

# Stefan Weckx

## List of Publications by Year in descending order

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Version: 2024-02-01

63  
papers

3,715  
citations

168829

31  
h-index

150775

59  
g-index

68  
all docs

68  
docs citations

68  
times ranked

4266  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-Based Characterization of a Plasmid-Associated Micrococcin P1 Biosynthetic Gene Cluster and Virulence Factors in <i>Mammaliococcus sciuri</i> IMDO-S72. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0208821.	1.4	11
2	Traditional Fermented Foods from Ecuador: A Review with a Focus on Microbial Diversity. <i>Foods</i> , 2022, 11, 1854.	1.9	13
3	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.	4.1	17
4	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.	1.5	28
5	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.	1.6	12
6	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.	2.1	8
7	The metagenome-assembled genome of <i>Candidatus Oenococcus aquikefiri</i> from water kefir represents the species <i>Oenococcus siceræ</i> . <i>Food Microbiology</i> , 2020, 88, 103402.	2.1	24
8	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.	1.9	14
9	Temporal Shotgun Metagenomics Revealed the Potential Metabolic Capabilities of Specific Microorganisms During Lambic Beer Production. <i>Frontiers in Microbiology</i> , 2020, 11, 1692.	1.5	21
10	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.	2.1	5
11	Amplicon-Based High-Throughput Sequencing Method Capable of Species-Level Identification of Coagulase-Negative Staphylococci in Diverse Communities. <i>Microorganisms</i> , 2020, 8, 897.	1.6	10
12	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.	1.9	42
13	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.	2.1	34
14	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.	1.5	27
15	Omics approaches to understand sourdough fermentation processes. <i>International Journal of Food Microbiology</i> , 2019, 302, 90-102.	2.1	44
16	Following Coffee Production from Cherries to Cup: Microbiological and Metabolomic Analysis of Wet Processing of <i>Coffea arabica</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	83
17	Shotgun Metagenomics of a Water Kefir Fermentation Ecosystem Reveals a Novel <i>Oenococcus</i> Species. <i>Frontiers in Microbiology</i> , 2019, 10, 479.	1.5	80
18	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.	1.5	15

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19	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.	1.5	48
20	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.	2.1	37
21	Comparative genome analysis of <i>Lactobacillus mudanjiangensis</i> , an understudied member of the <i>Lactobacillus plantarum</i> group. <i>Microbial Genomics</i> , 2019, 5, .	1.0	9
22	<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.	1.2	25
23	Carrot Juice Fermentations as Man-Made Microbial Ecosystems Dominated by Lactic Acid Bacteria. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	62
24	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
25	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.	1.5	43
26	Exploring the Impacts of Postharvest Processing on the Microbiota and Metabolite Profiles during Green Coffee Bean Production. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	162
27	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.	2.1	22
28	The cocoa bean fermentation process: from ecosystem analysis to starter culture development. <i>Journal of Applied Microbiology</i> , 2016, 121, 5-17.	1.4	208
29	Bifidobacterial inulin-type fructan degradation capacity determines cross-feeding interactions between bifidobacteria and <i>Faecalibacterium prausnitzii</i> . <i>International Journal of Food Microbiology</i> , 2016, 231, 76-85.	2.1	101
30	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.	1.2	56
31	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. <i>Food Microbiology</i> , 2015, 50, 54-63.	2.1	88
32	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. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7767-7781.	1.4	186
33	Microbial communities involved in KaÅŸar cheese ripening. <i>Food Microbiology</i> , 2015, 46, 587-595.	2.1	22
34	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.	1.4	26
35	The Ability of Bifidobacteria To Degrade Arabinoxylan Oligosaccharide Constituents and Derived Oligosaccharides Is Strain Dependent. <i>Applied and Environmental Microbiology</i> , 2014, 80, 204-217.	1.4	114
36	Microbial ecology of sourdough fermentations: Diverse or uniform?. <i>Food Microbiology</i> , 2014, 37, 11-29.	2.1	334

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37	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.	1.0	16
38	Complete genome sequence and comparative analysis of <i>Acetobacter pasteurianus</i> 386B, a strain well-adapted to the cocoa bean fermentation ecosystem. <i>BMC Genomics</i> , 2013, 14, 526.	1.2	81
39	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.	1.4	66
40	Phylogenetic Analysis of a Spontaneous Cocoa Bean Fermentation Metagenome Reveals New Insights into Its Bacterial and Fungal Community Diversity. <i>PLoS ONE</i> , 2012, 7, e38040.	1.1	112
41	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.	1.4	35
42	New insights into the exopolysaccharide production of <i>Streptococcus thermophilus</i> . <i>International Dairy Journal</i> , 2011, 21, 586-591.	1.5	33
43	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.	1.4	37
44	Influence of Temperature and Backslopping Time on the Microbiota of a Type I Propagated Laboratory Wheat Sourdough Fermentation. <i>Applied and Environmental Microbiology</i> , 2011, 77, 2716-2726.	1.4	95
45	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.	1.4	21
46	Production of conjugated linoleic acid and conjugated linolenic acid isomers by <i>Bifidobacterium</i> species. <i>Applied Microbiology and Biotechnology</i> , 2010, 87, 2257-2266.	1.7	127
47	Lactic acid bacteria community dynamics and metabolite production of rye sourdough fermentations share characteristics of wheat and spelt sourdough fermentations. <i>Food Microbiology</i> , 2010, 27, 1000-1008.	2.1	109
48	Community Dynamics of Bacteria in Sourdough Fermentations as Revealed by Their Metatranscriptome. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5402-5408.	1.4	67
49	In Vitro Kinetic Analysis of Fermentation of Prebiotic Inulin-Type Fructans by <i>Bifidobacterium</i> Species Reveals Four Different Phenotypes. <i>Applied and Environmental Microbiology</i> , 2009, 75, 454-461.	1.4	106
50	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.	1.4	19
51	Biodiversity, ecological determinants, and metabolic exploitation of sourdough microbiota. <i>Food Microbiology</i> , 2009, 26, 666-675.	2.1	277
52	Metagenome and metatranscriptome analysis: Does the flag always cover the cargo?. <i>International Journal of Food Microbiology</i> , 2009, 133, 292-293.	2.1	2
53	Environmental pH determines citrulline and ornithine release through the arginine deiminase pathway in <i>Lactobacillus fermentum</i> IMDO 130101. <i>International Journal of Food Microbiology</i> , 2009, 135, 216-222.	2.1	71
54	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.	1.2	17

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55	SNPbox. <i>Methods in Molecular Biology</i> , 2007, 402, 178-199.	0.4	2
56	novoSNP, a novel computational tool for sequence variation discovery. <i>Genome Research</i> , 2005, 15, 436-442.	2.4	254
57	SNPbox: a modular software package for large-scale primer design. <i>Bioinformatics</i> , 2005, 21, 385-387.	1.8	31
58	Synaptopodin and 4 novel genes identified in primary sensory neurons. <i>Molecular and Cellular Neurosciences</i> , 2005, 30, 316-325.	1.0	3
59	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.	2.6	48
60	SSHSuite: an integrated software package for analysis of large-scale suppression subtractive hybridization data. <i>BioTechniques</i> , 2004, 36, 1043-1045.	0.8	7
61	SNPbox: web-based high-throughput primer design from gene to genome. <i>Nucleic Acids Research</i> , 2004, 32, W170-W172.	6.5	25
62	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
63	Microbiomes Associated With the Surfaces of Northern Argentinian Fruits Show a Wide Species Diversity. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5