematic and Applied Microbiology, 2005, 28, 187-195. | 2.8 | 34 |
| 440 | Enrichment and Detection of Microorganisms Involved in Direct and Indirect Methanogenesis from Methanol in an Anaerobic Thermophilic Bioreactor. Microbial Ecology, 2005, 50, 440-446. | 2.8 | 27 |
| 441 | Different control mechanisms regulate glucoamylase and protease gene transcription in Aspergillus oryzae in solid-state and submerged fermentation. Applied Microbiology and Biotechnology, 2005, 67, 75-82. | 3.6 | 48 |
| 442 | Deletion ofsigBinBacillus cereusaffects spore properties. FEMS Microbiology Letters, 2005, 252, 169-173. | 1.8 | 11 |
| 443 | An agr -Like Two-Component Regulatory System in Lactobacillus plantarum Is Involved in Production of a Novel Cyclic Peptide and Regulation of Adherence. Journal of Bacteriology, 2005, 187, 5224-5235. | 2.2 | 144 |
| 444 | Exploring Lactobacillus plantarum Genome Diversity by Using Microarrays. Journal of Bacteriology, 2005, 187, 6119-6127. | 2.2 | 229 |
| 445 | Engineering a Selectable Marker for Hyperthermophiles. Journal of Biological Chemistry, 2005, 280, 11422-11431. | 3.4 | 78 |
| 446 | Deletion of the sigB Gene in Bacillus cereus ATCC 14579 Leads to Hydrogen Peroxide Hyperresistance. Applied and Environmental Microbiology, 2005, 71, 6427-6430. | 3.1 | 18 |
| 447 | Overproduction of Heterologous Mannitol 1-Phosphatase: a Key Factor for Engineering Mannitol Production by Lactococcus lactis. Applied and Environmental Microbiology, 2005, 71, 1507-1514. | 3.1 | 57 |
| 448 | The first true obligately syntrophic propionate-oxidizing bacterium, Pelotomaculum schinkii sp. nov., co-cultured with Methanospirillum hungatei, and emended description of the genus Pelotomaculum. International Journal of Systematic and Evolutionary Microbiology, 2005, 55, 1697-1703. | 1.7 | 139 |
| 449 | gerR , a Novel ger Operon Involved in l -Alanine- and Inosine-Initiated Germination of Bacillus cereus ATCC 14579. Applied and Environmental Microbiology, 2005, 71, 774-781. | 3.1 | 72 |
| 450 | Representational Difference Analysis and Real-Time PCR for Strain-Specific Quantification of Lactobacillus sobrius sp. nov. Applied and Environmental Microbiology, 2005, 71, 7578-7581. | 3.1 | 38 |

| # | Article | IF | Citations |
|---|---|---|---|
| 451 | Lipotechoic acid in lactobacilli: D-Alanine makes the difference. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10763-10764. | 7.1 | 16 |
| 452 | Colonic Microbiota Signatures across Five Northern European Countries. Applied and Environmental Microbiology, 2005, 71, 4153-4155. | 3.1 | 243 |
| 453 | Cloning and Expression of Islandisin, a New Thermostable Subtilisin from Fervidobacterium islandicum , in Escherichia coli. Applied and Environmental Microbiology, 2005, 71, 3951-3958. | 3.1 | 28 |
| 454 | Biodiversity-Based Identification and Functional Characterization of the Mannose-Specific Adhesin ofLactobacillus plantarum. Journal of Bacteriology, 2005, 187, 6128-6136. | 2.2 | 272 |
| 455 | Genome-based in silico detection of putative manganese transport systems in Lactobacillus plantarum and their genetic analysis. Microbiology (United Kingdom), 2005, 151, 1229-1238. | 1.8 | 68 |
| 456 | Complete Sequences of Four Plasmids of Lactococcus lactis subsp. cremoris SK11 Reveal Extensive Adaptation to the Dairy Environment. Applied and Environmental Microbiology, 2005, 71, 8371-8382. | 3.1 | 150 |
| 457 | Genetic Diversity of Viable, Injured, and Dead Fecal Bacteria Assessed by Fluorescence-Activated Cell Sorting and 16S rRNA Gene Analysis. Applied and Environmental Microbiology, 2005, 71, 4679-4689. | 3.1 | 190 |
| 458 | Analysis of the Role of RsbV, RsbW, and RsbY in Regulating Ïƒ B Activity in Bacillus cereus. Journal of Bacteriology, 2005, 187, 5846-5851. | 2.2 | 43 |
| 459 | Influence of Glutamate on Growth, Sporulation, and Spore Properties of Bacillus cereus ATCC 14579 in Defined Medium. Applied and Environmental Microbiology, 2005, 71, 3248-3254. | 3.1 | 48 |
| 460 | Functional Analysis of Three Plasmids from Lactobacillus plantarum. Applied and Environmental Microbiology, 2005, 71, 1223-1230. | 3.1 | 100 |
| 461 | Diversity, vitality and activities of intestinal lactic acid bacteria and bifidobacteria assessed by molecular approaches. FEMS Microbiology Reviews, 2005, 29, 477-490. | 8.6 | 75 |
| 462 | Specific Response of a Novel and Abundant Lactobacillus amylovorus -Like Phylotype to Dietary Prebiotics in the Guts of Weaning Piglets. Applied and Environmental Microbiology, 2004, 70, 3821-3830. | 3.1 | 185 |
| 463 | Identification and Functional Characterization of the Lactococcus lactis rfb Operon, Required for dTDP-Rhamnose Biosynthesis. Journal of Bacteriology, 2004, 186, 1239-1248. | 2.2 | 40 |
| 464 | Insertion-Sequence-Mediated Mutations Isolated During Adaptation to Growth and Starvation in Lactococcus lactis. Genetics, 2004, 168, 1145-1157. | 2.9 | 38 |
| 465 | Selection and Characterization of Conditionally Active Promoters in Lactobacillus plantarum , Using Alanine Racemase as a Promoter Probe. Applied and Environmental Microbiology, 2004, 70, 310-317. | 3.1 | 37 |
| 466 | Genetic Characterization of the Bile Salt Response in Lactobacillus plantarum and Analysis of Responsive Promoters In Vitro and In Situ in the Gastrointestinal Tract. Journal of Bacteriology, 2004, 186, 7829-7835. | 2.2 | 130 |
| 467 | Development and Application of a Selective PCR-Denaturing Gradient Gel Electrophoresis Approach To Detect a Recently Cultivated Bacillus Group Predominant in Soil. Applied and Environmental Microbiology, 2004, 70, 5801-5809. | 3.1 | 15 |
| 468 | Growth and Sporulation of Bacillus cereus ATCC 14579 under Defined Conditions: Temporal Expression of Genes for Key Sigma Factors. Applied and Environmental Microbiology, 2004, 70, 2514-2519. | 3.1 | 67 |

| # | Article | IF | Citations |
|---|---|---|---|
| 469 | Transformation of Folate-Consuming Lactobacillus gasseri into a Folate Producer. Applied and Environmental Microbiology, 2004, 70, 3146-3148. | 3.1 | 64 |
| 470 | The Alternative Sigma Factor Ïƒ B of Bacillus cereus : Response to Stress and Role in Heat Adaptation. Journal of Bacteriology, 2004, 186, 316-325. | 2.2 | 72 |
| 471 | Identification of ÏƒB-Dependent Genes in Bacillus cereus by Proteome and In Vitro Transcription Analysis. Journal of Bacteriology, 2004, 186, 4100-4109. | 2.2 | 26 |
| 472 | Substrate-Induced Production and Secretion of Cellulases by Clostridium acetobutylicum. Applied and Environmental Microbiology, 2004, 70, 5238-5243. | 3.1 | 57 |
| 473 | Identification and Functional Verification of Archaeal-Type Phosphoenolpyruvate Carboxylase, a Missing Link in Archaeal Central Carbohydrate Metabolism. Journal of Bacteriology, 2004, 186, 7754-7762. | 2.2 | 33 |
| 474 | The intestinal mucosa as a habitat of the gut microbiota and a rational target for probiotic functionality and safety. Microbial Ecology in Health and Disease, 2004, 16, 137-144. | 3.5 | 11 |
| 475 | Molecular methods for the analysis of gut microbiota. Microbial Ecology in Health and Disease, 2004, 16, 71-85. | 3.5 | 25 |
| 476 | Akkermansia muciniphila gen. nov., sp. nov., a human intestinal mucin-degrading bacterium. International Journal of Systematic and Evolutionary Microbiology, 2004, 54, 1469-1476. | 1.7 | 1,566 |
| 477 | The food, GI-tract functionality and human health cluster: PROEUHEALTH and beyond. Microbial Ecology in Health and Disease, 2004, 16, 66-70. | 3.5 | 1 |
| 478 | Engineering metabolic highways in Lactococci and other lactic acid bacteria. Trends in Biotechnology, 2004, 22, 72-79. | 9.3 | 126 |
| 479 | Anaerobic Microbial Dehalogenation. Annual Review of Microbiology, 2004, 58, 43-73. | 7.3 | 433 |
| 480 | Post-genomics of lactic acid bacteria and other food-grade bacteria to discover gut functionality. Current Opinion in Biotechnology, 2004, 15, 86-93. | 6.6 | 53 |
| 481 | Identification of Lactobacillus plantarum Genes That Are Induced in the Gastrointestinal Tract of Mice. Journal of Bacteriology, 2004, 186, 5721-5729. | 2.2 | 211 |
| 482 | Autoregulation of subtilin biosynthesis in Bacillus subtilis: the role of the spa-box in subtilin-responsive promoters. Peptides, 2004, 25, 1415-1424. | 2.4 | 39 |
| 483 | Optimising single cell activity assessment of Lactobacillus plantarum by fluorescent in situ hybridisation as affected by growth. Journal of Microbiological Methods, 2004, 59, 109-115. | 1.6 | 16 |
| 484 | Crystal Structure of Fervidolysin from Fervidobacterium pennivorans, a Keratinolytic Enzyme Related to Subtilisin. Journal of Molecular Biology, 2004, 335, 787-797. | 4.2 | 56 |
| 485 | Progress in Food-related Research Focussing on Bacillus cereus. Microbes and Environments, 2004, 19, 265-269. | 1.6 | 5 |
| 486 | Microbial Functionality in the Human Gastrointestinal Tract. Microbes and Environments, 2004, 19, 276-280. | 1.6 | 3 |

| # | Article | IF | Citations |
|---|---|---|---|
| 487 | TRASH: a novel metal-binding domain predicted to be involved in heavy-metal sensing, trafficking and resistance. Trends in Biochemical Sciences, 2003, 28, 170-173. | 7.5 | 65 |
| 488 | Analysis of 16S rDNA reveals bacterial shift during in vitro fermentation of fermentable carbohydrate using piglet faeces as inoculum. Anaerobe, 2003, 9, 175-180. | 2.1 | 47 |
| 489 | Development of bacterial and bifidobacterial communities in feces of newborn babies. Anaerobe, 2003, 9, 219-229. | 2.1 | 171 |
| 490 | Molecular characterization of H2O2-forming NADH oxidases from Archaeoglobus fulgidus. FEBS Journal, 2003, 270, 2885-2894. | 0.2 | 46 |
| 491 | The Lrp family of transcriptional regulators. Molecular Microbiology, 2003, 48, 287-294. | 2.5 | 252 |
| 492 | Effect of fermentable carbohydrates on piglet faecal bacterial communities as revealed by denaturing gradient gel electrophoresis analysis of 16S ribosomal DNA. FEMS Microbiology Ecology, 2003, 43, 225-235. | 2.7 | 150 |
| 493 | Increased Production of Folate by Metabolic Engineering of Lactococcus lactis. Applied and Environmental Microbiology, 2003, 69, 3069-3076. | 3.1 | 169 |
| 494 | Complete genome sequence of Lactobacillus plantarum WCFS1. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1990-1995. | 7.1 | 1,326 |
| 495 | Bacterial gene expression detected in human faeces by reverse transcription-PCR. Journal of Microbiological Methods, 2003, 55, 133-140. | 1.6 | 14 |
| 496 | Engineering of Carbon Distribution between Glycolysis and Sugar Nucleotide Biosynthesis in Lactococcus lactis. Applied and Environmental Microbiology, 2003, 69, 1129-1135. | 3.1 | 58 |
| 497 | ControlledModulation of Folate Polyglutamyl Tail Length by Metabolic Engineeringof Lactococcuslactis. Applied and Environmental Microbiology, 2003, 69, 7101-7107. | 3.1 | 42 |
| 498 | Production by Clostridium acetobutylicum ATCC 824 of CelG, a Cellulosomal Glycoside Hydrolase Belonging to Family 9. Applied and Environmental Microbiology, 2003, 69, 869-877. | 3.1 | 31 |
| 499 | Characterization, Expression, and Mutation of the Lactococcus lactis galPMKTE Genes, Involved in Galactose Utilization via the Leloir Pathway. Journal of Bacteriology, 2003, 185, 870-878. | 2.2 | 80 |
| 500 | Description of Sulfurospirillum halorespirans sp. nov., an anaerobic, tetrachloroethene-respiring bacterium, and transfer of Dehalospirillum multivorans to the genus Sulfurospirillum as Sulfurospirillum multivorans comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2003, 53, 787-793. | 1.7 | 176 |
| 501 | High-throughput PCR Screening of Genes for Three-component Regulatory System Putatively Involved in Quorum Sensing from Low-G+C Gram-positive Bacteria. Bioscience, Biotechnology and Biochemistry, 2003, 67, 480-489. | 1.3 | 22 |
| 502 | Identification and Molecular Characterization of a Novel Type of Î±-galactosidase fromPyrococcus furiosus. Biocatalysis and Biotransformation, 2003, 21, 243-252. | 2.0 | 27 |
| 503 | Increased Exopolysaccharide Production in Lactococcus lactis due to Increased Levels of Expression of the NIZO B40 eps Gene Cluster. Applied and Environmental Microbiology, 2003, 69, 5029-5031. | 3.1 | 53 |
| 504 | Effect of fermentable carbohydrates on piglet faecal bacterial communities as revealed by denaturing gradient gel electrophoresis analysis of 16S ribosomal DNA. FEMS Microbiology Ecology, 2003, 43, 225-235. | 2.7 | 2 |

| # | Article | IF | Citations |
|---|---|---|---|
| 505 | Quantification of Uncultured Ruminococcus obeum -Like Bacteria in Human Fecal Samples by Fluorescent In Situ Hybridization and Flow Cytometry Using 16S rRNA-Targeted Probes. Applied and Environmental Microbiology, 2002, 68, 4225-4232. | 3.1 | 115 |
| 506 | The Sulfolobus solfataricus Lrp-like Protein LysM Regulates Lysine Biosynthesis in Response to Lysine Availability. Journal of Biological Chemistry, 2002, 277, 29537-29549. | 3.4 | 98 |
| 507 | Characterization of Plasmid pRT1 from Pyrococcus sp. Strain JT1. Journal of Bacteriology, 2002, 184, 2561-2566. | 2.2 | 30 |
| 508 | Diversity of Bifidobacterium and Lactobacillus spp. in Breast-Fed and Formula-Fed Infants as Assessed by 16S rDNA Sequence Differences. Microbial Ecology in Health and Disease, 2002, 14, 97-105. | 3.5 | 43 |
| 509 | Food, GI-tract Functionality and Human Health Cluster: PROEUHEALTH. Microbial Ecology in Health and Disease, 2002, 14, 65-74. | 3.5 | 12 |
| 510 | Diversity, Dynamics, and Activity of Bacterial Communities during Production of an Artisanal Sicilian Cheese as Evaluated by 16S rRNA Analysis. Applied and Environmental Microbiology, 2002, 68, 1882-1892. | 3.1 | 332 |
| 511 | Use of the alr Gene as a Food-Grade Selection Marker in Lactic Acid Bacteria. Applied and Environmental Microbiology, 2002, 68, 5663-5670. | 3.1 | 85 |
| 512 | Molecular and Biochemical Characterization of a Distinct Type of Fructose-1,6-Bisphosphatase from Pyrococcus furiosus. Journal of Bacteriology, 2002, 184, 3401-3405. | 2.2 | 32 |
| 513 | Multiparametric Flow Cytometry and Cell Sorting for the Assessment of Viable, Injured, and Dead Bifidobacterium Cells during Bile Salt Stress. Applied and Environmental Microbiology, 2002, 68, 5209-5216. | 3.1 | 252 |
| 514 | Mucosa-Associated Bacteria in the Human Gastrointestinal Tract Are Uniformly Distributed along the Colon and Differ from the Community Recovered from Feces. Applied and Environmental Microbiology, 2002, 68, 3401-3407. | 3.1 | 716 |
| 515 | Molecular Monitoring of Succession of Bacterial Communities in Human Neonates. Applied and Environmental Microbiology, 2002, 68, 219-226. | 3.1 | 730 |
| 516 | Genetics of Streptococci, Lactococci, and Enterococci: Review of the Sixth International Conference. Journal of Bacteriology, 2002, 184, 6085-6092. | 2.2 | 19 |
| 517 | Molecular analysis of the role of two aromatic aminotransferases and a broad-specificity aspartate aminotransferase in the aromatic amino acid metabolism ofPyrococcus furiosus. Archaea, 2002, 1, 133-141. | 2.3 | 20 |
| 518 | Molecular characterization of fervidolysin, a subtilisin-like serine protease from the thermophilic bacterium Fervidobacterium pennivorans. Extremophiles, 2002, 6, 185-194. | 2.3 | 43 |
| 519 | Aspergillus oryzaein solid-state and submerged fermentations. FEMS Yeast Research, 2002, 2, 245-248. | 2.3 | 75 |
| 520 | Cell to cell communication by autoinducing peptides in gram-positive bacteria. Antonie Van Leeuwenhoek, 2002, 81, 233-243. | 1.7 | 248 |
| 521 | The Intestinal LABs. Antonie Van Leeuwenhoek, 2002, 82, 341-352. | 1.7 | 133 |
| 522 | Molecular Diversity of Lactobacillus spp. and Other Lactic Acid Bacteria in the Human Intestine as Determined by Specific Amplification of 16S Ribosomal DNA. Applied and Environmental Microbiology, 2002, 68, 114-123. | 3.1 | 619 |

| # | Article | IF | Citations |
|---|---|---|---|
| 523 | Bifidobacterial Diversity in Human Feces Detected by Genus-Specific PCR and Denaturing Gradient Gel Electrophoresis. Applied and Environmental Microbiology, 2001, 67, 504-513. | 3.1 | 392 |
| 524 | A two-component signal-transduction cascade in Carnobacterium piscicola LV17B: two signaling peptides and one sensor-transmitter. Peptides, 2001, 22, 1597-1601. | 2.4 | 31 |
| 525 | Sugar catabolism and its impact on the biosynthesis and engineering of exopolysaccharide production in lactic acid bacteria. International Dairy Journal, 2001, 11, 723-732. | 3.0 | 117 |
| 526 | Purification, characterization, and molecular modeling of pyrolysin and other extracellular thermostable serine proteases from hyperthermophilic microorganisms. Methods in Enzymology, 2001, 330, 383-393. | 1.0 | 16 |
| 527 | [4] ADP-dependent glucokinase and phosphofructokinase from Pyrococcus furiosus. Methods in Enzymology, 2001, 331, 41-53. | 1.0 | 16 |
| 528 | A Desulfitobacterium strain isolated from human feces that does not dechlorinate chloroethenes or chlorophenols. Archives of Microbiology, 2001, 175, 389-394. | 2.2 | 32 |
| 529 | Two distinct enzyme systems are responsible for tetrachloroethene and chlorophenol reductive dehalogenation in Desulfitobacterium strain PCE1. Archives of Microbiology, 2001, 176, 165-169. | 2.2 | 54 |
| 530 | Genetic and biochemical characterization of a short-chain alcohol dehydrogenase from the hyperthermophilic archaeonPyrococcus furiosus. FEBS Journal, 2001, 268, 3062-3068. | 0.2 | 50 |
| 531 | Gelatinase biosynthesis-activating pheromone: a peptide lactone that mediates a quorum sensing in Enterococcus faecalis. Molecular Microbiology, 2001, 41, 145-154. | 2.5 | 234 |
| 532 | Advances in genomics for microbial food fermentations and safety. Current Opinion in Biotechnology, 2001, 12, 493-498. | 6.6 | 44 |
| 533 | The NADH oxidase fromPyrococcus furiosus. FEBS Journal, 2001, 268, 5816-5823. | 0.2 | 60 |
| 534 | Improved oligosaccharide synthesis by protein engineering of ?-glucosidase CelB from hyperthermophilicPyrococcus furiosus. Biotechnology and Bioengineering, 2001, 73, 203-210. | 3.3 | 77 |
| 535 | Crystal structure of the Lrp-like transcriptional regulator from the archaeon Pyrococcus furiosus. EMBO Journal, 2001, 20, 990-997. | 7.8 | 135 |
| 536 | Polymerase Chain Reaction and Denaturing Gradient Gel Electrophoresis Monitoring of Fecal Bifidobacterium Populations in a Prebiotic and Probiotic Feeding Trial. Systematic and Applied Microbiology, 2001, 24, 227-231. | 2.8 | 94 |
| 537 | DNA Isolation Protocols Affect the Detection Limit of PCRApproaches of Bacteria in Samples from the HumanGastrointestinal Tract. Systematic and Applied Microbiology, 2001, 24, 405-410. | 2.8 | 102 |
| 538 | Functional Analysis of the Lactococcus lactis galU and galE Genes and Their Impact on Sugar Nucleotide and Exopolysaccharide Biosynthesis. Applied and Environmental Microbiology, 2001, 67, 3033-3040. | 3.1 | 117 |
| 539 | Î²-glucosidase CelB from Pyrococcus furiosus: Production by Escherichia coli, purification, and in vitro evolution. Methods in Enzymology, 2001, 330, 364-379. | 1.0 | 23 |
| 540 | ADP-Dependent Phosphofructokinases in Mesophilic and Thermophilic Methanogenic Archaea. Journal of Bacteriology, 2001, 183, 7145-7153. | 2.2 | 51 |

| # | Article | IF | Citations |
|---|---|---|---|
| 541 | The Phosphoglucose Isomerase from the Hyperthermophilic ArchaeonPyrococcus furiosus Is a Unique Glycolytic Enzyme That Belongs to the Cupin Superfamily. Journal of Biological Chemistry, 2001, 276, 40926-40932. | 3.4 | 49 |
| 542 | Relationship between Glycolysis and Exopolysaccharide Biosynthesis in Lactococcus lactis. Applied and Environmental Microbiology, 2001, 67, 33-41. | 3.1 | 121 |
| 543 | Cold Shock Proteins ofLactococcus lactisMG1363 Are Involved in Cryoprotection and in the Production of Cold-Induced Proteins. Applied and Environmental Microbiology, 2001, 67, 5171-5178. | 3.1 | 58 |
| 544 | Development of a Gene Cloning and Inactivation System for Halorespiring Desulfitobacterium dehalogenans. Applied and Environmental Microbiology, 2001, 67, 591-597. | 3.1 | 15 |
| 545 | Activation of Silent gal Genes in the lac-gal Regulon of Streptococcus thermophilus. Journal of Bacteriology, 2001, 183, 1184-1194. | 2.2 | 117 |
| 546 | Energy Yield of Respiration on Chloroaromatic Compounds in Desulfitobacterium dehalogenans. Applied and Environmental Microbiology, 2001, 67, 3958-3963. | 3.1 | 35 |
| 547 | Clostridium beijerinckii Cells Expressing Neocallimastix patriciarum Glycoside Hydrolases Show Enhanced Lichenan Utilization and Solvent Production. Applied and Environmental Microbiology, 2001, 67, 5127-5133. | 3.1 | 41 |
| 548 | Characterization of Î²-glycosylhydrolases from Pyrococcus furiosus. Methods in Enzymology, 2001, 330, 329-346. | 1.0 | 19 |
| 549 | Chapter 4 The role of cold-shock proteins in low-temperature adaptation. Cell and Molecular Response To Stress, 2001, 2, 43-56. | 0.4 | 3 |
| 550 | Hierarchical control versus autoregulation of carbohydrate utilization in bacteria. Journal of Molecular Microbiology and Biotechnology, 2001, 3, 401-13. | 1.0 | 25 |
| 551 | Spatial distribution of 16S rRNA levels from uncultured acidobacteria in soil. Letters in Applied Microbiology, 2000, 31, 118-122. | 2.2 | 18 |
| 552 | Halorespiring bacteriaâ€“molecular characterization and detection. Enzyme and Microbial Technology, 2000, 27, 812-820. | 3.2 | 50 |
| 553 | Nucleotide Sequence Analysis of the Lactococcal EPS Plasmid pNZ4000. Plasmid, 2000, 43, 130-136. | 1.4 | 52 |
| 554 | Utilisation of saccharides in extruded domestic organic waste by Clostridium acetobutylicum ATCC 824 for production of acetone, butanol and ethanol. Applied Microbiology and Biotechnology, 2000, 54, 162-167. | 3.6 | 73 |
| 555 | Activity and stability of hyperthermophilic enzymes: a comparative study on two archaeal Î²-glycosidases. Extremophiles, 2000, 4, 157-164. | 2.3 | 32 |
| 556 | An Lrp-like Transcriptional Regulator from the ArchaeonPyrococcus furiosus Is Negatively Autoregulated. Journal of Biological Chemistry, 2000, 275, 38160-38169. | 3.4 | 79 |
| 557 | Transcriptional Regulation of the cpr Gene Cluster inortho-Chlorophenol-Respiring Desulfitobacterium dehalogenans. Journal of Bacteriology, 2000, 182, 5683-5691. | 2.2 | 100 |
| 558 | Response of a Soil Bacterial Community to Grassland Succession as Monitored by 16S rRNA Levels of the Predominant Ribotypes. Applied and Environmental Microbiology, 2000, 66, 3998-4003. | 3.1 | 97 |

| # | Article | IF | Citations |
|---|---|---|---|
| 559 | Control of Lactose Transport, Î²-Galactosidase Activity, and Glycolysis by CcpA in Streptococcus thermophilus : Evidence for Carbon Catabolite Repression by a Non-Phosphoenolpyruvate-Dependent Phosphotransferase System Sugar. Journal of Bacteriology, 2000, 182, 5982-5989. | 2.2 | 111 |
| 560 | Physiological and Regulatory Effects of Controlled Overproduction of Five Cold Shock Proteins of Lactococcus lactis MG1363. Applied and Environmental Microbiology, 2000, 66, 3756-3763. | 3.1 | 43 |
| 561 | Changes in Glycolytic Activity of Lactococcus lactis Induced by Low Temperature. Applied and Environmental Microbiology, 2000, 66, 3686-3691. | 3.1 | 74 |
| 562 | Deletion of Various Carboxy-Terminal Domains of Lactococcus lactis SK11 Proteinase: Effects on Activity, Specificity, and Stability of the Truncated Enzyme. Applied and Environmental Microbiology, 2000, 66, 2859-2865. | 3.1 | 15 |
| 563 | Purification and Characterization of the Alanine Aminotransferase from the Hyperthermophilic Archaeon Pyrococcus furiosus and Its Role in Alanine Production. Journal of Bacteriology, 2000, 182, 2559-2566. | 2.2 | 74 |
| 564 | Improving Low-Temperature Catalysis in the Hyperthermostable Pyrococcus furiosus Î²-Glucosidase CelB by Directed Evolution. Biochemistry, 2000, 39, 3656-3665. | 2.5 | 83 |
| 565 | Temperature and Denaturing Gradient Gel Electrophoresis Analysis of 16S rRNA from Human Faecal Samples. Bioscience and Microflora, 2000, 19, 93-98. | 0.5 | 15 |
| 566 | A molecular view of the intestinal ecosystem. Current Issues in Intestinal Microbiology, 2000, 1, 1-12. | 2.5 | 115 |
| 567 | Molecular and Biochemical Characterization of the ADP-dependent Phosphofructokinase from the Hyperthermophilic Archaeon Pyrococcus furiosus. Journal of Biological Chemistry, 1999, 274, 21023-21028. | 3.4 | 91 |
| 568 | Purification and Molecular Characterization ofortho-Chlorophenol Reductive Dehalogenase, a Key Enzyme of Halorespiration in Desulfitobacterium dehalogenans. Journal of Biological Chemistry, 1999, 274, 20287-20292. | 3.4 | 154 |
| 569 | Food biotechnology: Frontiers of food functionalityEditorial overview. Current Opinion in Biotechnology, 1999, 10, 483-484. | 6.6 | 2 |
| 570 | Genetics and engineering of microbial exopolysaccharides for food: approaches for the production of existing and novel polysaccharides. Current Opinion in Biotechnology, 1999, 10, 498-504. | 6.6 | 92 |
| 571 | Conversion of Lactococcus lactis from homolactic to homoalanine fermentation through metabolic engineering. Nature Biotechnology, 1999, 17, 588-592. | 17.5 | 174 |
| 572 | Glutamate dehydrogenase from hyperthermophilic Bacteria and Archaea: determinants of thermostability and catalysis at extremely high temperatures. Journal of Molecular Catalysis B: Enzymatic, 1999, 7, 133-145. | 1.8 | 5 |
| 573 | In vivo nuclear magnetic resonance studies of glycolytic kinetics inLactococcus lactis. , 1999, 64, 200-212. | | 107 |
| 574 | Gene expression systems for lactic acid bacteria. Current Opinion in Microbiology, 1999, 2, 289-295. | 5.1 | 151 |
| 575 | Molecular approaches to study probiotic bacteria. Trends in Food Science and Technology, 1999, 10, 400-404. | 15.1 | 31 |
| 576 | Lantibiotics: biosynthesis, mode of action and applications. Natural Product Reports, 1999, 16, 575-587. | 10.3 | 123 |

| # | Article | IF | Citations |
|---|---|---|---|
| 577 | Engineering activity and stability of Thermotoga maritima glutamate dehydrogenase. II: construction of a 16-residue ion-pair network at the subunit interface. Journal of Molecular Biology, 1999, 289, 357-369. | 4.2 | 66 |
| 578 | Searching for predominant soil bacteria: 16S rDNA cloning versus strain cultivation. FEMS Microbiology Ecology, 1999, 30, 137-145. | 2.7 | 5 |
| 579 | Cold Shock Proteins and Low-Temperature Response of Streptococcus thermophilus CNRZ302. Applied and Environmental Microbiology, 1999, 65, 4436-4442. | 3.1 | 51 |
| 580 | Reductive Dechlorination of Tetrachloroethene to cis -1,2-Dichloroethene by a Thermophilic Anaerobic Enrichment Culture. Applied and Environmental Microbiology, 1999, 65, 2312-2316. | 3.1 | 37 |
| 581 | Exopolysaccharide Biosynthesis in Lactococcus lactis NIZO B40: Functional Analysis of the Glycosyltransferase Genes Involved in Synthesis of the Polysaccharide Backbone. Journal of Bacteriology, 1999, 181, 338-340. | 2.2 | 74 |
| 582 | Transcriptional Regulation in the Hyperthermophilic Archaeon Pyrococcus furiosus : Coordinated Expression of Divergently Oriented Genes in Response to Î²-Linked Glucose Polymers. Journal of Bacteriology, 1999, 181, 3777-3783. | 2.2 | 21 |
| 583 | Acetate Utilization in Lactococcus lactis Deficient in Lactate Dehydrogenase: a Rescue Pathway for Maintaining Redox Balance. Journal of Bacteriology, 1999, 181, 5521-5526. | 2.2 | 48 |
| 584 | Functional Analysis of Glycosyltransferase Genes from Lactococcus lactis and Other Gram-Positive Cocci: Complementation, Expression, and Diversity. Journal of Bacteriology, 1999, 181, 6347-6353. | 2.2 | 96 |
| 585 | Random Transposition by Tn 916 in Desulfitobacterium dehalogenans Allows for Isolation and Characterization of Halorespiration-Deficient Mutants. Journal of Bacteriology, 1999, 181, 6882-6888. | 2.2 | 33 |
| 586 | Molecular Characterization of the Lactococcus lactis ptsHI Operon and Analysis of the Regulatory Role of HPr. Journal of Bacteriology, 1999, 181, 764-771. | 2.2 | 48 |
| 587 | Characterization of the Divergent sacBK and sacAR Operons, Involved in Sucrose Utilization by Lactococcus lactis. Journal of Bacteriology, 1999, 181, 1924-1926. | 2.2 | 35 |
| 588 | Use of marker genes in competition studies of Rhizobium. Plant and Soil, 1998, 204, 35-45. | 3.7 | 28 |
| 589 | Demonstration of safety of probiotics â€" a review. International Journal of Food Microbiology, 1998, 44, 93-106. | 4.7 | 701 |
| 590 | Insights into the molecular basis of thermal stability from the analysis of ion-pair networks in the Glutamate Dehydrogenase family. FEBS Journal, 1998, 255, 336-346. | 0.2 | 103 |
| 591 | Sugar utilization and its control in hyperthermophiles. Extremophiles, 1998, 2, 201-205. | 2.3 | 42 |
| 592 | Synthesis of oligosaccharides catalyzed by thermostable Î²-glucosidase fromPyrococcus furiosus. Applied Biochemistry and Biotechnology, 1998, 75, 269-278. | 2.9 | 18 |
| 593 | Transcriptional activation of the glycolytic las operon and catabolite repression of the gal operon in Lactococcus lactis are mediated by the catabolite control protein CcpA. Molecular Microbiology, 1998, 30, 789-798. | 2.5 | 173 |
| 594 | Making More of Milk Sugar by Engineering Lactic Acid Bacteria. International Dairy Journal, 1998, 8, 227-233. | 3.0 | 21 |

| # | Article | IF | Citations |
|---|---|---|---|
| 595 | Engineering activity and stability of Thermotoga maritima glutamate dehydrogenase. I. introduction of a six-residue ion-pair network in the hinge region. Journal of Molecular Biology, 1998, 280, 287-296. | 4.2 | 33 |
| 596 | Quorum sensing-controlled gene expression in lactic acid bacteria. Journal of Biotechnology, 1998, 64, 15-21. | 3.8 | 641 |
| 597 | The Ferredoxin-dependent Conversion of Glyceraldehyde-3-phosphate in the Hyperthermophilic ArchaeonPyrococcus furiosus Represents a Novel Site of Glycolytic Regulation. Journal of Biological Chemistry, 1998, 273, 28149-28154. | 3.4 | 99 |
| 598 | Genetics of galactose utilisation via the Leloir pathway in lactic acid bacteria. Dairy Science and Technology, 1998, 78, 77-84. | 0.9 | 79 |
| 599 | Use of the Lactococcal nisA Promoter To Regulate Gene Expression in Gram-Positive Bacteria: Comparison of Induction Level and Promoter Strength. Applied and Environmental Microbiology, 1998, 64, 2763-2769. | 3.1 | 171 |
| 600 | Temperature Gradient Gel Electrophoresis Analysis of 16S rRNA from Human Fecal Samples Reveals Stable and Host-Specific Communities of Active Bacteria. Applied and Environmental Microbiology, 1998, 64, 3854-3859. | 3.1 | 1,186 |
| 601 | Redistribution mÃ©tabolique chez une souche de Lactobacillus plantarum dÃ©ficiente en lactate deshydrogÃ©nase. Dairy Science and Technology, 1998, 78, 107-116. | 0.9 | 6 |
| 602 | Regulation of the carbohydrate metabolism in Lactococcus lactis and other lactic acid bacteria. Dairy Science and Technology, 1998, 78, 69-76. | 0.9 | 8 |
| 603 | Quantification of 16S rRNAs in Complex Bacterial Communities by Multiple Competitive Reverse Transcription-PCR in Temperature Gradient Gel Electrophoresis Fingerprints. Applied and Environmental Microbiology, 1998, 64, 4581-4587. | 3.1 | 205 |
| 604 | In Situ Detection of an Uncultured Predominant Bacillus in Dutch Grassland Soils. Applied and Environmental Microbiology, 1998, 64, 4588-4590. | 3.1 | 41 |
| 605 | Cofactor Engineering: a Novel Approach to Metabolic Engineering in Lactococcus lactis by Controlled Expression of NADH Oxidase. Journal of Bacteriology, 1998, 180, 3804-3808. | 2.2 | 217 |
| 606 | Characterization of Multiple Regions Involved in Replication and Mobilization of Plasmid pNZ4000 Coding for Exopolysaccharide Production in Lactococcus lactis. Journal of Bacteriology, 1998, 180, 5285-5290. | 2.2 | 46 |
| 607 | Molecular and Biochemical Characterization of an Endo-Î²-1,3-glucanase of the Hyperthermophilic ArchaeonPyrococcus furiosus. Journal of Biological Chemistry, 1997, 272, 31258-31264. | 3.4 | 130 |
| 608 | Characterization of a locus from Carnobacterium piscicola LV17B involved in bacteriocin production and immunity: evidence for global inducer-mediated transcriptional regulation. Journal of Bacteriology, 1997, 179, 6163-6171. | 2.2 | 116 |
| 609 | Crystal structure of glutamate dehydrogenase from the hyperthermophilic eubacterium Thermotoga maritima at 3.0 Ã... resolution. Journal of Molecular Biology, 1997, 267, 916-932. | 4.2 | 146 |
| 610 | Food-grade controlled lysis of Lactococcus lactis for accelerated cheese ripening. Nature Biotechnology, 1997, 15, 976-979. | 17.5 | 146 |
| 611 | Controlled overproduction of proteins by lactic acid bacteria. Trends in Biotechnology, 1997, 15, 135-140. | 9.3 | 208 |
| 612 | Glutamate dehydrogenase from the hyperthermophilic bacterium Thermotoga maritima: molecular characterization and phylogenetic implications. Extremophiles, 1997, 1, 53-61. | 2.3 | 19 |

| # | Article | IF | Citations |
|---|---|---|---|
| 613 | Expression systems for industrial Gram-positive bacteria with low guanine and cytosine content. Current Opinion in Biotechnology, 1997, 8, 547-553. | 6.6 | 48 |
| 614 | Characterization of Rhizobium etli and other Rhizobium spp. that nodulate Phaseolus vulgaris L. in an Austrian soil. Molecular Ecology, 1997, 6, 601-608. | 3.9 | 38 |
| 615 | Molecular characterization of the plasmidâ€encoded eps gene cluster essential for exopolysaccharide biosynthesis in Lactococcus lactis. Molecular Microbiology, 1997, 24, 387-397. | 2.5 | 257 |
| 616 | Quorum sensing by peptide pheromones and twoâ€component signalâ€transduction systems in Gramâ€positive bacteria. Molecular Microbiology, 1997, 24, 895-904. | 2.5 | 710 |
| 617 | Stabilization of Enzymes against Thermal Stress and Freeze-Drying by Mannosylglycerate. Applied and Environmental Microbiology, 1997, 63, 4020-4025. | 3.1 | 111 |
| 618 | Controlled gene expression systems for lactic acid bacteria: transferable nisin-inducible expression cassettes for Lactococcus, Leuconostoc, and Lactobacillus spp. Applied and Environmental Microbiology, 1997, 63, 4581-4584. | 3.1 | 231 |
| 619 | A Cell-Free Transcription System for the Hyperthermophilic Archaeon Pyrococcus Furiosus. Nucleic Acids Research, 1996, 24, 2369-2376. | 14.5 | 75 |
| 620 | Identical transcriptional control of the divergently transcribed prtP and prtM genes that are required for proteinase production in lactococcus lactis SK11. Journal of Bacteriology, 1996, 178, 1525-1531. | 2.2 | 37 |
| 621 | Functional analysis of promoters in the nisin gene cluster of Lactococcus lactis. Journal of Bacteriology, 1996, 178, 3434-3439. | 2.2 | 316 |
| 622 | Crystallization and preliminary structural studies of lactose-specific enzyme IIA from Lactococcus lactis. Acta Crystallographica Section D: Biological Crystallography, 1996, 52, 1199-1201. | 2.5 | 2 |
| 623 | Metabolic engineering of sugar catabolism in lactic acid bacteria. Antonie Van Leeuwenhoek, 1996, 70, 223-242. | 1.7 | 134 |
| 624 | Genetics of subtilin and nisin biosyntheses. Antonie Van Leeuwenhoek, 1996, 69, 109-117. | 1.7 | 57 |
| 625 | Protein engineering of lantibiotics. Antonie Van Leeuwenhoek, 1996, 69, 161-170. | 1.7 | 119 |
| 626 | Comparison of lantibiotic gene clusters and encoded proteins. Antonie Van Leeuwenhoek, 1996, 69, 171-184. | 1.7 | 156 |
| 627 | Immunological crossreactivity to the catabolite control protein CcpA fromBacillus megateriumis found in many Gram-positive bacteria. FEMS Microbiology Letters, 1996, 139, 109-115. | 1.8 | 46 |
| 628 | Sugar metabolism of hyperthermophiles. FEMS Microbiology Reviews, 1996, 18, 119-137. | 8.6 | 107 |
| 629 | Carbon Monoxide Dehydrogenase from GÃ¶1. Journal of Biological Chemistry, 1996, 271, 14256-14263. | 3.4 | 27 |
| 630 | Isolation and Characterization of the Hyperthermostable Serine Protease, Pyrolysin, and Its Gene from the Hyperthermophilic Archaeon Pyrococcus furiosus. Journal of Biological Chemistry, 1996, 271, 20426-20431. | 3.4 | 72 |

| # | Article | IF | Citations |
|---|---|---|---|
| 631 | Sugar metabolism of hyperthermophiles. FEMS Microbiology Reviews, 1996, 18, 119-137. | 8.6 | 8 |
| 632 | Controlled gene expression systems for Lactococcus lactis with the food-grade inducer nisin. Applied and Environmental Microbiology, 1996, 62, 3662-3667. | 3.1 | 752 |
| 633 | Simultaneous detection of different Rhizobium strains marked with either the Escherichia coli gusA gene or the Pyrococcus furiosus celB gene. Applied and Environmental Microbiology, 1996, 62, 4191-4194. | 3.1 | 25 |
| 634 | Food-grade cloning and expression system for Lactococcus lactis. Applied and Environmental Microbiology, 1996, 62, 1008-1013. | 3.1 | 127 |
| 635 | Rapid and sensitive method for the detection of Mycobacterium chlorophenolicum PCP-1 in soil based on 16S rRNA gene-targeted PCR. Applied and Environmental Microbiology, 1996, 62, 1478-1480. | 3.1 | 23 |
| 636 | The lactose transporter in Leuconostoc lactis is a new member of the LacS subfamily of galactoside-pentose-hexuronide translocators. Applied and Environmental Microbiology, 1996, 62, 1574-1582. | 3.1 | 30 |
| 637 | Detection and localization of syntrophic propionate-oxidizing bacteria in granular sludge by in situ hybridization using 16S rRNA-based oligonucleotide probes. Applied and Environmental Microbiology, 1996, 62, 1656-1663. | 3.1 | 151 |
| 638 | Population dynamics of propionate-oxidizing bacteria under methanogenic and sulfidogenic conditions in anaerobic granular sludge. Applied and Environmental Microbiology, 1996, 62, 2163-2168. | 3.1 | 76 |
| 639 | Characterization of the celB gene coding for beta-glucosidase from the hyperthermophilic archaeon Pyrococcus furiosus and its expression and site-directed mutation in Escherichia coli. Journal of Bacteriology, 1995, 177, 7105-7111. | 2.2 | 128 |
| 640 | Maturation pathway of nisin and other lantibiotics: post-translationally modified antimicrobial peptides exported by Gram-positive bacteria. Molecular Microbiology, 1995, 17, 427-437. | 2.5 | 194 |
| 641 | Medium-dependent regulation of proteinase gene expression in Lactococcus lactis: control of transcription initiation by specific dipeptides. Journal of Bacteriology, 1995, 177, 2982-2989. | 2.2 | 86 |
| 642 | Purification and Characterization of a Novel ADP-dependent Glucokinase from the Hyperthermophilic Archaeon Pyrococcus furiosus. Journal of Biological Chemistry, 1995, 270, 30453-30457. | 3.4 | 117 |
| 643 | Homology modelling of the Lactococcus lactis leader peptidase NisP and its interaction with the precursor of the lantibiotic nisin. Protein Engineering, Design and Selection, 1995, 8, 117-125. | 2.1 | 39 |
| 644 | Exchange of domains of glutamate dehydrogenase from the hyperthermophilic archaeon Pyrococcus furiosus and the mesophilic bacterium Clostridium difficile: effects on catalysis, thermoactivity and stability. Protein Engineering, Design and Selection, 1995, 8, 1287-1294. | 2.1 | 22 |
| 645 | Identification and characterization of the insertion element IS1070 from leuconostoc lactis NZ6009. Gene, 1995, 155, 95-100. | 2.2 | 27 |
| 646 | Characterization and heterologous expression of the tetL gene and identification of iso-ISS1 elements from Enterococcus faecalis plasmid pJH1. Gene, 1995, 160, 89-93. | 2.2 | 16 |
| 647 | Autoregulation of Nisin Biosynthesis in Lactococcus lactis by Signal Transduction. Journal of Biological Chemistry, 1995, 270, 27299-27304. | 3.4 | 483 |
| 648 | Elucidation of the Primary Structure of the Lantibiotic Epilancin K7 from Staphylococcus epidermidis K7. Cloning and Characterisation of the Epilancin-K7-Encoding Gene and NMR Analysis of Mature Epilancin K7. FEBS Journal, 1995, 230, 587-600. | 0.2 | 90 |

| # | Article | IF | Citations |
|---|---|---|---|
| 649 | Metabolic engineering of Lactococcus lactis: influence of the overproduction of alpha-acetolactate synthase in strains deficient in lactate dehydrogenase as a function of culture conditions. Applied and Environmental Microbiology, 1995, 61, 3967-3971. | 3.1 | 93 |
| 650 | Detection and characterization of lactose-utilizing Lactococcus spp. in natural ecosystems. Applied and Environmental Microbiology, 1995, 61, 788-792. | 3.1 | 160 |
| 651 | Genetic marking of Lactococcus lactis shows its survival in the human gastrointestinal tract. Applied and Environmental Microbiology, 1995, 61, 2771-2774. | 3.1 | 187 |
| 652 | Improvement of solubility and stability of the antimicrobial peptide nisin by protein engineering. Applied and Environmental Microbiology, 1995, 61, 2873-2878. | 3.1 | 274 |
| 653 | Characterization of plasmid-encoded citrate permease (citP) genes from Leuconostoc species reveals high sequence conservation with the Lactococcus lactis citP gene. Applied and Environmental Microbiology, 1995, 61, 3172-3176. | 3.1 | 33 |
| 654 | Analysis of the binding site of the LysR-type transcriptional activator TcbR on the tcbR and tcbC divergent promoter sequences. Journal of Bacteriology, 1994, 176, 1850-1856. | 2.2 | 23 |
| 655 | Identification and characterization of genes involved in excision of the Lactococcus lactis conjugative transposon Tn5276. Journal of Bacteriology, 1994, 176, 2165-2171. | 2.2 | 49 |
| 656 | Evidence for a large dispensable segment in the subtilisin-like catalytic domain of the Lactococcus lactis cell-envelope proteinas. Protein Engineering, Design and Selection, 1994, 7, 991-996. | 2.1 | 32 |
| 657 | Genetics of lactose utilization in lactic acid bacteria. FEMS Microbiology Reviews, 1994, 15, 217-237. | 8.6 | 178 |
| 658 | Molecular and Comparative Analysis of the HyperthermostablePyrococcus FuriosusGlutamate Dehydrogenase and its Gene. Biocatalysis, 1994, 11, 131-141. | 0.9 | 6 |
| 659 | Use of the Escherichia coli beta-glucuronidase (gusA) gene as a reporter gene for analyzing promoters in lactic acid bacteria. Applied and Environmental Microbiology, 1994, 60, 587-593. | 3.1 | 185 |
| 660 | Distribution and evolution of nisin-sucrose elements in Lactococcus lactis. Applied and Environmental Microbiology, 1994, 60, 1798-1804. | 3.1 | 33 |
| 661 | Evidence for the operation of a novel Embden-Meyerhof pathway that involves ADP-dependent kinases during sugar fermentation by Pyrococcus furiosus. Journal of Biological Chemistry, 1994, 269, 17537-41. | 3.4 | 175 |
| 662 | Influence of amino acid substitutions in the nisin leader peptide on biosynthesis and secretion of nisin by Lactococcus lactis. Journal of Biological Chemistry, 1994, 269, 3555-62. | 3.4 | 132 |
| 663 | Distribution and characterization of plasmid-related sequences in the chromosomal DNA of different thermophilic Methanobacterium strains. Molecular Genetics and Genomics, 1993, 240, 81-91. | 2.4 | 6 |
| 664 | Functional analysis of the Lactococcus lactis usp45 secretion signal in the secretion of a homologous proteinase and a heterologous Î±-amylase. Molecular Genetics and Genomics, 1993, 240, 428-434. | 2.4 | 86 |
| 665 | Characterization of the nisin gene cluster nisABTCIPR of Lactococcus lactis. FEBS Journal, 1993, 216, 281-291. | 0.2 | 495 |
| 666 | Biosynthesis and secretion of a precursor of nisin Z byLactococcus lactis, directed by the leader peptide of the homologous lantibiotic subtilin fromBacillus subtilis. FEBS Letters, 1993, 330, 23-27. | 2.8 | 79 |

| # | Article | IF | Citations |
|---|---|---|---|
| 667 | Overproduction of bovine Î²-casein in Escherichia coli and engineering of its main chymosin cleavage site. Protein Engineering, Design and Selection, 1993, 6, 763-770. | 2.1 | 15 |
| 668 | The glutamate dehydrogenase-encoding gene of the hyperthermophilic archaeon Pyrococcus furiosus: sequence, transcription and analysis of the deduced amino acid sequence. Gene, 1993, 132, 143-148. | 2.2 | 59 |
| 669 | Lysines 72, 80 and 213 and aspartic acid 210 of the Lactococcus lactis LacR repressor are involved in the response to the inducer tagatose-6-phosphate leading to induction of lac operon expression. Protein Engineering, Design and Selection, 1993, 6, 201-206. | 2.1 | 38 |
| 670 | Engineering of the substrate-binding region of the sublilisin-like, cell-envelop proteinase of Lactococcus lactis. Protein Engineering, Design and Selection, 1993, 6, 927-937. | 2.1 | 42 |
| 671 | Efficient random mutagenesis method with adjustable mutation frequency by use of PCR and dITP. Nucleic Acids Research, 1993, 21, 777-778. | 14.5 | 160 |
| 672 | Characterization of the Lactococcus lactis nisin A operon genes nisP, encoding a subtilisin-like serine protease involved in precursor processing, and nisR, encoding a regulatory protein involved in nisin biosynthesis. Journal of Bacteriology, 1993, 175, 2578-2588. | 2.2 | 305 |
| 673 | Cloning, nucleotide sequence, and regulatory analysis of the Lactococcus lactis dnaJ gene. Journal of Bacteriology, 1993, 175, 1637-1644. | 2.2 | 130 |
| 674 | Integration and gene replacement in the Lactococcus lactis lac operon: induction of a cryptic phospho-beta-glucosidase in LacG-deficient strains. Journal of Bacteriology, 1993, 175, 5168-5175. | 2.2 | 28 |
| 675 | Properties of nisin Z and distribution of its gene, nisZ, in Lactococcus lactis. Applied and Environmental Microbiology, 1993, 59, 213-218. | 3.1 | 193 |
| 676 | Structure, organization, and expression of the lct gene for lacticin 481, a novel lantibiotic produced by Lactococcus lactis. Journal of Biological Chemistry, 1993, 268, 16361-8. | 3.4 | 114 |
| 677 | Identification of the CTAG-recognizing restriction-modification systemsMthZI andMthFI fromMethanobacterium thermoformicicumand characterization of the plasmid-encodedmthZIMgene. Nucleic Acids Research, 1992, 20, 5047-5052. | 14.5 | 25 |
| 678 | Modular organization of related Archaeal plasmids encoding different restriction-modification systems inMethanobacterium thermoformicicum. Nucleic Acids Research, 1992, 20, 6501-6507. | 14.5 | 46 |
| 679 | Characterization of the novel nisin-sucrose conjugative transposon Tn5276 and its insertion in Lactococcus lactis. Journal of Bacteriology, 1992, 174, 1280-1287. | 2.2 | 204 |
| 680 | Characterization of the Lactococcus lactis lactose operon promoter: contribution of flanking sequences and LacR repressor to promoter activity. Journal of Bacteriology, 1992, 174, 2273-2280. | 2.2 | 128 |
| 681 | Leuconostoc lactis beta-galactosidase is encoded by two overlapping genes. Journal of Bacteriology, 1992, 174, 4475-4481. | 2.2 | 81 |
| 682 | Location, characterization and expression of lytic enzyme-encoding gene, lytA, of Lactococcus lactis bacteriophage Ït US3 â€. Gene, 1992, 118, 115-120. | 2.2 | 61 |
| 683 | Transcriptional regulation of the Tn5276-located Lactococcus lactis sucrose operon and characterization of the sac A gene encoding sucrose-6-phosphate hydrolase. Gene, 1992, 121, 55-61. | 2.2 | 40 |
| 684 | Characterization of theLactococcus lactis pepNgene encoding an aminopeptidase homologous to mammalian aminopeptidase N. FEBS Letters, 1992, 306, 9-16. | 2.8 | 74 |

| # | Article | IF | Citations |
|---|---|---|---|
| 685 | Characterization of the archaeal, plasmid-encoded type II restriction-modification system MthTI from Methanobacterium thermoformicicum THF: homology to the bacterial NgoPII system from Neisseria gonorrhoeae. Journal of Bacteriology, 1992, 174, 5719-5726. | 2.2 | 50 |
| 686 | Proteinase overproduction in Lactococcus lactis strains: regulation and effect on growth and acidification in milk. Applied and Environmental Microbiology, 1992, 58, 78-84. | 3.1 | 48 |
| 687 | Engineering dehydrated amino acid residues in the antimicrobial peptide nisin. Journal of Biological Chemistry, 1992, 267, 24340-6. | 3.4 | 133 |
| 688 | Homology modelling and protein engineering strategy of subtilases, the family of subtilisin-like serine proteinases. Protein Engineering, Design and Selection, 1991, 4, 719-737. | 2.1 | 331 |
| 689 | Molecular organization of the minimal replicon of novel, narrow-host-range, lactococcal plasmid pCI305. Plasmid, 1991, 25, 16-26. | 1.4 | 66 |
| 690 | Sequence analysis of the Pseudomonas sp. strain P51 tcb gene cluster, which encodes metabolism of chlorinated catechols: evidence for specialization of catechol 1,2-dioxygenases for chlorinated substrates. Journal of Bacteriology, 1991, 173, 2425-2434. | 2.2 | 181 |
| 691 | Characterization of the Pseudomonas sp. strain P51 gene tcbR, a LysR-type transcriptional activator of the tcbCDEF chlorocatechol oxidative operon, and analysis of the regulatory region. Journal of Bacteriology, 1991, 173, 3700-3708. | 2.2 | 94 |
| 692 | Identification of a novel composite transposable element, Tn5280, carrying chlorobenzene dioxygenase genes of Pseudomonas sp. strain P51. Journal of Bacteriology, 1991, 173, 7077-7083. | 2.2 | 130 |
| 693 | Cloning and characterization of plasmid-encoded genes for the degradation of 1,2-dichloro-, 1,4-dichloro-, and 1,2,4-trichlorobenzene of Pseudomonas sp. strain P51. Journal of Bacteriology, 1991, 173, 6-15. | 2.2 | 183 |
| 694 | Cloning, sequence analysis, and functional expression of the acetyl coenzyme A synthetase gene from Methanothrix soehngenii in Escherichia coli. Journal of Bacteriology, 1991, 173, 6383-6389. | 2.2 | 74 |
| 695 | Identification and characterization of the lantibiotic nisin Z, a natural nisin variant. FEBS Journal, 1991, 201, 581-584. | 0.2 | 377 |
| 696 | Improved site-directed mutagenesis method using PCR. Nucleic Acids Research, 1991, 19, 4558-4558. | 14.5 | 117 |
| 697 | Engineering of the Lactococcus lactis serine proteinase by construction of hybrid enzymes. Protein Engineering, Design and Selection, 1991, 4, 479-484. | 2.1 | 83 |
| 698 | Identification of mesophilic lactic acid bacteria by using polymerase chain reaction-amplified variable regions of 16S rRNA and specific DNA probes. Applied and Environmental Microbiology, 1991, 57, 3390-3393. | 3.1 | 247 |
| 699 | Detection of Plasmid Transfer from Pseudomonas fluorescens to Indigenous Bacteria in Soil by Using Bacteriophage ÏŧR2f for Donor Counterselection. Applied and Environmental Microbiology, 1991, 57, 3482-3488. | 3.1 | 117 |
| 700 | Characterization and overexpression of the Lactococcus lactis pepN gene and localization of its product, aminopeptidase N. Applied and Environmental Microbiology, 1991, 57, 2555-2561. | 3.1 | 101 |
| 701 | Cloning, expression, and sequence analysis of the genes for carbon monoxide dehydrogenase of Methanothrix soehngenii. Journal of Biological Chemistry, 1991, 266, 6883-7. | 3.4 | 54 |
| 702 | Molecular cloning, characterization, and nucleotide sequence of the tagatose 6-phosphate pathway gene cluster of the lactose operon of Lactococcus lactis. Journal of Biological Chemistry, 1991, 266, 7176-81. | 3.4 | 99 |

| # | Article | IF | Citations |
|---|---|---|---|
| 703 | Nucleotide sequence and expression in Escherichia coli of the Lactococcus lactis citrate permease gene. Journal of Bacteriology, 1990, 172, 5789-5794. | 2.2 | 75 |
| 704 | Organization of a ribosomal RNA gene cluster from the ArchaebacteriumMethanothrix soehngenii. Nucleic Acids Research, 1990, 18, 1306-1306. | 14.5 | 10 |
| 705 | Nucleotide sequence of IS904 fromLactococcus lactissubsp.lactisstrain NIZO R5. Nucleic Acids Research, 1990, 18, 4253-4254. | 14.5 | 58 |
| 706 | Cloning of usp45, a gene encoding a secreted protein from Lactococcus lactis subsp. lactis MG1363. Gene, 1990, 95, 155-160. | 2.2 | 222 |
| 707 | Insertion elements on lactococcal proteinase plasmids. Applied and Environmental Microbiology, 1990, 56, 1890-1896. | 3.1 | 61 |
| 708 | Characterization of the lactose-specific enzymes of the phosphotransferase system in Lactococcus lactis. Journal of Biological Chemistry, 1990, 265, 22554-60. | 3.4 | 114 |
| 709 | Nucleotide sequence of a 16S rRNA encoding gene from the ArchaebacteriumMethanothrix soehngenii. Nucleic Acids Research, 1989, 17, 9469-9469. | 14.5 | 17 |
| 710 | Cloning and expression of the Lactococcus lactis subsp. Cremoris SK11 gene encoding an extracellular serine proteinase. Gene, 1989, 85, 169-176. | 2.2 | 137 |
| 711 | Gene Organization and Expression in Mesophilic Lactic Acid Bacteria. Journal of Dairy Science, 1989, 72, 3398-3405. | 3.4 | 26 |
| 712 | A maturation protein is essential for production of active forms of Lactococcus lactis SK11 serine proteinase located in or secreted from the cell envelope. Journal of Bacteriology, 1989, 171, 2795-2802. | 2.2 | 186 |
| 713 | Plasmid transformation by electroporation of Leuconostoc paramesenteroides and its use in molecular cloning. Applied and Environmental Microbiology, 1989, 55, 1483-1489. | 3.1 | 53 |
| 714 | Primary structure and organization of the gene for a procaryotic, cell envelope-located serine proteinase. Journal of Biological Chemistry, 1989, 264, 13579-85. | 3.4 | 149 |
| 715 | Proteinases of Streptococcus cremoris: physiological and genetic analysis. Antonie Van Leeuwenhoek, 1985, 51, 565-566. | 1.7 | 6 |
| 716 | A shoot-specific mRNA from pea: nucleotide sequence and regulation as compared to light-induced mRNAs. Plant Molecular Biology, 1985, 4, 95-102. | 3.9 | 17 |
| 717 | Transformation of Bacillus subtilis competent cells: Identification and regulation of the rec E gene product. Molecular Genetics and Genomics, 1983, 190, 56-64. | 2.4 | 39 |
| 718 | Cloning and expression of the Escherichia coli recA gene in Bacillus subtilis. Gene, 1983, 25, 301-308. | 2.2 | 58 |
| 719 | Transformation of Bacillus subtilis competent cells: Identification of a protein involved in recombination. Molecular Genetics and Genomics, 1982, 187, 439-445. | 2.4 | 33 |
| 720 | Plasmid DNA in Streptococcus cremoris Wg2: Influence of pH on Selection in Chemostats of a Variant Lacking a Protease Plasmid. Applied and Environmental Microbiology, 1982, 43, 1272-1277. | 3.1 | 92 |

| # | Article | IF | Citations |
|---|---|---|---|
| 721 | Fate of plasmid DNA in transformation of Bacillus subtilis protoplasts. Molecular Genetics and Genomics, 1981, 182, 39-43. | 2.4 | 32 |
| 722 | Plasmid transformation in Bacillus subtilis: Fate of plasmid DNA. Molecular Genetics and Genomics, 1981, 181, 424-433. | 2.4 | 86 |
| 723 | l-Aspartate fermentation by a free-livingCampylobacter species. Archives of Microbiology, 1978, 117, 109-114. | 2.2 | 28 |
| 724 | Future Development of Probiotic Dairy Products. , 0, , 195-206. | | 0 |
| 725 | The Human Intestinal Microbiota and Its Impact on Health. , 0, , 11-32. | | 1 |