

Laura Treu

List of Publications by Year in descending order

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104
papers

5,654
citations

81900

39
h-index

85541

71
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108
all docs

108
docs citations

108
times ranked

4715
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of bacterial communities isolated from municipal waste compost and screening of their plant-interactive phenotypes. <i>Science of the Total Environment</i> , 2022, 806, 150592.	8.0	4
2	Thermophilic anaerobic digestion of olive mill wastewater in an upflow packed bed reactor: Evaluation of 16S rRNA amplicon sequencing for microbial analysis. <i>Journal of Environmental Management</i> , 2022, 301, 113853.	7.8	13
3	In-situ biogas upgrading assisted by bioaugmentation with hydrogenotrophic methanogens during mesophilic and thermophilic co-digestion. <i>Bioresource Technology</i> , 2022, 348, 126754.	9.6	22
4	KEMET – A python tool for KEGG Module evaluation and microbial genome annotation expansion. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1481-1486.	4.1	11
5	Preliminary investigation of microorganisms potentially involved in microplastics degradation using an integrated metagenomic and biochemical approach. <i>Science of the Total Environment</i> , 2022, 843, 157017.	8.0	13
6	Valorization of palm oil mill wastewater for integrated production of microbial oil and biogas in a biorefinery approach. <i>Journal of Cleaner Production</i> , 2021, 296, 126606.	9.3	11
7	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.	10.0	77
8	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
9	Evolution of the microbial community structure in biogas reactors inoculated with seeds from different origin. <i>Science of the Total Environment</i> , 2021, 773, 144981.	8.0	12
10	Microbial dynamics in biogas digesters treating lipid-rich substrates via genome-centric metagenomics. <i>Science of the Total Environment</i> , 2021, 778, 146296.	8.0	17
11	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.	4.2	10
12	Pilot-scale biomethanation in a trickle bed reactor: Process performance and microbiome functional reconstruction. <i>Energy Conversion and Management</i> , 2021, 244, 114491.	9.2	39
13	Comprehensive evaluation of different strategies to recover methanogenic performance in ammonia-stressed reactors. <i>Bioresource Technology</i> , 2021, 336, 125329.	9.6	25
14	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.	9.6	19
15	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.	3.5	9
16	Metagenomic insights into bioaugmentation and biovalorization of oily industrial wastes by lipolytic oleaginous yeast <i>Yarrowia lipolytica</i> during successive batch fermentation. <i>Biotechnology and Applied Biochemistry</i> , 2020, 67, 1020-1029.	3.1	7
17	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
18	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.	5.3	18

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19	Microbiota of the Therapeutic Euganean Thermal Muds with a Focus on the Main Cyanobacteria Species. <i>Microorganisms</i> , 2020, 8, 1590.	3.6	23
20	Insights into Ammonia Adaptation and Methanogenic Precursor Oxidation by Genome-Centric Analysis. <i>Environmental Science & Technology</i> , 2020, 54, 12568-12582.	10.0	57
21	Evolutionary Study of the Crassphage Virus at Gene Level. <i>Viruses</i> , 2020, 12, 1035.	3.3	8
22	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
23	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
24	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
25	Modeling temperature response in bioenergy production: Novel solution to a common challenge of anaerobic digestion. <i>Applied Energy</i> , 2020, 263, 114646.	10.1	28
26	Metabolic dependencies govern microbial syntrophies during methanogenesis in an anaerobic digestion ecosystem. <i>Microbiome</i> , 2020, 8, 22.	11.1	91
27	Human waste anaerobic digestion as a promising low-carbon strategy: Operating performance, microbial dynamics and environmental footprint. <i>Journal of Cleaner Production</i> , 2020, 256, 120414.	9.3	26
28	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
29	Long-term preserved and rapidly revived methanogenic cultures: Microbial dynamics and preservation mechanisms. <i>Journal of Cleaner Production</i> , 2020, 263, 121577.	9.3	11
30	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
31	Complete genome sequence of Nitratireductor 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
32	Genomic Comparison of <i>Lactobacillus helveticus</i> Strains Highlights Probiotic Potential. <i>Frontiers in Microbiology</i> , 2019, 10, 1380.	3.5	50
33	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
34	Hydrogenotrophic methanogens are the key for a successful bioaugmentation to alleviate ammonia inhibition in thermophilic anaerobic digesters. <i>Bioresource Technology</i> , 2019, 293, 122070.	9.6	66
35	Exoelectrogenic Anaerobic Granular Sludge for Simultaneous Electricity Generation and Wastewater Treatment. <i>Environmental Science & Technology</i> , 2019, 53, 12130-12140.	10.0	40
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	Bioaugmentation strategy for overcoming ammonia inhibition during biomethanation of a protein-rich substrate. <i>Chemosphere</i> , 2019, 231, 415-422.	8.2	66
38	Enhancing anaerobic digestion of agricultural residues by microaerobic conditions. <i>Biomass Conversion and Biorefinery</i> , 2019, , 1.	4.6	6
39	Acclimatization contributes to stable anaerobic digestion of organic fraction of municipal solid waste under extreme ammonia levels: Focusing on microbial community dynamics. <i>Bioresource Technology</i> , 2019, 286, 121376.	9.6	89
40	Draft genome sequence data of <i>Lactobacillus paracasei</i> strain DTA83 isolated from infant stools. <i>Data in Brief</i> , 2019, 22, 1064-1067.	1.0	7
41	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.	4.1	9
42	A Cryptic Non-Inducible Prophage Confers Phage-Immunity on the <i>Streptococcus thermophilus</i> M17PTZA496. <i>Viruses</i> , 2019, 11, 7.	3.3	26
43	Microbial profiling during anaerobic digestion of cheese whey in reactors operated at different conditions. <i>Bioresource Technology</i> , 2019, 275, 375-385.	9.6	59
44	Novel ecological insights and functional roles during anaerobic digestion of saccharides unveiled by genome-centric metagenomics. <i>Water Research</i> , 2019, 151, 271-279.	11.3	83
45	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.	8.0	85
46	16s rRNA gene sequencing and radioisotopic analysis reveal the composition of ammonia acclimatized methanogenic consortia. <i>Bioresource Technology</i> , 2019, 272, 54-62.	9.6	32
47	Metagenomic binning reveals the functional roles of core abundant microorganisms in twelve full-scale biogas plants. <i>Water Research</i> , 2018, 140, 123-134.	11.3	122
48	Genome Sequence of <i>Rhizobium sllae</i> HCNT1 Isolated from <i>Hedysarum coronarium</i> Nodules and Featuring Peculiar Denitrification Phenotypes. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
49	Taxonomy of anaerobic digestion microbiome reveals biases associated with the applied high throughput sequencing strategies. <i>Scientific Reports</i> , 2018, 8, 1926.	3.3	70
50	Biogas upgrading and utilization: Current status and perspectives. <i>Biotechnology Advances</i> , 2018, 36, 452-466.	11.7	885
51	Performance and genome-centric metagenomics of thermophilic single and two-stage anaerobic digesters treating cheese wastes. <i>Water Research</i> , 2018, 134, 181-191.	11.3	56
52	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
53	Hybrid biogas upgrading in a two-stage thermophilic reactor. <i>Energy Conversion and Management</i> , 2018, 168, 1-10.	9.2	71
54	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.	3.3	26

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55	Acclimation to extremely high ammonia levels in continuous biomethanation process and the associated microbial community dynamics. <i>Bioresource Technology</i> , 2018, 247, 616-623.	9.6	133
56	Converting mesophilic upflow sludge blanket (UASB) reactors to thermophilic by applying axenic methanogenic culture bioaugmentation. <i>Chemical Engineering Journal</i> , 2018, 332, 508-516.	12.7	30
57	Microbial activity response to hydrogen injection in thermophilic anaerobic digesters revealed by genome-centric metatranscriptomics. <i>Microbiome</i> , 2018, 6, 194.	11.1	39
58	Short communication: Comparison of growth kinetics at different temperatures of <i>Streptococcus macedonicus</i> and <i>Streptococcus thermophilus</i> strains of dairy origin. <i>Journal of Dairy Science</i> , 2018, 101, 7812-7816.	3.4	18
59	Whole genome comparison of two <i>Starmerella bacillaris</i> strains with other wine yeasts uncovers genes involved in modulating important winemaking traits. <i>FEMS Yeast Research</i> , 2018, 18, .	2.3	15
60	Effect of different initial pH on the growth of <i>Streptococcus macedonicus</i> and <i>Streptococcus thermophilus</i> strains. <i>International Dairy Journal</i> , 2018, 86, 65-68.	3.0	12
61	Hydrogen-Fueled Microbial Pathways in Biogas Upgrading Systems Revealed by Genome-Centric Metagenomics. <i>Frontiers in Microbiology</i> , 2018, 9, 1079.	3.5	66
62	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
63	Electricity generation and microbial communities in microbial fuel cell powered by macroalgal biomass. <i>Bioelectrochemistry</i> , 2018, 123, 145-149.	4.6	65
64	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
65	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
66	Differences in Carbohydrates Utilization and Antibiotic Resistance Between <i>Streptococcus macedonicus</i> and <i>Streptococcus thermophilus</i> Strains Isolated from Dairy Products in Italy. <i>Current Microbiology</i> , 2018, 75, 1334-1344.	2.2	17
67	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
68	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
69	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
70	Microbial population dynamics in urban organic waste anaerobic co-digestion with mixed sludge during a change in feedstock composition and different hydraulic retention times. <i>Water Research</i> , 2017, 118, 261-271.	11.3	136
71	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
72	Ex-situ biogas upgrading and enhancement in different reactor systems. <i>Bioresource Technology</i> , 2017, 225, 429-437.	9.6	249

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73	Microbial community changes in methanogenic granules during the transition from mesophilic to thermophilic conditions. Applied Microbiology and Biotechnology, 2017, 101, 1313-1322.	3.6	51
74	Enriched ammonia-tolerant methanogenic cultures as bioaugmentation inocula in continuous biomethanation processes. Journal of Cleaner Production, 2017, 166, 1305-1313.	9.3	53
75	Anaerobic granular sludge for simultaneous biomethanation of synthetic wastewater and CO with focus on the identification of CO-converting microorganisms. Water Research, 2017, 126, 19-28.	11.3	41
76	Co-fermentation of onion and whey: A promising synbiotic combination. Journal of Functional Foods, 2017, 39, 233-237.	3.4	16
77	Whole-Genome Sequence of <i>Starmerella bacillaris</i> PAS13, a Nonconventional Enological Yeast with Antifungal Activity. Genome Announcements, 2017, 5, .	0.8	15
78	Draft Genome Sequence of the Yeast <i>Starmerella bacillaris</i> (syn., <i>Candida</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 547 Td (Announcements, 2017, 5, .	0.8	17
79	Process performance and comparative metagenomic analysis during co-digestion of manure and lignocellulosic biomass for biogas production. Applied Energy, 2017, 185, 126-135.	10.1	132
80	Genome comparison and physiological characterization of eight <i>Streptococcus thermophilus</i> strains isolated from Italian dairy products. Food Microbiology, 2017, 63, 47-57.	4.2	34
81	Whole-Genome Sequences of Three <i>Streptococcus macedonicus</i> Strains Isolated from Italian Cheeses in the Veneto Region. Genome Announcements, 2017, 5, .	0.8	8
82	The Complete Genome Sequence of <i>Trueperella pyogenes</i> UFV1 Reveals a Processing System Involved in the Quorum-Sensing Signal Response. Genome Announcements, 2017, 5, .	0.8	3
83	Deeper insight into the structure of the anaerobic digestion microbial community; the biogas microbiome database is expanded with 157 new genomes. Bioresource Technology, 2016, 216, 260-266.	9.6	132
84	Potential use of <i>scotta</i> , the by-product of the ricotta cheese manufacturing process, for the production of fermented drinks. Journal of Dairy Research, 2016, 83, 104-108.	1.4	18
85	Untangling the Effect of Fatty Acid Addition at Species Level Revealed Different Transcriptional Responses of the Biogas Microbial Community Members. Environmental Science & Technology, 2016, 50, 6079-6090.	10.0	79
86	Metagenomic analysis and functional characterization of the biogas microbiome using high throughput shotgun sequencing and a novel binning strategy. Biotechnology for Biofuels, 2016, 9, 26.	6.2	248
87	Dynamic functional characterization and phylogenetic changes due to Long Chain Fatty Acids pulses in biogas reactors. Scientific Reports, 2016, 6, 28810.	3.3	58
88	Different mechanisms of resistance modulate sulfite tolerance in wine yeasts. Applied Microbiology and Biotechnology, 2016, 100, 797-813.	3.6	42
89	New steady-state microbial community compositions and process performances in biogas reactors induced by temperature disturbances. Biotechnology for Biofuels, 2015, 8, 3.	6.2	68
90	Biogas Upgrading via Hydrogenotrophic Methanogenesis in Two-Stage Continuous Stirred Tank Reactors at Mesophilic and Thermophilic Conditions. Environmental Science & Technology, 2015, 49, 12585-12593.	10.0	287

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91	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
92	Genome Sequence of <i>Lactobacillus fabifermentans</i> Strain T30PCM01, Isolated from Fermenting Grape Marc. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
93	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
94	Genome Sequences of Four Italian <i>Streptococcus thermophilus</i> Strains of Dairy Origin. <i>Genome Announcements</i> , 2014, 2, .	0.8	18
95	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
96	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
97	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
98	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
99	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
100	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
101	Microbial analysis in biogas reactors suffering by foaming incidents. <i>Bioresource Technology</i> , 2014, 167, 24-32.	9.6	38
102	Temperature-dependent global gene expression in the Antarctic archaeon <i>Methanococcoides burtonii</i> . <i>Environmental Microbiology</i> , 2011, 13, 2018-2038.	3.8	62
103	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.	3.8	4
104	Protein evolution in deep sea bacteria: an analysis of amino acids substitution rates. <i>BMC Evolutionary Biology</i> , 2008, 8, 313.	3.2	37