

Laura Treu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4814934/publications.pdf>

Version: 2024-02-01

104
papers

5,654
citations

81900

39
h-index

85541

71
g-index

108
all docs

108
docs citations

108
times ranked

4715
citing authors

#	ARTICLE	IF	CITATIONS
1	Biogas upgrading and utilization: Current status and perspectives. <i>Biotechnology Advances</i> , 2018, 36, 452-466.	11.7	885
2	Biogas Upgrading via Hydrogenotrophic Methanogenesis in Two-Stage Continuous Stirred Tank Reactors at Mesophilic and Thermophilic Conditions. <i>Environmental Science & Technology</i> , 2015, 49, 12585-12593.	10.0	287
3	Ex-situ biogas upgrading and enhancement in different reactor systems. <i>Bioresource Technology</i> , 2017, 225, 429-437.	9.6	249
4	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
5	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
6	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
7	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
8	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
9	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
10	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
11	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
12	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
13	Metabolic dependencies govern microbial syntrophies during methanogenesis in an anaerobic digestion ecosystem. <i>Microbiome</i> , 2020, 8, 22.	11.1	91
14	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
15	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
16	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
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	Hybrid biogas upgrading in a two-stage thermophilic reactor. <i>Energy Conversion and Management</i> , 2018, 168, 1-10.	9.2	71
22	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
23	New steady-state microbial community compositions and process performances in biogas reactors induced by temperature disturbances. <i>Biotechnology for Biofuels</i> , 2015, 8, 3.	6.2	68
24	Hydrogen-Fueled Microbial Pathways in Biogas Upgrading Systems Revealed by Genome-Centric Metagenomics. <i>Frontiers in Microbiology</i> , 2018, 9, 1079.	3.5	66
25	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
26	Bioaugmentation strategy for overcoming ammonia inhibition during biomethanation of a protein-rich substrate. <i>Chemosphere</i> , 2019, 231, 415-422.	8.2	66
27	Electricity generation and microbial communities in microbial fuel cell powered by macroalgal biomass. <i>Bioelectrochemistry</i> , 2018, 123, 145-149.	4.6	65
28	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
29	Temperature-dependent global gene expression in the Antarctic archaeon <i>Methanococcoides burtonii</i> . <i>Environmental Microbiology</i> , 2011, 13, 2018-2038.	3.8	62
30	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
31	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
32	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
33	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
34	Insights into Ammonia Adaptation and Methanogenic Precursor Oxidation by Genome-Centric Analysis. <i>Environmental Science & Technology</i> , 2020, 54, 12568-12582.	10.0	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.	11.3	56
36	Enriched ammonia-tolerant methanogenic cultures as bioaugmentation inocula in continuous biomethanation processes. <i>Journal of Cleaner Production</i> , 2017, 166, 1305-1313.	9.3	53

#	ARTICLE	IF	CITATIONS
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.	3.6	51
38	Genomic Comparison of <i>Lactobacillus helveticus</i> Strains Highlights Probiotic Potential. <i>Frontiers in Microbiology</i> , 2019, 10, 1380.	3.5	50
39	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
40	Different mechanisms of resistance modulate sulfite tolerance in wine yeasts. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 797-813.	3.6	42
41	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
42	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
43	Exoelectrogenic Anaerobic Granular Sludge for Simultaneous Electricity Generation and Wastewater Treatment. <i>Environmental Science & Technology</i> , 2019, 53, 12130-12140.	10.0	40
44	Microbial activity response to hydrogen injection in thermophilic anaerobic digesters revealed by genome-centric metatranscriptomics. <i>Microbiome</i> , 2018, 6, 194.	11.1	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.	9.2	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.	3.6	38
47	Microbial analysis in biogas reactors suffering by foaming incidents. <i>Bioresource Technology</i> , 2014, 167, 24-32.	9.6	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.	3.6	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.	4.2	34
51	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
52	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
53	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
54	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

#	ARTICLE	IF	CITATIONS
55	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
56	A Cryptic Non-Inducible Prophage Confers Phage-Immunity on the <i>Streptococcus thermophilus</i> M17PTZA496. <i>Viruses</i> , 2019, 11, 7.	3.3	26
57	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
58	Comprehensive evaluation of different strategies to recover methanogenic performance in ammonia-stressed reactors. <i>Bioresource Technology</i> , 2021, 336, 125329.	9.6	25
59	Microbiota of the Therapeutic Euganean Thermal Muds with a Focus on the Main Cyanobacteria Species. <i>Microorganisms</i> , 2020, 8, 1590.	3.6	23
60	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
61	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
62	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
63	Genome Sequences of Four Italian <i>Streptococcus thermophilus</i> Strains of Dairy Origin. <i>Genome Announcements</i> , 2014, 2, .	0.8	18
64	Potential use of <i>scotta</i> , the by-product of the ricotta cheese manufacturing process, for the production of fermented drinks. <i>Journal of Dairy Research</i> , 2016, 83, 104-108.	1.4	18
65	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
66	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
67	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
68	Draft Genome Sequence of the Yeast <i>Starmerella bacillaris</i> (syn., <i>Candida</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 Td (<i>Announcements</i> , 2017, 5, .	0.8	17
69	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
70	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
71	Co-fermentation of onion and whey: A promising synbiotic combination. <i>Journal of Functional Foods</i> , 2017, 39, 233-237.	3.4	16
72	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

#	ARTICLE	IF	CITATIONS
73	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
74	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
75	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
76	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
77	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
78	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
79	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
80	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
81	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
82	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
83	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
84	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
85	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
86	Metabolomic Alterations Do Not Induce Metabolic Burden in the Industrial Yeast M2n[pBKD2-Pccbgl1]-C1 Engineered by Multiple λ -Integration of a Fungal β -Glucosidase Gene. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 376.	4.1	9
87	Natural <i>Saccharomyces cerevisiae</i> Strain Reveals Peculiar Genomic Traits for Starch-to-Bioethanol Production: the Design of an Amylolytic Consolidated Bioprocessing Yeast. <i>Frontiers in Microbiology</i> , 2021, 12, 768562.	3.5	9
88	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
89	Whole-Genome Sequences of Three <i>Streptococcus macedonicus</i> Strains Isolated from Italian Cheeses in the Veneto Region. <i>Genome Announcements</i> , 2017, 5, .	0.8	8
90	Evolutionary Study of the Crassphage Virus at Gene Level. <i>Viruses</i> , 2020, 12, 1035.	3.3	8

#	ARTICLE	IF	CITATIONS
91	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
92	Metagenomic insights into bioaugmentation and biovalorization of oily industrial wastes by lipolytic oleaginous yeast <i>Yarrowia lipolytica</i> during successive batch fermentation. Biotechnology and Applied Biochemistry, 2020, 67, 1020-1029.	3.1	7
93	Study of microbial dynamics during optimization of hydrogen production from food waste by using LCFA-rich agent. Bioresource Technology Reports, 2019, 5, 157-163.	2.7	6
94	Enhancing anaerobic digestion of agricultural residues by microaerobic conditions. Biomass Conversion and Biorefinery, 2019, , 1.	4.6	6
95	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
96	Genome Sequence of <i>Lactobacillus fabifermentans</i> Strain T30PCM01, Isolated from Fermenting Grape Marc. Genome Announcements, 2014, 2, .	0.8	4
97	Draft Genome Sequences of Three Virulent <i>Streptococcus thermophilus</i> Bacteriophages Isolated from the Dairy Environment in the Veneto Region of Italy. Genome Announcements, 2018, 6, .	0.8	4
98	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. Scientific Reports, 2020, 10, 5520.	3.3	4
99	Characterization of bacterial communities isolated from municipal waste compost and screening of their plant-interactive phenotypes. Science of the Total Environment, 2022, 806, 150592.	8.0	4
100	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
101	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
102	Complete genome sequence of <i>Nitratireductor</i> sp. strain OM-1: A lipid-producing bacterium with potential use in wastewater treatment. Biotechnology Reports (Amsterdam, Netherlands), 2019, 24, e00366.	4.4	3
103	Genome Sequence of <i>Rhizobium sulae</i> HCNT1 Isolated from <i>Hedysarum coronarium</i> Nodules and Featuring Peculiar Denitrification Phenotypes. Genome Announcements, 2018, 6, .	0.8	2
104	The hidden layers of microbial community structure: extracting the concealed diversity dimensions from our sequencing data. FEMS Microbiology Letters, 2020, 367, .	1.8	1