Richard van Kranenburg

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Relaxed control of sugar utilization in Parageobacillus thermoglucosidasius DSM 2542. Microbiological Research, 2022, 256, 126957.	2.5	6
2	Breaking the Restriction Barriers and Applying CRISPRi as a Gene Silencing Tool in Pseudoclostridium thermosuccinogenes. Microorganisms, 2022, 10, 698.	1.6	2
3	The PEP-pyruvate-oxaloacetate node: variation at the heart of metabolism. FEMS Microbiology Reviews, 2021, 45, .	3.9	22
4	Development of a Cas12a-Based Genome Editing Tool for Moderate Thermophiles. CRISPR Journal, 2021, 4, 82-91.	1.4	10
5	A navigation guide of synthetic biology tools for Pseudomonas putida. Biotechnology Advances, 2021, 49, 107732.	6.0	48
6	ReScribe: An Unrestrained Tool Combining Multiplex Recombineering and Minimal-PAM ScCas9 for Genome Recoding <i>Pseudomonas putida</i> . ACS Synthetic Biology, 2021, 10, 2672-2688.	1.9	7
7	The pentose phosphate pathway of cellulolytic clostridia relies on 6-phosphofructokinase instead of transaldolase. Journal of Biological Chemistry, 2020, 295, 1867-1878.	1.6	14
8	CRISPR interference (CRISPRi) as transcriptional repression tool for <i>Hungateiclostridium thermocellum</i> DSM 1313. Microbial Biotechnology, 2020, 13, 339-349.	2.0	15
9	Characterization of sporulation dynamics of Pseudoclostridium thermosuccinogenes using flow cytometry. Anaerobe, 2020, 63, 102208.	1.0	8
10	Effects of CO2 limitation on the metabolism of Pseudoclostridium thermosuccinogenes. BMC Microbiology, 2020, 20, 149.	1.3	5
11	Assessing Cofactor Usage in Pseudoclostridium thermosuccinogenes via Heterologous Expression of Central Metabolic Enzymes. Frontiers in Microbiology, 2019, 10, 1162.	1.5	7
12	Investigating the Central Metabolism of Clostridium thermosuccinogenes. Applied and Environmental Microbiology, 2018, 84, .	1.4	18
13	Hijacking CRISPR-Cas for high-throughput bacterial metabolic engineering: advances and prospects. Current Opinion in Biotechnology, 2018, 50, 146-157.	3.3	59
14	Complete Genome Sequence of Geobacillus thermodenitrificans T12, A Potential Host for Biotechnological Applications. Current Microbiology, 2018, 75, 49-56.	1.0	15
15	Engineering Geobacillus thermodenitrificans to introduce cellulolytic activity; expression of native and heterologous cellulase genes. BMC Biotechnology, 2018, 18, 42.	1.7	15
16	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
17	Efficient Genome Editing of a Facultative Thermophile Using Mesophilic spCas9. ACS Synthetic Biology, 2017, 6, 849-861.	1.9	56
18	Characterizing a thermostable Cas9 for bacterial genome editing and silencing. Nature Communications, 2017, 8, 1647.	5.8	112

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19	Biochemical characterization of the xylan hydrolysis profile of the extracellular endo-xylanase from Geobacillus thermodenitrificans T12. BMC Biotechnology, 2017, 17, 44.	1.7	15
20	Isolation of a genetically accessible thermophilic xylan degrading bacterium from compost. Biotechnology for Biofuels, 2016, 9, 210.	6.2	20
21	Complete genome sequence of thermophilic Bacillus smithii type strain DSM 4216T. Standards in Genomic Sciences, 2016, 11, 52.	1.5	13
22	Next Generation Prokaryotic Engineering: The CRISPR-Cas Toolkit. Trends in Biotechnology, 2016, 34, 575-587.	4.9	113
23	Establishment of markerless gene deletion tools in thermophilic Bacillus smithii and construction of multiple mutant strains. Microbial Cell Factories, 2015, 14, 99.	1.9	18
24	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.	1.4	42
25	Sustainable Production of Bio-Based Chemicals by Extremophiles. Current Biotechnology, 2013, 2, 360-379.	0.2	26
26	Functional Analysis of the ComK Protein of Bacillus coagulans. PLoS ONE, 2013, 8, e53471.	1.1	8
27	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.	2.1	45
28	Analysis of acidâ€stressed <i>Bacillus cereus</i> reveals a major oxidative response and inactivationâ€associated radical formation. Environmental Microbiology, 2010, 12, 873-885.	1.8	88
29	Genetic Tool Development for a New Host for Biotechnology, the Thermotolerant Bacterium <i>Bacillus coagulans</i> . Applied and Environmental Microbiology, 2010, 76, 4085-4088.	1.4	37
30	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.	1.4	150
31	Functional Analysis of Three Plasmids from Lactobacillus plantarum. Applied and Environmental Microbiology, 2005, 71, 1223-1230.	1.4	100
32	Complete genome sequence of Lactobacillus plantarum WCFS1. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1990-1995.	3.3	1,326
33	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.	1.5	55
34	Identification and Genetic Characterization of a Novel Proteinase, PrtR, from the Human Isolate Lactobacillus rhamnosus BGT10. Applied and Environmental Microbiology, 2003, 69, 5802-5811.	1.4	56
35	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.	1.4	53
36	Regulation of the metC-cysK Operon, Involved in Sulfur Metabolism in Lactococcus lactis. Journal of Bacteriology, 2002, 184, 82-90.	1.0	79

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37	Flavour formation from amino acids by lactic acid bacteria: predictions from genome sequence analysis. International Dairy Journal, 2002, 12, 111-121.	1.5	182
38	Sugar catabolism and its impact on the biosynthesis and engineering of exopolysaccharide production in lactic acid bacteria. International Dairy Journal, 2001, 11, 723-732.	1.5	117
39	Nucleotide Sequence Analysis of the Lactococcal EPS Plasmid pNZ4000. Plasmid, 2000, 43, 130-136.	0.4	52
40	Molecular and Functional Analyses of the <i>metC</i> Gene of <i>Lactococcus lactis</i> , Encoding Cystathionine β-Lyase. Applied and Environmental Microbiology, 2000, 66, 42-48.	1.4	73
41	Cheese flavour development by enzymatic conversions of peptides and amino acids. Food Research International, 2000, 33, 153-160.	2.9	82
42	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.	3.3	92
43	Exopolysaccharide Biosynthesis in <i>Lactococcus lactis</i> NIZO B40: Functional Analysis of the Glycosyltransferase Genes Involved in Synthesis of the Polysaccharide Backbone. Journal of Bacteriology, 1999, 181, 338-340.	1.0	74
44	Functional Analysis of Glycosyltransferase Genes from <i>Lactococcus lactis</i> and Other Gram-Positive Cocci: Complementation, Expression, and Diversity. Journal of Bacteriology, 1999, 181, 6347-6353.	1.0	96
45	Making More of Milk Sugar by Engineering Lactic Acid Bacteria. International Dairy Journal, 1998, 8, 227-233.	1.5	21
46	Characterization of Multiple Regions Involved in Replication and Mobilization of Plasmid pNZ4000 Coding for Exopolysaccharide Production in <i>Lactococcus lactis</i> . Journal of Bacteriology, 1998, 180, 5285-5290.	1.0	46
47	Molecular characterization of the plasmidâ€encoded eps gene cluster essential for exopolysaccharide biosynthesis in Lactococcus lactis. Molecular Microbiology, 1997, 24, 387-397.	1.2	257
48	Carbon Monoxide Dehydrogenase from Gö1. Journal of Biological Chemistry, 1996, 271, 14256-14263.	1.6	27