

Stefano Campanaro

List of Publications by Year in descending order

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107
papers

9,837
citations

81743

39
h-index

38300

95
g-index

111
all docs

111
docs citations

111
times ranked

11095
citing authors

#	ARTICLE	IF	CITATIONS
1	Functional profiling of the <i>Saccharomyces cerevisiae</i> genome. <i>Nature</i> , 2002, 418, 387-391.	13.7	3,938
2	Biogas upgrading and utilization: Current status and perspectives. <i>Biotechnology Advances</i> , 2018, 36, 452-466.	6.0	885
3	Life at Depth: <i>Photobacterium profundum</i> Genome Sequence and Expression Analysis. <i>Science</i> , 2005, 307, 1459-1461.	6.0	266
4	Quantitative Proteomic Comparison of Rat Mitochondria from Muscle, Heart, and Liver. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 608-619.	2.5	250
5	Ex-situ biogas upgrading and enhancement in different reactor systems. <i>Bioresource Technology</i> , 2017, 225, 429-437.	4.8	249
6	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
7	Piezophilic adaptation: a genomic point of view. <i>Journal of Biotechnology</i> , 2006, 126, 11-25.	1.9	169
8	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
9	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.	4.8	132
10	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.	5.1	132
11	Metagenomic binning reveals the functional roles of core abundant microorganisms in twelve full-scale biogas plants. <i>Water Research</i> , 2018, 140, 123-134.	5.3	122
12	Effects of different feedstocks-based biochar on soil remediation: A review. <i>Environmental Pollution</i> , 2022, 294, 118655.	3.7	116
13	Optimization of hydrogen dispersion in thermophilic up-flow reactors for ex situ biogas upgrading. <i>Bioresource Technology</i> , 2017, 234, 310-319.	4.8	110
14	Microbial diversity and dynamicity of biogas reactors due to radical changes of feedstock composition. <i>Bioresource Technology</i> , 2015, 176, 56-64.	4.8	101
15	Laterally transferred elements and high pressure adaptation in <i>Photobacterium profundum</i> strains. <i>BMC Genomics</i> , 2005, 6, 122.	1.2	91
16	Metabolic dependencies govern microbial syntrophies during methanogenesis in an anaerobic digestion ecosystem. <i>Microbiome</i> , 2020, 8, 22.	4.9	91
17	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.	1.6	90
18	Process performance and microbial community structure in thermophilic trickling biofilter reactors for biogas upgrading. <i>Science of the Total Environment</i> , 2019, 655, 529-538.	3.9	85

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19	Novel ecological insights and functional roles during anaerobic digestion of saccharides unveiled by genome-centric metagenomics. <i>Water Research</i> , 2019, 151, 271-279.	5.3	83
20	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.	4.6	79
21	Genome-Centric Metatranscriptomics Analysis Reveals the Role of Hydrochar in Anaerobic Digestion of Waste Activated Sludge. <i>Environmental Science & Technology</i> , 2021, 55, 8351-8361.	4.6	77
22	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.	6.6	76
23	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, .	1.4	72
24	Gene expression profiling in dysferlinopathies using a dedicated muscle microarray. <i>Human Molecular Genetics</i> , 2002, 11, 3283-3298.	1.4	70
25	Taxonomy of anaerobic digestion microbiome reveals biases associated with the applied high throughput sequencing strategies. <i>Scientific Reports</i> , 2018, 8, 1926.	1.6	70
26	Hydrogen-Fueled Microbial Pathways in Biogas Upgrading Systems Revealed by Genome-Centric Metagenomics. <i>Frontiers in Microbiology</i> , 2018, 9, 1079.	1.5	66
27	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.	1.0	63
28	Temperature-dependent global gene expression in the Antarctic archaeon <i>Methanococcoides burtonii</i> . <i>Environmental Microbiology</i> , 2011, 13, 2018-2038.	1.8	62
29	Valorization of sewage sludge for volatile fatty acids production and role of microbiome on acidogenic fermentation. <i>Bioresource Technology</i> , 2019, 291, 121817.	4.8	62
30	The impact of genomic variability on gene expression in environmental <i>Saccharomyces cerevisiae</i> strains. <i>Environmental Microbiology</i> , 2014, 16, 1378-1397.	1.8	59
31	Microbial profiling during anaerobic digestion of cheese whey in reactors operated at different conditions. <i>Bioresource Technology</i> , 2019, 275, 375-385.	4.8	59
32	ALMS1-Deficient Fibroblasts Over-Express Extra-Cellular Matrix Components, Display Cell Cycle Delay and Are Resistant to Apoptosis. <i>PLoS ONE</i> , 2011, 6, e19081.	1.1	58
33	Dynamic functional characterization and phylogenetic changes due to Long Chain Fatty Acids pulses in biogas reactors. <i>Scientific Reports</i> , 2016, 6, 28810.	1.6	58
34	Insights into Ammonia Adaptation and Methanogenic Precursor Oxidation by Genome-Centric Analysis. <i>Environmental Science & Technology</i> , 2020, 54, 12568-12582.	4.6	57
35	Performance and genome-centric metagenomics of thermophilic single and two-stage anaerobic digesters treating cheese wastes. <i>Water Research</i> , 2018, 134, 181-191.	5.3	56
36	Pattern recognition in gene expression profiling using DNA array: a comparative study of different statistical methods applied to cancer classification. <i>Human Molecular Genetics</i> , 2003, 12, 823-836.	1.4	51

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37	Microbial community changes in methanogenic granules during the transition from mesophilic to thermophilic conditions. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 1313-1322.	1.7	51
38	Genomic Comparison of <i>Lactobacillus helveticus</i> Strains Highlights Probiotic Potential. <i>Frontiers in Microbiology</i> , 2019, 10, 1380.	1.5	50
39	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.	1.5	47
40	Revealing metabolic mechanisms of interaction in the anaerobic digestion microbiome by flux balance analysis. <i>Metabolic Engineering</i> , 2020, 62, 138-149.	3.6	45
41	Different mechanisms of resistance modulate sulfite tolerance in wine yeasts. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 797-813.	1.7	42
42	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.	5.3	41
43	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.	1.5	40
44	Microbial activity response to hydrogen injection in thermophilic anaerobic digesters revealed by genome-centric metatranscriptomics. <i>Microbiome</i> , 2018, 6, 194.	4.9	39
45	Pilot-scale biomethanation in a trickle bed reactor: Process performance and microbiome functional reconstruction. <i>Energy Conversion and Management</i> , 2021, 244, 114491.	4.4	39
46	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.	1.7	38
47	Microbial analysis in biogas reactors suffering by foaming incidents. <i>Bioresource Technology</i> , 2014, 167, 24-32.	4.8	38
48	Protein evolution in deep sea bacteria: an analysis of amino acids substitution rates. <i>BMC Evolutionary Biology</i> , 2008, 8, 313.	3.2	37
49	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.	1.7	35
50	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.	2.1	34
51	Multi-Tasking Role of the Mechanosensing Protein Ankrd2 in the Signaling Network of Striated Muscle. <i>PLoS ONE</i> , 2011, 6, e25519.	1.1	31
52	The Ankrd2, Cdkn1c and Calcyclin Genes are Under the Control of MyoD During Myogenic Differentiation. <i>Journal of Molecular Biology</i> , 2005, 349, 349-366.	2.0	30
53	Converting mesophilic upflow sludge blanket (UASB) reactors to thermophilic by applying axenic methanogenic culture bioaugmentation. <i>Chemical Engineering Journal</i> , 2018, 332, 508-516.	6.6	30
54	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.	1.2	28

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55	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
56	Dynamic membrane bioreactor (DMBR) for the treatment of landfill leachate; bioreactor's performance and metagenomic insights into microbial community evolution. <i>Environmental Pollution</i> , 2018, 243, 326-335.	3.7	27
57	Genomic analysis and immune response in a murine mastitis model of vB_EcoM-UFV13, a potential biocontrol agent for use in dairy cows. <i>Scientific Reports</i> , 2018, 8, 6845.	1.6	26
58	A Cryptic Non-Inducible Prophage Confers Phage-Immunity on the <i>Streptococcus thermophilus</i> M17PTZA496. <i>Viruses</i> , 2019, 11, 7.	1.5	26
59	Comprehensive evaluation of different strategies to recover methanogenic performance in ammonia-stressed reactors. <i>Bioresource Technology</i> , 2021, 336, 125329.	4.8	25
60	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.	2.1	23
61	Microbiota of the Therapeutic Euganean Thermal Muds with a Focus on the Main Cyanobacteria Species. <i>Microorganisms</i> , 2020, 8, 1590.	1.6	23
62	Evaluation of acidogenesis products' effect on biogas production performed with metagenomics and isotopic approaches. <i>Biotechnology for Biofuels</i> , 2021, 14, 125.	6.2	23
63	Intermittent aeration of landfill simulation bioreactors: Effects on emissions and microbial community. <i>Waste Management</i> , 2020, 117, 146-156.	3.7	22
64	Biological CO ₂ fixation in up-flow reactors via exogenous H ₂ addition. <i>Journal of Biotechnology</i> , 2020, 319, 1-7.	1.9	22
65	In-situ biogas upgrading assisted by bioaugmentation with hydrogenotrophic methanogens during mesophilic and thermophilic co-digestion. <i>Bioresource Technology</i> , 2022, 348, 126754.	4.8	22
66	Single TRAM domain RNA-binding proteins in <i>A</i> archaea: functional insight from Ctr3 from the Antarctic methanogen <i>Methanococcus burtonii</i> . <i>Environmental Microbiology</i> , 2016, 18, 2810-2824.	1.8	21
67	Genes involved in TGF β 1-driven epithelial-mesenchymal transition of renal epithelial cells are topologically related in the human interactome map. <i>BMC Genomics</i> , 2007, 8, 383.	1.2	20
68	Co-digestion of cheese whey with sewage sludge for caproic acid production: Role of microbiome and polyhydroxyalkanoates potential production. <i>Bioresource Technology</i> , 2021, 337, 125388.	4.8	19
69	Genome Sequences of Four Italian <i>Streptococcus thermophilus</i> Strains of Dairy Origin. <i>Genome Announcements</i> , 2014, 2, .	0.8	18
70	New insights into the variability of lactic acid production in <i>Lachancea thermotolerans</i> at the phenotypic and genomic level. <i>Microbiological Research</i> , 2020, 238, 126525.	2.5	18
71	miR-7 Controls the Dopaminergic/Oligodendroglial Fate through Wnt/ β 2-catenin Signaling Regulation. <i>Cells</i> , 2020, 9, 711.	1.8	18
72	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

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73	Draft Genome Sequence of the Yeast <i>Starmerella bacillaris</i> (syn., <i>Candida</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 507 Announcements, 2017, 5, .	0.8	17
74	Interplay between gut microbiota and <i>p66Shc</i> affects obesity-associated insulin resistance. FASEB Journal, 2018, 32, 4004-4015.	0.2	17
75	Microbial dynamics in biogas digesters treating lipid-rich substrates via genome-centric metagenomics. Science of the Total Environment, 2021, 778, 146296.	3.9	17
76	Muscle Research and Gene Ontology: New standards for improved data integration. BMC Medical Genomics, 2009, 2, 6.	0.7	16
77	Transcriptome structure variability in <i>Saccharomyces cerevisiae</i> strains determined with a newly developed assembly software. BMC Genomics, 2014, 15, 1045.	1.2	15
78	Whole-Genome Sequence of <i>Starmerella bacillaris</i> PAS13, a Nonconventional Enological Yeast with Antifungal Activity. Genome Announcements, 2017, 5, .	0.8	15
79	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, .	1.1	15
80	Characterization of the planktonic microbiome in upflow anaerobic sludge blanket reactors during adaptation of mesophilic methanogenic granules to thermophilic operational conditions. Anaerobe, 2017, 46, 69-77.	1.0	14
81	How Microbiome Composition Correlates with Biochemical Changes during Sauerkraut Fermentation: a Focus on Neglected Bacterial Players and Functionalities. Microbiology Spectrum, 2022, 10, .	1.2	14
82	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. FEMS Yeast Research, 2020, 20, .	1.1	13
83	How multiple farming conditions correlate with the composition of the raw cow's milk lactic microbiome. Environmental Microbiology, 2021, 23, 1702-1716.	1.8	13
84	Preliminary investigation of microorganisms potentially involved in microplastics degradation using an integrated metagenomic and biochemical approach. Science of the Total Environment, 2022, 843, 157017.	3.9	13
85	In vitro fermentation of key dietary compounds with rumen fluid: A genome-centric perspective. Science of the Total Environment, 2017, 584-585, 683-691.	3.9	12
86	Evolution of the microbial community structure in biogas reactors inoculated with seeds from different origin. Science of the Total Environment, 2021, 773, 144981.	3.9	12
87	Gene disruption and basic phenotypic analysis of nine novel yeast genes from chromosome XIV. Yeast, 2000, 16, 1089-1097.	0.8	11
88	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.	4.6	11
89	KEMET – A python tool for KEGG Module evaluation and microbial genome annotation expansion. Computational and Structural Biotechnology Journal, 2022, 20, 1481-1486.	1.9	11
90	A global gene evolution analysis on Vibrionaceae family using phylogenetic profile. BMC Bioinformatics, 2007, 8, S23.	1.2	10

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91	Large-scale sequencing and comparative analysis of oenological <i>Saccharomyces cerevisiae</i> strains supported by nanopore refinement of key genomes. <i>Food Microbiology</i> , 2021, 97, 103753.	2.1	10
92	Metabolomic Alterations Do Not Induce Metabolic Burden in the Industrial Yeast M2n[pBKD2-Pccbgl1]-C1 Engineered by Multiple $\hat{\Gamma}$ -Integration of a Fungal $\hat{\Gamma}^2$ -Glucosidase Gene. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 376.	2.0	9
93	Natural <i>Saccharomyces cerevisiae</i> Strain Reveals Peculiar Genomic Traits for Starch-to-Bioethanol Production: the Design of an Amyolytic Consolidated Bioprocessing Yeast. <i>Frontiers in Microbiology</i> , 2021, 12, 768562.	1.5	9
94	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
95	Evolutionary Study of the Crassphage Virus at Gene Level. <i>Viruses</i> , 2020, 12, 1035.	1.5	8
96	Draft genome sequence data of <i>Lactobacillus paracasei</i> strain DTA83 isolated from infant stools. <i>Data in Brief</i> , 2019, 22, 1064-1067.	0.5	7
97	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.	1.5	6
98	Role prediction of Gram-negative species in the resistome of raw cow's milk. <i>International Journal of Food Microbiology</i> , 2021, 340, 109045.	2.1	6
99	The RNA polymerase subunits E/F from the Antarctic archaeon <i>Methanococcoides burtonii</i> bind to specific species of mRNA. <i>Environmental Microbiology</i> , 2011, 13, 2039-2055.	1.8	4
100	Genome Sequence of <i>Lactobacillus fabifermentans</i> Strain T30PCM01, Isolated from Fermenting Grape Marc. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
101	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
102	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.	1.6	4
103	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
104	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. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
105	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.	2.1	3
106	The hidden layers of microbial community structure: extracting the concealed diversity dimensions from our sequencing data. <i>FEMS Microbiology Letters</i> , 2020, 367, .	0.7	1
107	Editorial: Meta-omic Approaches to the Complex Anaerobic Communities in Wastewater Treatment Plants and Digesters. <i>Frontiers in Microbiology</i> , 2021, 12, 664716.	1.5	0