

Stefan Weckx

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

3,715
citations

147801

31
h-index

133252

59
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68
all docs

68
docs citations

68
times ranked

3951
citing authors

#	ARTICLE	IF	CITATIONS
1	Microbial ecology of sourdough fermentations: Diverse or uniform?. Food Microbiology, 2014, 37, 11-29.	4.2	334
2	Biodiversity, ecological determinants, and metabolic exploitation of sourdough microbiota. Food Microbiology, 2009, 26, 666-675.	4.2	277
3	novoSNP, a novel computational tool for sequence variation discovery. Genome Research, 2005, 15, 436-442.	5.5	254
4	The cocoa bean fermentation process: from ecosystem analysis to starter culture development. Journal of Applied Microbiology, 2016, 121, 5-17.	3.1	208
5	Mutual Cross-Feeding Interactions between <i>Bifidobacterium longum</i> subsp. <i>longum</i> NCC2705 and <i>Eubacterium rectale</i> ATCC 33656 Explain the Bifidogenic and Butyrogenic Effects of Arabinoxylan Oligosaccharides. Applied and Environmental Microbiology, 2015, 81, 7767-7781.	3.1	186
6	Exploring the Impacts of Postharvest Processing on the Microbiota and Metabolite Profiles during Green Coffee Bean Production. Applied and Environmental Microbiology, 2017, 83, .	3.1	162
7	Production of conjugated linoleic acid and conjugated linolenic acid isomers by <i>Bifidobacterium</i> species. Applied Microbiology and Biotechnology, 2010, 87, 2257-2266.	3.6	127
8	The Ability of <i>Bifidobacteria</i> To Degrade Arabinoxylan Oligosaccharide Constituents and Derived Oligosaccharides Is Strain Dependent. Applied and Environmental Microbiology, 2014, 80, 204-217.	3.1	114
9	Phylogenetic Analysis of a Spontaneous Cocoa Bean Fermentation Metagenome Reveals New Insights into Its Bacterial and Fungal Community Diversity. PLoS ONE, 2012, 7, e38040.	2.5	112
10	Lactic acid bacteria community dynamics and metabolite production of rye sourdough fermentations share characteristics of wheat and spelt sourdough fermentations. Food Microbiology, 2010, 27, 1000-1008.	4.2	109
11	In Vitro Kinetic Analysis of Fermentation of Prebiotic Inulin-Type Fructans by <i>Bifidobacterium</i> Species Reveals Four Different Phenotypes. Applied and Environmental Microbiology, 2009, 75, 454-461.	3.1	106
12	<i>Bifidobacterial</i> inulin-type fructan degradation capacity determines cross-feeding interactions between <i>bifidobacteria</i> and <i>Faecalibacterium prausnitzii</i> . International Journal of Food Microbiology, 2016, 231, 76-85.	4.7	101
13	Influence of Temperature and Backslopping Time on the Microbiota of a Type I Propagated Laboratory Wheat Sourdough Fermentation. Applied and Environmental Microbiology, 2011, 77, 2716-2726.	3.1	95
14	Applying meta-pathway analyses through metagenomics to identify the functional properties of the major bacterial communities of a single spontaneous cocoa bean fermentation process sample. Food Microbiology, 2015, 50, 54-63.	4.2	88
15	Following Coffee Production from Cherries to Cup: Microbiological and Metabolomic Analysis of Wet Processing of <i>Coffea arabica</i> . Applied and Environmental Microbiology, 2019, 85, .	3.1	83
16	Complete genome sequence and comparative analysis of <i>Acetobacter pasteurianus</i> 386B, a strain well-adapted to the cocoa bean fermentation ecosystem. BMC Genomics, 2013, 14, 526.	2.8	81
17	Shotgun Metagenomics of a Water Kefir Fermentation Ecosystem Reveals a Novel <i>Oenococcus</i> Species. Frontiers in Microbiology, 2019, 10, 479.	3.5	80
18	Environmental pH determines citrulline and ornithine release through the arginine deiminase pathway in <i>Lactobacillus fermentum</i> IMDO 130101. International Journal of Food Microbiology, 2009, 135, 216-222.	4.7	71

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19	Community Dynamics of Bacteria in Sourdough Fermentations as Revealed by Their Metatranscriptome. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5402-5408.	3.1	67
20	Expression of the Arginine Deiminase Pathway Genes in <i>Lactobacillus sakei</i> Is Strain Dependent and Is Affected by the Environmental pH. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4874-4883.	3.1	66
21	Carrot Juice Fermentations as Man-Made Microbial Ecosystems Dominated by Lactic Acid Bacteria. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	62
22	Comparative genome analysis of the candidate functional starter culture strains <i>Lactobacillus fermentum</i> 222 and <i>Lactobacillus plantarum</i> 80 for controlled cocoa bean fermentation processes. <i>BMC Genomics</i> , 2015, 16, 766.	2.8	56
23	Linkage and Association Studies Identify a Novel Locus for Alzheimer Disease at 7q36 in a Dutch Population-Based Sample. <i>American Journal of Human Genetics</i> , 2005, 77, 643-652.	6.2	48
24	Influence of Various Processing Parameters on the Microbial Community Dynamics, Metabolomic Profiles, and Cup Quality During Wet Coffee Processing. <i>Frontiers in Microbiology</i> , 2019, 10, 2621.	3.5	48
25	Omics approaches to understand sourdough fermentation processes. <i>International Journal of Food Microbiology</i> , 2019, 302, 90-102.	4.7	44
26	Amplicon and shotgun metagenomic sequencing indicates that microbial ecosystems present in cheese brines reflect environmental inoculation during the cheese production process. <i>International Dairy Journal</i> , 2018, 87, 44-53.	3.0	43
27	Temporal shotgun metagenomics of an Ecuadorian coffee fermentation process highlights the predominance of lactic acid bacteria. <i>Current Research in Biotechnology</i> , 2020, 2, 1-15.	3.7	42
28	Linoleate isomerase activity occurs in lactic acid bacteria strains and is affected by pH and temperature. <i>Journal of Applied Microbiology</i> , 2011, 111, 593-606.	3.1	37
29	The addition of citrate stimulates the production of acetoin and diacetyl by a citrate-positive <i>Lactobacillus crustorum</i> strain during wheat sourdough fermentation. <i>International Journal of Food Microbiology</i> , 2019, 289, 88-105.	4.7	37
30	Metatranscriptome Analysis for Insight into Whole-Ecosystem Gene Expression during Spontaneous Wheat and Spelt Sourdough Fermentations. <i>Applied and Environmental Microbiology</i> , 2011, 77, 618-626.	3.1	35
31	Comparative genomics of <i>Lactobacillus fermentum</i> suggests a free-living lifestyle of this lactic acid bacterial species. <i>Food Microbiology</i> , 2020, 89, 103448.	4.2	34
32	New insights into the exopolysaccharide production of <i>Streptococcus thermophilus</i> . <i>International Dairy Journal</i> , 2011, 21, 586-591.	3.0	33
33	SNPbox: a modular software package for large-scale primer design. <i>Bioinformatics</i> , 2005, 21, 385-387.	4.1	31
34	A Combined Metagenomics and Metatranscriptomics Approach to Unravel Costa Rican Cocoa Box Fermentation Processes Reveals Yet Unreported Microbial Species and Functionalities. <i>Frontiers in Microbiology</i> , 2021, 12, 641185.	3.5	28
35	Curing of Cocoa Beans: Fine-Scale Monitoring of the Starter Cultures Applied and Metabolomics of the Fermentation and Drying Steps. <i>Frontiers in Microbiology</i> , 2020, 11, 616875.	3.5	27
36	Coagulase-Negative Staphylococci Favor Conversion of Arginine into Ornithine despite a Widespread Genetic Potential for Nitric Oxide Synthase Activity. <i>Applied and Environmental Microbiology</i> , 2014, 80, 7741-7751.	3.1	26

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37	SNPbox: web-based high-throughput primer design from gene to genome. <i>Nucleic Acids Research</i> , 2004, 32, W170-W172.	14.5	25
38	<i>Acetobacter oryzafermentans</i> sp. nov., isolated from Korean traditional vinegar and reclassification of the type strains of <i>Acetobacter pasteurianus</i> subsp. <i>ascendens</i> (Henneberg 1898) and <i>Acetobacter pasteurianus</i> subsp. <i>paradoxus</i> (Frateur 1950) as <i>Acetobacter ascendens</i> sp. nov., comb. nov.. <i>Systematic and Applied Microbiology</i> , 2018, 41, 324-332.	2.8	25
39	The metagenome-assembled genome of <i>Candidatus Oenococcus aquikefiri</i> from water kefir represents the species <i>Oenococcus sicerae</i> . <i>Food Microbiology</i> , 2020, 88, 103402.	4.2	24
40	Microbial communities involved in KaÅŸar cheese ripening. <i>Food Microbiology</i> , 2015, 46, 587-595.	4.2	22
41	Assessment of the contribution of cocoa-derived strains of <i>Acetobacter ghanensis</i> and <i>Acetobacter senegalensis</i> to the cocoa bean fermentation process through a genomic approach. <i>Food Microbiology</i> , 2016, 58, 68-78.	4.2	22
42	Adaptation of <i>Lactobacillus plantarum</i> IMDO 130201, a Wheat Sourdough Isolate, to Growth in Wheat Sourdough Simulation Medium at Different pH Values through Differential Gene Expression. <i>Applied and Environmental Microbiology</i> , 2011, 77, 3406-3412.	3.1	21
43	Temporal Shotgun Metagenomics Revealed the Potential Metabolic Capabilities of Specific Microorganisms During Lambic Beer Production. <i>Frontiers in Microbiology</i> , 2020, 11, 1692.	3.5	21
44	Development and Validation of a Species-Independent Functional Gene Microarray That Targets Lactic Acid Bacteria. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6488-6495.	3.1	19
45	Thermodynamic Behavior of Short Oligonucleotides in Microarray Hybridizations Can Be Described Using Gibbs Free Energy in a Nearest-Neighbor Model. <i>Journal of Physical Chemistry B</i> , 2007, 111, 13583-13590.	2.6	17
46	Next-generation sequencing to enhance the taxonomic resolution of the microbiological analysis of meat and meat-derived products. <i>Current Opinion in Food Science</i> , 2021, 37, 58-65.	8.0	17
47	A putative transport protein is involved in citrulline excretion and re-uptake during arginine deiminase pathway activity by <i>Lactobacillus sakei</i> . <i>Research in Microbiology</i> , 2013, 164, 216-225.	2.1	16
48	Genome-Scale Metabolic Reconstruction of <i>Acetobacter pasteurianus</i> 386B, a Candidate Functional Starter Culture for Cocoa Bean Fermentation. <i>Frontiers in Microbiology</i> , 2019, 10, 2801.	3.5	15
49	Application of a High-Throughput Amplicon Sequencing Method to Chart the Bacterial Communities that Are Associated with European Fermented Meats from Different Origins. <i>Foods</i> , 2020, 9, 1247.	4.3	14
50	Traditional Fermented Foods from Ecuador: A Review with a Focus on Microbial Diversity. <i>Foods</i> , 2022, 11, 1854.	4.3	13
51	The Microbiota of Modified-Atmosphere-Packaged Cooked Charcuterie Products throughout Their Shelf-Life Period, as Revealed by a Complementary Combination of Culture-Dependent and Culture-Independent Analysis. <i>Microorganisms</i> , 2021, 9, 1223.	3.6	12
52	Genome-Based Characterization of a Plasmid-Associated Micrococcal P1 Biosynthetic Gene Cluster and Virulence Factors in <i>Mammaliococcus sciuri</i> IMDO-S72. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0208821.	3.1	11
53	Amplicon-Based High-Throughput Sequencing Method Capable of Species-Level Identification of Coagulase-Negative Staphylococci in Diverse Communities. <i>Microorganisms</i> , 2020, 8, 897.	3.6	10
54	Comparative genome analysis of <i>Lactobacillus mudanjiangensis</i> , an understudied member of the <i>Lactobacillus plantarum</i> group. <i>Microbial Genomics</i> , 2019, 5, .	2.0	9

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55	High-throughput amplicon sequencing to assess the impact of processing factors on the development of microbial communities during spontaneous meat fermentation. <i>International Journal of Food Microbiology</i> , 2021, 354, 109322.	4.7	8
56	SSHSuite: an integrated software package for analysis of large-scale suppression subtractive hybridization data. <i>BioTechniques</i> , 2004, 36, 1043-1045.	1.8	7
57	Complete and Annotated Genome Sequence of the Sourdough Lactic Acid Bacterium <i>Lactobacillus fermentum</i> IMDO 130101. <i>Genome Announcements</i> , 2018, 6, .	0.8	6
58	Genome-scale metabolic modeling of <i>Acetobacter pasteurianus</i> 386B reveals its metabolic adaptation to cocoa fermentation conditions. <i>Food Microbiology</i> , 2020, 92, 103597.	4.2	5
59	Microbiomes Associated With the Surfaces of Northern Argentinian Fruits Show a Wide Species Diversity. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	5
60	Synaptopodin and 4 novel genes identified in primary sensory neurons. <i>Molecular and Cellular Neurosciences</i> , 2005, 30, 316-325.	2.2	3
61	Metagenome and metatranscriptome analysis: Does the flag always cover the cargo?. <i>International Journal of Food Microbiology</i> , 2009, 133, 292-293.	4.7	2
62	SNPbox. <i>Methods in Molecular Biology</i> , 2007, 402, 178-199.	0.9	2
63	Oxidative destabilization of lysozyme and the chaperone-like activity of a heat-shock protein: a student experiment. <i>Biochemical Education</i> , 1998, 26, 324-327.	0.1	1