

# Frank R Bengelsdorf

## List of Publications by Year in descending order

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Version: 2024-02-01

42  
papers

1,415  
citations

393982

19  
h-index

329751

37  
g-index

44  
all docs

44  
docs citations

44  
times ranked

1249  
citing authors

#	ARTICLE	IF	CITATIONS
1	Bacterial synthesis gas (syngas) fermentation. Environmental Technology (United Kingdom), 2013, 34, 1639-1651.	1.2	187
2	Using gas mixtures of CO, CO <sub>2</sub> and H <sub>2</sub> as microbial substrates: the do's and don'ts of successful technology transfer from laboratory to production scale. Microbial Biotechnology, 2018, 11, 606-625.	2.0	126
3	Bacterial Anaerobic Synthesis Gas (Syngas) and CO <sub>2</sub> + H <sub>2</sub> Fermentation. Advances in Applied Microbiology, 2018, 103, 143-221.	1.3	118
4	Acetone production with metabolically engineered strains of Acetobacterium woodii. Metabolic Engineering, 2016, 36, 37-47.	3.6	111
5	Industrial Acetogenic Biocatalysts: A Comparative Metabolic and Genomic Analysis. Frontiers in Microbiology, 2016, 7, 1036.	1.5	85
6	The Complete Genome Sequence of Clostridium aceticum: a Missing Link between Rnf- and Cytochrome-Containing Autotrophic Acetogens. MBio, 2015, 6, e01168-15.	1.8	75
7	Improved operating strategy for continuous fermentation of carbon monoxide to fuel-ethanol by clostridia. Applied Energy, 2016, 169, 210-217.	5.1	55
8	Caproicibacter fermentans gen. nov., sp. nov., a new caproate-producing bacterium and emended description of the genus Caproiciproducens. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4269-4279.	0.8	49
9	Gas fermentation for commodity chemicals and fuels. Microbial Biotechnology, 2017, 10, 1167-1170.	2.0	47
10	Dynamics of biofilm formation during anaerobic digestion of organic waste. Anaerobe, 2014, 29, 44-51.	1.0	46
11	Anaerobic Production of Poly(3-hydroxybutyrate) and Its Precursor 3-Hydroxybutyrate from Synthesis Gas by Autotrophic Clostridia. Biomacromolecules, 2019, 20, 3271-3282.	2.6	46
12	Stability of a biogas-producing bacterial, archaeal and fungal community degrading food residues. FEMS Microbiology Ecology, 2013, 84, 201-212.	1.3	44
13	Fungi open new possibilities for anaerobic fermentation of organic residues. Energy, Sustainability and Society, 2014, 4, .	1.7	41
14	Production of the biocommodities butanol and acetone from methanol with fluorescent FAST-tagged proteins using metabolically engineered strains of Eubacterium limosum. Biotechnology for Biofuels, 2021, 14, 117.	6.2	36
15	Functionally redundant but dissimilar microbial communities within biogas reactors treating maize silage in co-fermentation with sugar beet silage. Microbial Biotechnology, 2015, 8, 828-836.	2.0	31
16	Electron availability in CO <sub>2</sub> , CO and H <sub>2</sub> mixtures constrains flux distribution, energy management and product formation in <i>Clostridium ljungdahlii</i> . Microbial Biotechnology, 2020, 13, 1831-1846.	2.0	27
17	Complete Genome Sequence of the Type Strain of the Acetogenic Bacterium Moorella thermoacetica DSM 521 <sup>T</sup> . Genome Announcements, 2015, 3, .	0.8	25
18	Different response of bacteria, archaea and fungi to process parameters in nine full-scale anaerobic digesters. Microbial Biotechnology, 2019, 12, 1210-1225.	2.0	23

#	ARTICLE	IF	CITATIONS
19	Induced heterologous expression of the arginine deiminase pathway promotes growth advantages in the strict anaerobe <i>Acetobacterium woodii</i> . <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 687-699.	1.7	23
20	Complete Genome Sequence of the Acetogenic Bacterium <i>Moorella thermoacetica</i> DSM 2955 <sup>T</sup>. <i>Genome Announcements</i> , 2015, 3, .	0.8	21
21	Genome Sequence of the Caproic Acid-Producing Bacterium <i>Caproiciproducens galactitolivorans</i> BS-1 <sup>T</sup> (JCM 30532). <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	18
22	Genome Sequence of the Acetogenic Bacterium <i>Oxobacter pfennigii</i> DSM 3222 <sup>T</sup>. <i>Genome Announcements</i> , 2015, 3, .	0.8	17
23	Autotrophic lactate production from H <sub>2</sub> +CO <sub>2</sub> using recombinant and fluorescent FAST-tagged <i>Acetobacterium woodii</i> strains. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 1447-1458.	1.7	17
24	Isobutanol Production by Autotrophic Acetogenic Bacteria. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 657253.	2.0	16
25	Analysis of the key enzymes of butyric and acetic acid fermentation in biogas reactors. <i>Microbial Biotechnology</i> , 2015, 8, 865-873.	2.0	14
26	Genome Sequence of the Acetogenic Bacterium <i>Butyribacterium methylotrophicum</i> DSM 3468 <sup>T</sup>. <i>Genome Announcements</i> , 2016, 4, .	0.8	13
27	Syntrophic microbial communities on straw as biofilm carrier increase the methane yield of a biowaste-digesting biogas reactor. <i>AIMS Bioengineering</i> , 2015, 2, 264-276.	0.6	13
28	Genome Sequence of the Acetogenic Bacterium <i>Acetobacterium wieringae</i> DSM 1911 <sup>T</sup>. <i>Genome Announcements</i> , 2016, 4, .	0.8	12
29	Complete Genome Sequence of the Autotrophic Acetogen <i>Clostridium formicaceticum</i> DSM 92 <sup>T</sup> Using Nanopore and Illumina Sequencing Data. <i>Genome Announcements</i> , 2017, 5, .	0.8	12
30	Genome-Based Comparison of All Species of the Genus <i>Moorella</i> , and Status of the Species <i>Moorella thermoacetica</i> and <i>Moorella thermoautotrophica</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 3070.	1.5	12
31	Complete Genome Sequence of Rnf- and Cytochrome-Containing Autotrophic Acetogen <i>Clostridium aceticum</i> DSM 1496. <i>Genome Announcements</i> , 2015, 3, .	0.8	11
32	Identifying and Engineering Bottlenecks of Autotrophic Isobutanol Formation in Recombinant <i>C. ljungdahlii</i> by Systemic Analysis. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 647853.	2.0	10
33	Novel synthetic co-culture of <i>Acetobacterium woodii</i> and <i>Clostridium drakei</i> using CO <sub>2</sub> and in situ generated H <sub>2</sub> for the production of caproic acid via lactic acid. <i>Engineering in Life Sciences</i> , 2023, 23, .	2.0	7
34	Draft Genome Sequence of Purine-Degrading <i>Clostridium cylindrosporium</i> HC-1 (DSM 605). <i>Genome Announcements</i> , 2015, 3, .	0.8	6
35	Draft Genome Sequence of the Strict Anaerobe <i>Clostridium neopropionicum</i> X4 (DSM 3847 T). <i>Genome Announcements</i> , 2016, 4, .	0.8	6
36	Draft Genome Sequence of Purine-Degrading <i>Gottschalkia purinilyticum</i> (Formerly <i>Clostridium</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62	0.8	4

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37	Draft Genome Sequence of the Strict Anaerobe <i>Clostridium homopropionicum</i> LuHBu1 (DSM 5847). <i>Genome Announcements</i> , 2015, 3, .	0.8	4
38	Genome sequencing and description of <i>Oerskovia enterophila</i> VJag, an agar- and cellulose-degrading bacterium. <i>Standards in Genomic Sciences</i> , 2017, 12, 30.	1.5	2
39	Genome Sequence of the Facultative Anaerobe <i>Oerskovia enterophila</i> DFA-19 (DSM 43852 <sup>T</sup>) Tj ETQq1 1 0.784314 rgBT	0.8	1
40	Genome Sequence of <i>Enterococcus faecalis</i> Strain CG_E. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
41	Genome Sequence of <i>Lactobacillus sunkii</i> Strain CG_D. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
42	Biokatalytische Konversion. , 2020, , 99-119.		0