Douwe Van Sinderen

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484 papers	29,664 citations	85 h-index	151 g-index
509 ext. papers	35,650 ext. citations	5.5 avg, IF	7.18 L-index

#	Paper	IF	Citations
484	Gut microbiota composition correlates with diet and health in the elderly. *Nature*, **2012**, 488, 178-84	50.4	1987
483	Composition, variability, and temporal stability of the intestinal microbiota of the elderly. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108 Suppl 1, 4586-91	11.5	1105
482	Bacteria as vitamin suppliers to their host: a gut microbiota perspective. *Current Opinion in Biotechnology*, **2013**, 24, 160-8	11.4	766
481	Genomics of Actinobacteria: tracing the evolutionary history of an ancient phylum. *Microbiology and Molecular Biology Reviews*, **2007**, 71, 495-548	13.2	680
480	The First Microbial Colonizers of the Human Gut: Composition, Activities, and Health Implications of the Infant Gut Microbiota. *Microbiology and Molecular Biology Reviews*, **2017**, 81,	13.2	626
479	T-cell activation by transitory neo-antigens derived from distinct microbial pathways. *Nature*, **2014**, 509, 361-5	50.4	492
478	Carbohydrate metabolism in Bifidobacteria. *Genes and Nutrition*, **2011**, 6, 285-306	4.3	445
477	Diversity of bifidobacteria within the infant gut microbiota. *PLoS ONE*, **2012**, 7, e36957	3.7	415
476	Bifidobacteria and Their Role as Members of the Human Gut Microbiota. *Frontiers in Microbiology*, **2016**, 7, 925	5.7	366
475	Bifidobacterial surface-exopolysaccharide facilitates commensal-host interaction through immune modulation and pathogen protection. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 2108-13	11.5	364
474	Genome-scale analyses of health-promoting bacteria: probiogenomics. *Nature Reviews Microbiology* , **2009**, 7, 61-71	22.2	334
473	Complete genome sequence of the prototype lactic acid bacterium Lactococcus lactis subsp. cremoris MG1363. *Journal of Bacteriology*, **2007**, 189, 3256-70	3.5	314
472	Fermented functional foods based on probiotics and their biogenic metabolites. *Current Opinion in Biotechnology*, **2005**, 16, 198-203	11.4	301
471	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, 11217-22	11.5	290
470	Stress Physiology of Lactic Acid Bacteria. *Microbiology and Molecular Biology Reviews*, **2016**, 80, 837-90	13.2	276
469	Sequence and analysis of the genetic locus responsible for surfactin synthesis in Bacillus subtilis. *Molecular Microbiology*, **1993**, 8, 821-31	4.1	274
468	Genome analysis of Bifidobacterium bifidum PRL2010 reveals metabolic pathways for host-derived glycan foraging. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 19514-9	11.5	266

467	B-group vitamin production by lactic acid bacteria--current knowledge and potential applications. *Journal of Applied Microbiology*, **2011**, 111, 1297-309	4.7	263
466	Getting better with bifidobacteria. *Journal of Applied Microbiology*, **2005**, 98, 1303-15	4.7	244
465	Improvement of the quality and shelf life of wheat bread by fermentation with the antifungal strain Lactobacillus plantarum FST 1.7. *Journal of Cereal Science*, **2007**, 45, 309-318	3.8	238
464	Exploring the diversity of the bifidobacterial population in the human intestinal tract. *Applied and Environmental Microbiology*, **2009**, 75, 1534-45	4.8	237
463	Stable Engraftment of Bifidobacterium longum AH1206 in the Human Gut Depends on Individualized Features of the Resident Microbiome. *Cell Host and Microbe*, **2016**, 20, 515-526	23.4	222
462	Assessing the fecal microbiota: an optimized ion torrent 16S rRNA gene-based analysis protocol. *PLoS ONE*, **2013**, 8, e68739	3.7	205
461	Characterization of the genetic locus responsible for the production of ABP-118, a novel bacteriocin produced by the probiotic bacterium Lactobacillus salivarius subsp. salivarius UCC118. *Microbiology (United Kingdom)*, **2002**, 148, 973-984	2.9	199
460	comK encodes the competence transcription factor, the key regulatory protein for competence development in Bacillus subtilis. *Molecular Microbiology*, **1995**, 15, 455-62	4.1	198
459	Current perspectives on antifungal lactic acid bacteria as natural bio-preservatives. *Trends in Food Science and Technology*, **2013**, 33, 93-109	15.3	189
458	Molecular dialogue between the human gut microbiota and the host: a Lactobacillus and Bifidobacterium perspective. *Cellular and Molecular Life Sciences*, **2014**, 71, 183-203	10.3	188
457	Multireplicon genome architecture of Lactobacillus salivarius. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 6718-23	11.5	183
456	Role of sortase-dependent pili of Bifidobacterium bifidum PRL2010 in modulating bacterium-host interactions. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 11151-6	11.5	172
455	Sequence analysis and molecular characterization of the temperate lactococcal bacteriophage r1t. *Molecular Microbiology*, **1996**, 19, 1343-55	4.1	170
454	Bifidobacteria exhibit social behavior through carbohydrate resource sharing in the gut. *Scientific Reports*, **2015**, 5, 15782	4.9	168
453	Riboflavin production in Lactococcus lactis: potential for in situ production of vitamin-enriched foods. *Applied and Environmental Microbiology*, **2004**, 70, 5769-77	4.8	166
452	Maternal inheritance of bifidobacterial communities and bifidophages in infants through vertical transmission. *Microbiome*, **2017**, 5, 66	16.6	163
451	Genomic encyclopedia of type strains of the genus Bifidobacterium. *Applied and Environmental Microbiology*, **2014**, 80, 6290-302	4.8	162
450	Human gut microbiota and bifidobacteria: from composition to functionality. *Antonie Van Leeuwenhoek*, **2008**, 94, 35-50	2.1	158

449	A small gene, designated comS, located within the coding region of the fourth amino acid-activation domain of srfA, is required for competence development in Bacillus subtilis. *Molecular Microbiology*, **1995**, 15, 55-63	4.1	153
448	Exploring Vertical Transmission of Bifidobacteria from Mother to Child. *Applied and Environmental Microbiology*, **2015**, 81, 7078-87	4.8	150
447	Insights into the taxonomy, genetics and physiology of bifidobacteria. *Antonie Van Leeuwenhoek*, **2004**, 86, 205-23	2.1	150
446	Selective carbohydrate utilization by lactobacilli and bifidobacteria. *Journal of Applied Microbiology*, **2013**, 114, 1132-46	4.7	147
445	Bacteriophages as biocontrol agents of food pathogens. *Current Opinion in Biotechnology*, **2011**, 22, 157-63	11.4	141
444	Host-microbe interactions that facilitate gut colonization by commensal bifidobacteria. *Trends in Microbiology*, **2012**, 20, 467-76	12.4	139
443	Analysis of bifidobacterial evolution using a multilocus approach. *International Journal of Systematic and Evolutionary Microbiology*, **2006**, 56, 2783-2792	2.2	136
442	Gut microbiota composition and Clostridium difficile infection in hospitalized elderly individuals: a metagenomic study. *Scientific Reports*, **2016**, 6, 25945	4.9	132
441	Lactic acid bacteria with potential to eliminate fungal spoilage in foods. *Journal of Applied Microbiology*, **2008**, 104, 915-23	4.7	129
440	Screening for and identification of starch-, amylopectin-, and pullulan-degrading activities in bifidobacterial strains. *Applied and Environmental Microbiology*, **2006**, 72, 5289-96	4.8	128
439	Enhancing the Microbiological Stability of Malt and Beer □A Review. *Journal of the Institute of Brewing*, **2005**, 111, 355-371	2	124
438	Cross-feeding by Bifidobacterium breve UCC2003 during co-cultivation with Bifidobacterium bifidum PRL2010 in a mucin-based medium. *BMC Microbiology*, **2014**, 14, 282	4.5	122
437	Genomics of the Genus Bifidobacterium Reveals Species-Specific Adaptation to the Glycan-Rich Gut Environment. *Applied and Environmental Microbiology*, **2016**, 82, 980-991	4.8	121
436	The Bifidobacterium dentium Bd1 genome sequence reflects its genetic adaptation to the human oral cavity. *PLoS Genetics*, **2009**, 5, e1000785	6	120
435	Bacterial vitamin B2, B11 and B12 overproduction: An overview. *International Journal of Food Microbiology*, **2009**, 133, 1-7	5.8	117
434	Bacteriophage orphan DNA methyltransferases: insights from their bacterial origin, function, and occurrence. *Applied and Environmental Microbiology*, **2013**, 79, 7547-55	4.8	116
433	Comparative genomics reveals close genetic relationships between phages from dairy bacteria and pathogenic Streptococci: evolutionary implications for prophage-host interactions. *Virology*, **2001**, 288, 325-41	3.6	115
432	Comparative and functional analysis of sortase-dependent proteins in the predicted secretome of Lactobacillus salivarius UCC118. *Applied and Environmental Microbiology*, **2006**, 72, 4143-53	4.8	114

431	Microbiomic analysis of the bifidobacterial population in the human distal gut. *ISME Journal*, **2009**, 3, 745-51	11.9	111
430	Identification and characterization of phage-resistance genes in temperate lactococcal bacteriophages. *Molecular Microbiology*, **2002**, 43, 509-20	4.1	109
429	Characterization of bacteriocin-like inhibitory substances (BLIS) from sourdough lactic acid bacteria and evaluation of their in vitro and in situ activity. *Journal of Applied Microbiology*, **2004**, 96, 521-34	4.7	108
428	Glycan Utilization and Cross-Feeding Activities by Bifidobacteria. *Trends in Microbiology*, **2018**, 26, 339-350	12.4	107
427	Deciphering bifidobacterial-mediated metabolic interactions and their impact on gut microbiota by a multi-omics approach. *ISME Journal*, **2016**, 10, 1656-68	11.9	107
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425	Characterization of virus-like particles associated with the human faecal and caecal microbiota. *Research in Microbiology*, **2014**, 165, 803-12	4	105
424	Genomics and ecological overview of the genus Bifidobacterium. *International Journal of Food Microbiology*, **2011**, 149, 37-44	5.8	104
423	The dilemma of phage taxonomy illustrated by comparative genomics of Sfi21-like Siphoviridae in lactic acid bacteria. *Journal of Bacteriology*, **2002**, 184, 6026-36	3.5	103
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419	High resolution in vivo bioluminescent imaging for the study of bacterial tumour targeting. *PLoS ONE*, **2012**, 7, e30940	3.7	100
418	Structure of the phage TP901-1 1.8 MDa baseplate suggests an alternative host adhesion mechanism. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 8954-8	11.5	100
417	Multivitamin production in Lactococcus lactis using metabolic engineering. *Metabolic Engineering*, **2004**, 6, 109-15	9.7	100
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415	Identification of universal gut microbial biomarkers of common human intestinal diseases by meta-analysis. *FEMS Microbiology Ecology*, **2017**, 93,	4.3	99
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413	Metabolism of sialic acid by Bifidobacterium breve UCC2003. *Applied and Environmental Microbiology*, **2014**, 80, 4414-26	4.8	98
412	Investigation of the evolutionary development of the genus Bifidobacterium by comparative genomics. *Applied and Environmental Microbiology*, **2014**, 80, 6383-94	4.8	95
411	Improvement and optimization of two engineered phage resistance mechanisms in Lactococcus lactis. *Applied and Environmental Microbiology*, **2001**, 67, 608-16	4.8	95
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406	Bifidobacterium asteroides PRL2011 genome analysis reveals clues for colonization of the insect gut. *PLoS ONE*, **2012**, 7, e44229	3.7	91
405	Characterization of ApuB, an extracellular type II amylopullulanase from Bifidobacterium breve UCC2003. *Applied and Environmental Microbiology*, **2008**, 74, 6271-9	4.8	90
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403	Insights into the biodiversity of the gut microbiota of broiler chickens. *Environmental Microbiology*, **2016**, 18, 4727-4738	5.2	89
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395	Investigation of the relationship between lactococcal host cell wall polysaccharide genotype and 936 phage receptor binding protein phylogeny. *Applied and Environmental Microbiology*, **2013**, 79, 4385-92	4.8	83
394	Bifidobacterium lactis DSM 10140: identification of the atp (atpBEFHAGDC) operon and analysis of its genetic structure, characteristics, and phylogeny. *Applied and Environmental Microbiology*, **2004**, 70, 3110-21	4.8	83
393	Characterization of the groEL and groES loci in Bifidobacterium breve UCC 2003: genetic, transcriptional, and phylogenetic analyses. *Applied and Environmental Microbiology*, **2004**, 70, 6197-209	4.8	82
392	Bifidobacteria and the infant gut: an example of co-evolution and natural selection. *Cellular and Molecular Life Sciences*, **2018**, 75, 103-118	10.3	81
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390	An analysis of bacteriocins produced by lactic acid bacteria isolated from malted barley. *Journal of Applied Microbiology*, **2001**, 91, 131-8	4.7	81
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386	Bacteriophage Tuc2009 encodes a tail-associated cell wall-degrading activity. *Journal of Bacteriology*, **2004**, 186, 3480-91	3.5	76
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363	Transcriptional and functional characterization of genetic elements involved in galacto-oligosaccharide utilization by Bifidobacterium breve UCC2003. *Microbial Biotechnology*, **2013**, 6, 67-79	6.3	63
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360	Probing direct interactions between CodY and the oppD promoter of Lactococcus lactis. *Journal of Bacteriology*, **2005**, 187, 512-21	3.5	63

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358	Comparative genomic and phylogenomic analyses of the Bifidobacteriaceae family. *BMC Genomics*, **2017**, 18, 568	4.5	62
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353	Obesity and microbiota: an example of an intricate relationship. *Genes and Nutrition*, **2017**, 12, 18	4.3	61
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336	Identification of the lower baseplate protein as the antireceptor of the temperate lactococcal bacteriophages TP901-1 and Tuc2009. *Journal of Bacteriology*, **2006**, 188, 55-63	3.5	56
335	Genome Analysis and Characterisation of the Exopolysaccharide Produced by Bifidobacterium longum subsp. longum 35624□*PLoS ONE*, **2016**, 11, e0162983	3.7	56
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