

Stefano Campanaro

List of Publications by Year in descending order

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107
papers

9,837
citations

81900
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38395
95
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111
all docs

111
docs citations

111
times ranked

11095
citing authors

#	ARTICLE	IF	CITATIONS
1	Effects of different feedstocks-based biochar on soil remediation: A review. Environmental Pollution, 2022, 294, 118655.	7.5	116
2	In-situ biogas upgrading assisted by bioaugmentation with hydrogenotrophic methanogens during mesophilic and thermophilic co-digestion. Bioresource Technology, 2022, 348, 126754.	9.6	22
3	KEMET – A python tool for KEGG Module evaluation and microbial genome annotation expansion. Computational and Structural Biotechnology Journal, 2022, 20, 1481-1486.	4.1	11
4	How Microbiome Composition Correlates with Biochemical Changes during Sauerkraut Fermentation: a Focus on Neglected Bacterial Players and Functionalities. Microbiology Spectrum, 2022, 10, .	3.0	14
5	Preliminary investigation of microorganisms potentially involved in microplastics degradation using an integrated metagenomic and biochemical approach. Science of the Total Environment, 2022, 843, 157017.	8.0	13
6	How multiple farming conditions correlate with the composition of the raw cow's milk lactic microbiome. Environmental Microbiology, 2021, 23, 1702-1716.	3.8	13
7	Role prediction of Gram-negative species in the resistome of raw cow's milk. International Journal of Food Microbiology, 2021, 340, 109045.	4.7	6
8	Editorial: Meta-omic Approaches to the Complex Anaerobic Communities in Wastewater Treatment Plants and Digesters. Frontiers in Microbiology, 2021, 12, 664716.	3.5	0
9	Valorization of palm oil mill wastewater for integrated production of microbial oil and biogas in a biorefinery approach. Journal of Cleaner Production, 2021, 296, 126606.	9.3	11
10	Genome-Centric Metatranscriptomics Analysis Reveals the Role of Hydrochar in Anaerobic Digestion of Waste Activated Sludge. Environmental Science & Technology, 2021, 55, 8351-8361.	10.0	77
11	Evaluation of acidogenesis products' effect on biogas production performed with metagenomics and isotopic approaches. Biotechnology for Biofuels, 2021, 14, 125.	6.2	23
12	Evolution of the microbial community structure in biogas reactors inoculated with seeds from different origin. Science of the Total Environment, 2021, 773, 144981.	8.0	12
13	Microbial dynamics in biogas digesters treating lipid-rich substrates via genome-centric metagenomics. Science of the Total Environment, 2021, 778, 146296.	8.0	17
14	Large-scale sequencing and comparative analysis of oenological Saccharomyces cerevisiae strains supported by nanopore refinement of key genomes. Food Microbiology, 2021, 97, 103753.	4.2	10
15	Pilot-scale biomethanation in a trickle bed reactor: Process performance and microbiome functional reconstruction. Energy Conversion and Management, 2021, 244, 114491.	9.2	39
16	Comprehensive evaluation of different strategies to recover methanogenic performance in ammonia-stressed reactors. Bioresource Technology, 2021, 336, 125329.	9.6	25
17	Co-digestion of cheese whey with sewage sludge for caproic acid production: Role of microbiome and polyhydroxyalkanoates potential production. Bioresource Technology, 2021, 337, 125388.	9.6	19
18	Natural Saccharomyces cerevisiae Strain Reveals Peculiar Genomic Traits for Starch-to-Bioethanol Production: the Design of an Amylolytic Consolidated Bioprocessing Yeast. Frontiers in Microbiology, 2021, 12, 768562.	3.5	9

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19	Intermittent aeration of landfill simulation bioreactors: Effects on emissions and microbial community. <i>Waste Management</i> , 2020, 117, 146-156.	7.4	22
20	Revealing metabolic mechanisms of interaction in the anaerobic digestion microbiome by flux balance analysis. <i>Metabolic Engineering</i> , 2020, 62, 138-149.	7.0	45
21	New insights into the variability of lactic acid production in <i>Lachanea thermotolerans</i> at the phenotypic and genomic level. <i>Microbiological Research</i> , 2020, 238, 126525.	5.3	18
22	Microbiota of the Therapeutic Euganean Thermal Muds with a Focus on the Main Cyanobacteria Species. <i>Microorganisms</i> , 2020, 8, 1590.	3.6	23
23	Insights into Ammonia Adaptation and Methanogenic Precursor Oxidation by Genome-Centric Analysis. <i>Environmental Science & Technology</i> , 2020, 54, 12568-12582.	10.0	57
24	Evolutionary Study of the Crassphage Virus at Gene Level. <i>Viruses</i> , 2020, 12, 1035.	3.3	8
25	Biological CO ₂ fixation in up-flow reactors via exogenous H ₂ addition. <i>Journal of Biotechnology</i> , 2020, 319, 1-7.	3.8	22
26	The impact of CUP1 gene copy-number and XVI-VIII/XV-XVI translocations on copper and sulfite tolerance in vineyard <i>Saccharomyces cerevisiae</i> strain populations. <i>FEMS Yeast Research</i> , 2020, 20, .	2.3	13
27	miR-7 Controls the Dopaminergic/Oligodendroglial Fate through Wnt/ β 2-catenin Signaling Regulation. <i>Cells</i> , 2020, 9, 711.	4.1	18
28	Effect of ammonia on anaerobic digestion of municipal solid waste: Inhibitory performance, bioaugmentation and microbiome functional reconstruction. <i>Chemical Engineering Journal</i> , 2020, 401, 126159.	12.7	76
29	New insights from the biogas microbiome by comprehensive genome-resolved metagenomics of nearly 1600 species originating from multiple anaerobic digesters. <i>Biotechnology for Biofuels</i> , 2020, 13, 25.	6.2	136
30	Metabolic dependencies govern microbial syntrophies during methanogenesis in an anaerobic digestion ecosystem. <i>Microbiome</i> , 2020, 8, 22.	11.1	91
31	Milk microbial composition of Brazilian dairy cows entering the dry period and genomic comparison between <i>Staphylococcus aureus</i> strains susceptible to the bacteriophage vB_SauM-UFV_DC4. <i>Scientific Reports</i> , 2020, 10, 5520.	3.3	4
32	The hidden layers of microbial community structure: extracting the concealed diversity dimensions from our sequencing data. <i>FEMS Microbiology Letters</i> , 2020, 367, .	1.8	1
33	Complete genome sequence of <i>Nitratireductor</i> sp. strain OM-1: A lipid-producing bacterium with potential use in wastewater treatment. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2019, 24, e00366.	4.4	3
34	Genomic Comparison of <i>Lactobacillus helveticus</i> Strains Highlights Probiotic Potential. <i>Frontiers in Microbiology</i> , 2019, 10, 1380.	3.5	50
35	Valorization of sewage sludge for volatile fatty acids production and role of microbiome on acidogenic fermentation. <i>Bioresource Technology</i> , 2019, 291, 121817.	9.6	62
36	Study of microbial dynamics during optimization of hydrogen production from food waste by using LCFA-rich agent. <i>Bioresource Technology Reports</i> , 2019, 5, 157-163.	2.7	6

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37	Draft genome sequence data of <i>Lactobacillus paracasei</i> strain DTA83 isolated from infant stools. Data in Brief, 2019, 22, 1064-1067.	1.0	7
38	Metabolomic Alterations Do Not Induce Metabolic Burden in the Industrial Yeast M2n[pBKD2-Pccbgl1]-C1 Engineered by Multiple \hat{I} -Integration of a Fungal \hat{I}^2 -Glucosidase Gene. Frontiers in Bioengineering and Biotechnology, 2019, 7, 376.	4.1	9
39	A Cryptic Non-Inducible Prophage Confers Phage-Immunity on the <i>Streptococcus thermophilus</i> M17PTZA496. Viruses, 2019, 11, 7.	3.3	26
40	Microbial profiling during anaerobic digestion of cheese whey in reactors operated at different conditions. Bioresource Technology, 2019, 275, 375-385.	9.6	59
41	Novel ecological insights and functional roles during anaerobic digestion of saccharides unveiled by genome-centric metagenomics. Water Research, 2019, 151, 271-279.	11.3	83
42	Process performance and microbial community structure in thermophilic trickling biofilter reactors for biogas upgrading. Science of the Total Environment, 2019, 655, 529-538.	8.0	85
43	Metagenomic binning reveals the functional roles of core abundant microorganisms in twelve full-scale biogas plants. Water Research, 2018, 140, 123-134.	11.3	122
44	Taxonomy of anaerobic digestion microbiome reveals biases associated with the applied high throughput sequencing strategies. Scientific Reports, 2018, 8, 1926.	3.3	70
45	Biogas upgrading and utilization: Current status and perspectives. Biotechnology Advances, 2018, 36, 452-466.	11.7	885
46	Performance and genome-centric metagenomics of thermophilic single and two-stage anaerobic digesters treating cheese wastes. Water Research, 2018, 134, 181-191.	11.3	56
47	Genome Sequence of <i>Enterococcus mundtii</i> EM01, Isolated from <i>Bombyx mori</i> Midgut and Responsible for Flacherie Disease in Silkworms Reared on an Artificial Diet. Genome Announcements, 2018, 6, .	0.8	3
48	Genomic analysis and immune response in a murine mastitis model of vB_EcoM-UFV13, a potential biocontrol agent for use in dairy cows. Scientific Reports, 2018, 8, 6845.	3.3	26
49	Converting mesophilic upflow sludge blanket (UASB) reactors to thermophilic by applying axenic methanogenic culture bioaugmentation. Chemical Engineering Journal, 2018, 332, 508-516.	12.7	30
50	Microbial activity response to hydrogen injection in thermophilic anaerobic digesters revealed by genome-centric metatranscriptomics. Microbiome, 2018, 6, 194.	11.1	39
51	Dynamic membrane bioreactor (DMBR) for the treatment of landfill leachate; bioreactor's performance and metagenomic insights into microbial community evolution. Environmental Pollution, 2018, 243, 326-335.	7.5	27
52	Whole genome comparison of two <i>Starmerella bacillaris</i> strains with other wine yeasts uncovers genes involved in modulating important winemaking traits. FEMS Yeast Research, 2018, 18, .	2.3	15
53	Interplay between gut microbiota and <i>p66Shc</i> affects obesity-associated insulin resistance. FASEB Journal, 2018, 32, 4004-4015.	0.5	17
54	Hydrogen-Fueled Microbial Pathways in Biogas Upgrading Systems Revealed by Genome-Centric Metagenomics. Frontiers in Microbiology, 2018, 9, 1079.	3.5	66

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55	Spatial Distribution and Diverse Metabolic Functions of Lignocellulose-Degrading Uncultured Bacteria as Revealed by Genome-Centric Metagenomics. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	72
56	Draft Genome Sequences of Three Virulent <i>Streptococcus thermophilus</i> Bacteriophages Isolated from the Dairy Environment in the Veneto Region of Italy. <i>Genome Announcements</i> , 2018, 6, .	0.8	4
57	Comparative Transcriptomic Analysis of <i>Streptococcus thermophilus</i> TH1436 and TH1477 Showing Different Capability in the Use of Galactose. <i>Frontiers in Microbiology</i> , 2018, 9, 1765.	3.5	40
58	Characterization of the planktonic microbiome in upflow anaerobic sludge blanket reactors during adaptation of mesophilic methanogenic granules to thermophilic operational conditions. <i>Anaerobe</i> , 2017, 46, 69-77.	2.1	14
59	In vitro fermentation of key dietary compounds with rumen fluid: A genome-centric perspective. <i>Science of the Total Environment</i> , 2017, 584-585, 683-691.	8.0	12
60	A novel archaeal species belonging to <i>Methanoculleus</i> genus identified via de-novo assembly and metagenomic binning process in biogas reactors. <i>Anaerobe</i> , 2017, 46, 23-32.	2.1	63
61	Optimization of hydrogen dispersion in thermophilic up-flow reactors for ex situ biogas upgrading. <i>Bioresource Technology</i> , 2017, 234, 310-319.	9.6	110
62	Ex-situ biogas upgrading and enhancement in different reactor systems. <i>Bioresource Technology</i> , 2017, 225, 429-437.	9.6	249
63	Microbial community changes in methanogenic granules during the transition from mesophilic to thermophilic conditions. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 1313-1322.	3.6	51
64	Anaerobic granular sludge for simultaneous biomethanation of synthetic wastewater and CO with focus on the identification of CO-converting microorganisms. <i>Water Research</i> , 2017, 126, 19-28.	11.3	41
65	Whole-Genome Sequence of <i>Starmerella bacillaris</i> PAS13, a Nonconventional Enological Yeast with Antifungal Activity. <i>Genome Announcements</i> , 2017, 5, .	0.8	15
66	Draft Genome Sequence of the Yeast <i>Starmerella bacillaris</i> (syn., <i>Candida</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 307 Td (< Announcements, 2017, 5, .	0.8	17
67	Process performance and comparative metagenomic analysis during co-digestion of manure and lignocellulosic biomass for biogas production. <i>Applied Energy</i> , 2017, 185, 126-135.	10.1	132
68	Genome comparison and physiological characterization of eight <i>Streptococcus thermophilus</i> strains isolated from Italian dairy products. <i>Food Microbiology</i> , 2017, 63, 47-57.	4.2	34
69	The Complete Genome Sequence of <i>Trueperella pyogenes</i> UFV1 Reveals a Processing System Involved in the Quorum-Sensing Signal Response. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
70	Whole-Metagenome-Sequencing-Based Community Profiles of <i>Vitis vinifera</i> L. cv. Corvina Berries Withered in Two Post-harvest Conditions. <i>Frontiers in Microbiology</i> , 2016, 7, 937.	3.5	47
71	Single <i>TRAM</i> domain <i>RNA</i> -binding proteins in <i>Archaea</i> : functional insight from <i>Ctr3</i> from the <i>Antarctic</i> methanogen <i>Methanococcoides burtonii</i> . <i>Environmental Microbiology</i> , 2016, 18, 2810-2824.	3.8	21
72	Direct 16S rRNA-seq from bacterial communities: a PCR-independent approach to simultaneously assess microbial diversity and functional activity potential of each taxon. <i>Scientific Reports</i> , 2016, 6, 32165.	3.3	90

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73	Deeper insight into the structure of the anaerobic digestion microbial community; the biogas microbiome database is expanded with 157 new genomes. <i>Bioresource Technology</i> , 2016, 216, 260-266.	9.6	132
74	Untangling the Effect of Fatty Acid Addition at Species Level Revealed Different Transcriptional Responses of the Biogas Microbial Community Members. <i>Environmental Science & Technology</i> , 2016, 50, 6079-6090.	10.0	79
75	Metagenomic analysis and functional characterization of the biogas microbiome using high throughput shotgun sequencing and a novel binning strategy. <i>Biotechnology for Biofuels</i> , 2016, 9, 26.	6.2	248
76	Dynamic functional characterization and phylogenetic changes due to Long Chain Fatty Acids pulses in biogas reactors. <i>Scientific Reports</i> , 2016, 6, 28810.	3.3	58
77	Different mechanisms of resistance modulate sulfite tolerance in wine yeasts. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 797-813.	3.6	42
78	Selection and validation of reference genes for quantitative real-time PCR studies during <i>Saccharomyces cerevisiae</i> alcoholic fermentation in the presence of sulfite. <i>International Journal of Food Microbiology</i> , 2015, 215, 49-56.	4.7	23
79	Microbial diversity and dynamicity of biogas reactors due to radical changes of feedstock composition. <i>Bioresource Technology</i> , 2015, 176, 56-64.	9.6	101
80	Genome Sequence of <i>Lactobacillus fabifermentans</i> Strain T30PCM01, Isolated from Fermenting Grape Marc. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
81	Genome Sequences of <i>Streptococcus thermophilus</i> Strains MTH17CL396 and M17PTZA496 from Fontina, an Italian PDO Cheese. <i>Genome Announcements</i> , 2014, 2, .	0.8	17
82	Genome Sequences of Four Italian <i>Streptococcus thermophilus</i> Strains of Dairy Origin. <i>Genome Announcements</i> , 2014, 2, .	0.8	18
83	Whole-Genome Sequence of <i>Streptococcus macedonicus</i> Strain 33MO, Isolated from the Curd of Morlacco Cheese in the Veneto Region (Italy). <i>Genome Announcements</i> , 2014, 2, .	0.8	8
84	Whole-Genome Sequences of <i>Streptococcus thermophilus</i> Strains TH1435 and TH1436, Isolated from Raw Goat Milk. <i>Genome Announcements</i> , 2014, 2, .	0.8	28
85	Transcriptome structure variability in <i>Saccharomyces cerevisiae</i> strains determined with a newly developed assembly software. <i>BMC Genomics</i> , 2014, 15, 1045.	2.8	15
86	Metagenomic analysis of the microbial community in fermented grape marc reveals that <i>Lactobacillus fabifermentans</i> is one of the dominant species: insights into its genome structure. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 6015-6037.	3.6	35
87	Oxidative stress response and nitrogen utilization are strongly variable in <i>Saccharomyces cerevisiae</i> wine strains with different fermentation performances. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 4119-4135.	3.6	38
88	The impact of genomic variability on gene expression in environmental <i>Saccharomyces cerevisiae</i> strains. <i>Environmental Microbiology</i> , 2014, 16, 1378-1397.	3.8	59
89	Microbial analysis in biogas reactors suffering by foaming incidents. <i>Bioresource Technology</i> , 2014, 167, 24-32.	9.6	38
90	The transcriptional landscape of the deep-sea bacterium <i>Photobacterium profundum</i> in both a <i>toxR</i> mutant and its parental strain. <i>BMC Genomics</i> , 2012, 13, 567.	2.8	28

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91	ALMS1-Deficient Fibroblasts Over-Express Extra-Cellular Matrix Components, Display Cell Cycle Delay and Are Resistant to Apoptosis. PLoS ONE, 2011, 6, e19081.	2.5	58
92	Multi-Tasking Role of the Mechanosensing Protein Ankrd2 in the Signaling Network of Striated Muscle. PLoS ONE, 2011, 6, e25519.	2.5	31
93	Temperatureâ€dependent global gene expression in the Antarctic archaeon <i>Methanococcoides burtonii</i> . Environmental Microbiology, 2011, 13, 2018-2038.	3.8	62
94	The RNA polymerase subunits E/F from the Antarctic archaeon <i>Methanococcoides burtonii</i> bind to specific species of mRNA. Environmental Microbiology, 2011, 13, 2039-2055.	3.8	4
95	Muscle Research and Gene Ontology: New standards for improved data integration. BMC Medical Genomics, 2009, 2, 6.	1.5	16
96	Protein evolution in deep sea bacteria: an analysis of amino acids substitution rates. BMC Evolutionary Biology, 2008, 8, 313.	3.2	37
97	A global gene evolution analysis on Vibrionaceae family using phylogenetic profile. BMC Bioinformatics, 2007, 8, S23.	2.6	10
98	Genes involved in TGFÎ²1-driven epithelial-mesenchymal transition of renal epithelial cells are topologically related in the human interactome map. BMC Genomics, 2007, 8, 383.	2.8	20
99	Quantitative Proteomic Comparison of Rat Mitochondria from Muscle, Heart, and Liver. Molecular and Cellular Proteomics, 2006, 5, 608-619.	3.8	250
100	Piezophilic adaptation: a genomic point of view. Journal of Biotechnology, 2006, 126, 11-25.	3.8	169
101	Laterally transferred elements and high pressure adaptation in Photobacterium profundum strains. BMC Genomics, 2005, 6, 122.	2.8	91
102	The Ankrd2, Cdkn1c and Calcyclin Genes are Under the Control of MyoD During Myogenic Differentiation. Journal of Molecular Biology, 2005, 349, 349-366.	4.2	30
103	Life at Depth: Photobacterium profundum Genome Sequence and Expression Analysis. Science, 2005, 307, 1459-1461.	12.6	266
104	Pattern recognition in gene expression profiling using DNA array: a comparative study of different statistical methods applied to cancer classification. Human Molecular Genetics, 2003, 12, 823-836.	2.9	51
105	Gene expression profiling in dysferlinopathies using a dedicated muscle microarray. Human Molecular Genetics, 2002, 11, 3283-3298.	2.9	70
106	Functional profiling of the Saccharomyces cerevisiae genome. Nature, 2002, 418, 387-391.	27.8	3,988
107	Gene disruption and basic phenotypic analysis of nine novel yeast genes from chromosome XIV. Yeast, 2000, 16, 1089-1097.	1.7	11