Richard van Kranenburg

List of Publications by Year
in descending order

48 papers	3,817 citations	218677 26 h-index	206112 48 g-index
50 all docs	50 docs citations	50 times ranked	3506 citing authors

#	Article	IF	Citations
1	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
2	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
3	Flavour formation from amino acids by lactic acid bacteria: predictions from genome sequence analysis. International Dairy Journal, 2002, 12, 111-121.	3.0	182
4	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
5	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
6	Next Generation Prokaryotic Engineering: The CRISPR-Cas Toolkit. Trends in Biotechnology, 2016, 34, 575-587.	9.3	113
7	Characterizing a thermostable Cas9 for bacterial genome editing and silencing. Nature Communications, 2017, 8, 1647.	12.8	112
8	Functional Analysis of Three Plasmids from Lactobacillus plantarum. Applied and Environmental Microbiology, 2005, 71, 1223-1230.	3.1	100
9	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
10	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
11	Analysis of acidâ€stressed Bacillus cereus reveals a major oxidative response and inactivationâ€associated radical formation. Environmental Microbiology, 2010, 12, 873-885.	3.8	88
12	Cheese flavour development by enzymatic conversions of peptides and amino acids. Food Research International, 2000, 33, 153-160.	6.2	82
13	Regulation of the metC-cysK Operon, Involved in Sulfur Metabolism in Lactococcus lactis. Journal of Bacteriology, 2002, 184, 82-90.	2.2	79
14	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
15	Molecular and Functional Analyses of the metC Gene of Lactococcus lactis , Encoding Cystathionine Î²-Lyase. Applied and Environmental Microbiology, 2000, 66, 42-48.	3.1	73
16	Hijacking CRISPR-Cas for high-throughput bacterial metabolic engineering: advances and prospects. Current Opinion in Biotechnology, 2018, 50, 146-157.	6.6	59
17	Identification and Genetic Characterization of a Novel Proteinase, PrtR, from the Human Isolate Lactobacillus rhamnosus BGT10. Applied and Environmental Microbiology, 2003, 69, 5802-5811.	3.1	56
18	Efficient Genome Editing of a Facultative Thermophile Using Mesophilic spCas9. ACS Synthetic Biology, 2017, 6, 849-861.	3.8	56

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19	Lactococcal aminotransferases AraT and BcaT are key enzymes for the formation of aroma compounds from amino acids in cheese. International Dairy Journal, 2003, 13, 805-812.	3.0	55
20	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
21	Nucleotide Sequence Analysis of the Lactococcal EPS Plasmid pNZ4000. Plasmid, 2000, 43, 130-136.	1.4	52
22	A navigation guide of synthetic biology tools for Pseudomonas putida. Biotechnology Advances, 2021, 49, 107732.	11.7	48
23	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
24	Comparative analysis of transcriptional and physiological responses of Bacillus cereus to organic and inorganic acid shocks. International Journal of Food Microbiology, 2010, 137, 13-21.	4.7	45
25	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
26	Genetic Tool Development for a New Host for Biotechnology, the Thermotolerant Bacterium Bacillus coagulans. Applied and Environmental Microbiology, 2010, 76, 4085-4088.	3.1	37
27	In vivo selection of sfGFP variants with improved and reliable functionality in industrially important thermophilic bacteria. Biotechnology for Biofuels, 2018, 11, 8.	6.2	33
28	Carbon Monoxide Dehydrogenase from GÃ¶1. Journal of Biological Chemistry, 1996, 271, 14256-14263.	3.4	27
29	Sustainable Production of Bio-Based Chemicals by Extremophiles. Current Biotechnology, 2013, 2, 360-379.	0.4	26
30	The PEP-pyruvate-oxaloacetate node: variation at the heart of metabolism. FEMS Microbiology Reviews, 2021, 45, .	8.6	22
31	Making More of Milk Sugar by Engineering Lactic Acid Bacteria. International Dairy Journal, 1998, 8, 227-233.	3.0	21
32	Isolation of a genetically accessible thermophilic xylan degrading bacterium from compost. Biotechnology for Biofuels, 2016, 9, 210.	6.2	20
33	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
34	Investigating the Central Metabolism of Clostridium thermosuccinogenes. Applied and Environmental Microbiology, 2018, 84, .	3.1	18
35	Biochemical characterization of the xylan hydrolysis profile of the extracellular endo-xylanase from Geobacillus thermodenitrificans T12. BMC Biotechnology, 2017, 17, 44.	3.3	15
36	Complete Genome Sequence of Geobacillus thermodenitrificans T12, A Potential Host for Biotechnological Applications. Current Microbiology, 2018, 75, 49-56.	2.2	15

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37	Engineering Geobacillus thermodenitrificans to introduce cellulolytic activity; expression of native and heterologous cellulase genes. BMC Biotechnology, 2018, 18, 42.	3.3	15
38	CRISPR interference (CRISPRi) as transcriptional repression tool for Hungateiclostridium thermocellum DSM 1313. Microbial Biotechnology, 2020, 13, 339-349.	4.2	15
39	The pentose phosphate pathway of cellulolytic clostridia relies on 6-phosphofructokinase instead of transaldolase. Journal of Biological Chemistry, 2020, 295, 1867-1878.	3.4	14
40	Complete genome sequence of thermophilic Bacillus smithii type strain DSM 4216T. Standards in Genomic Sciences, 2016, 11, 52.	1.5	13
41	Development of a Cas12a-Based Genome Editing Tool for Moderate Thermophiles. CRISPR Journal, 2021, 4, 82-91.	2.9	10
42	Characterization of sporulation dynamics of Pseudoclostridium thermosuccinogenes using flow cytometry. Anaerobe, 2020, 63, 102208.	2.1	8
43	Functional Analysis of the ComK Protein of Bacillus coagulans. PLoS ONE, 2013, 8, e53471.	2.5	8
44	Assessing Cofactor Usage in Pseudoclostridium thermosuccinogenes via Heterologous Expression of Central Metabolic Enzymes. Frontiers in Microbiology, 2019, 10, 1162.	3.5	7
45	ReScribe: An Unrestrained Tool Combining Multiplex Recombineering and Minimal-PAM ScCas9 for Genome Recoding Pseudomonas putida. ACS Synthetic Biology, 2021, 10, 2672-2688.	3.8	7
46	Relaxed control of sugar utilization in Parageobacillus thermoglucosidasius DSM 2542. Microbiological Research, 2022, 256, 126957.	5.3	6
47	Effects of CO2 limitation on the metabolism of Pseudoclostridium thermosuccinogenes. BMC Microbiology, 2020, 20, 149.	3.3	5
48	Breaking the Restriction Barriers and Applying CRISPRi as a Gene Silencing Tool in Pseudoclostridium thermosuccinogenes. Microorganisms, 2022, 10, 698.	3.6	2