

# Masaru K Nobu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2416856/publications.pdf>

Version: 2024-02-01

40  
papers

2,652  
citations

279487

23  
h-index

301761

39  
g-index

45  
all docs

45  
docs citations

45  
times ranked

3301  
citing authors

#	ARTICLE	IF	CITATIONS
1	High-rate cotreatment of purified terephthalate and dimethyl terephthalate manufacturing wastewater by a mesophilic upflow anaerobic sludge blanket reactor and the microbial ecology relevant to aromatic compound degradation. <i>Water Research</i> , 2022, 219, 118581.	5.3	20
2	<i>Koleobacter methoxysyntrophicus</i> gen. nov., sp. nov., a novel anaerobic bacterium isolated from deep subsurface oil field and proposal of <i>Koleobacteraceae</i> fam. nov. and <i>Koleobacterales</i> ord. nov. within the class <i>Clostridia</i> of the phylum <i>Firmicutes</i> . <i>Systematic and Applied Microbiology</i> , 2021, 44, 126154.	1.2	15
3	Ecogenomics Reveals Microbial Metabolic Networks in a Psychrophilic Methanogenic Bioreactor Treating Soy Sauce Production Wastewater. <i>Microbes and Environments</i> , 2021, 36, n/a.	0.7	9
4	Methanogenic archaea use a bacteria-like methyltransferase system to demethoxylate aromatic compounds. <i>ISME Journal</i> , 2021, 15, 3549-3565.	4.4	30
5	Assessing the effect of green tuff as a novel natural inorganic carrier on methane-producing activity of an anaerobic sludge microbiome. <i>Environmental Technology and Innovation</i> , 2021, 24, 101835.	3.0	3
6	Novel Syntrophic Isovalerate-Degrading Bacteria and Their Energetic Cooperation with Methanogens in Methanogenic Chemostats. <i>Environmental Science &amp; Technology</i> , 2020, 54, 9618-9628.	4.6	23
7	Influence of Green Tuff Fertilizer Application on Soil Microorganisms, Plant Growth, and Soil Chemical Parameters in Green Onion ( <i>Allium fistulosum</i> L.) Cultivation. <i>Agronomy</i> , 2020, 10, 929.	1.3	8
8	Catabolism and interactions of uncultured organisms shaped by eco-thermodynamics in methanogenic bioprocesses. <i>Microbiome</i> , 2020, 8, 111.	4.9	48
9	Metagenomic and Metatranscriptomic Analyses Revealed Uncultured Bacteroidales Populations as the Dominant Proteolytic Amino Acid Degraders in Anaerobic Digesters. <i>Frontiers in Microbiology</i> , 2020, 11, 593006.	1.5	57
10	Isolation of a member of the candidate phylum <i>Atribacteria</i> <sup>TM</sup> reveals a unique cell membrane structure. <i>Nature Communications</i> , 2020, 11, 6381.	5.8	62
11	A hydrogen-dependent geochemical analogue of primordial carbon and energy metabolism. <i>Nature Ecology and Evolution</i> , 2020, 4, 534-542.	3.4	140
12	Different Interspecies Electron Transfer Patterns during Mesophilic and Thermophilic Syntrophic Propionate Degradation in Chemostats. <i>Microbial Ecology</i> , 2020, 80, 120-132.	1.4	29
13	Identifying anaerobic amino acids degraders through the comparison of short-term and long-term enrichments. <i>Environmental Microbiology Reports</i> , 2020, 12, 173-184.	1.0	8
14	Isolation of an archaeon at the prokaryote-eukaryote interface. <i>Nature</i> , 2020, 577, 519-525.	13.7	449
15	Molecular Evolution of [NiFe] Hydrogenase-related Energy Conservation Systems. <i>Journal of Geography (Chigaku Zasshi)</i> , 2020, 129, 825-835.	0.1	2
16	Community analysis of gut microbiota in hornets, the largest eusocial wasps, <i>Vespa mandarinia</i> and <i>V. simillima</i> . <i>Scientific Reports</i> , 2019, 9, 9830.	1.6	37
17	Response of Propionate-Degrading Methanogenic Microbial Communities to Inhibitory Conditions. <i>Applied Biochemistry and Biotechnology</i> , 2019, 189, 233-248.	1.4	20
18	Using DNA-based stable isotope probing to reveal novel propionate- and acetate-oxidizing bacteria in propionate-fed mesophilic anaerobic chemostats. <i>Scientific Reports</i> , 2019, 9, 17396.	1.6	25

#	ARTICLE	IF	CITATIONS
19	Shaping microbial consortia in coupling glycerol fermentation and carboxylate chain elongation for Co-production of 1,3-propanediol and caproate: Pathways and mechanisms. <i>Water Research</i> , 2019, 148, 281-291.	5.3	30
20	Novel <i>Geobacter</i> species and diverse methanogens contribute to enhanced methane production in media-added methanogenic reactors. <i>Water Research</i> , 2018, 147, 403-412.	5.3	69
21	Co-occurrence network analysis reveals thermodynamics-driven microbial interactions in methanogenic bioreactors. <i>Environmental Microbiology Reports</i> , 2018, 10, 673-685.	1.0	22
22	Novel energy conservation strategies and behaviour of <i>Pelotomaculum schinkii</i> driving syntrophic propionate catabolism. <i>Environmental Microbiology</i> , 2018, 20, 4503-4511.	1.8	31
23	Impacts of biostimulation and bioaugmentation on the performance and microbial ecology in methanogenic reactors treating purified terephthalic acid wastewater. <i>Water Research</i> , 2017, 122, 308-316.	5.3	22
24	Thermodynamically diverse syntrophic aromatic compound catabolism. <i>Environmental Microbiology</i> , 2017, 19, 4576-4586.	1.8	32
25	Operation-driven heterogeneity and overlooked feed-associated populations in global anaerobic digester microbiome. <i>Water Research</i> , 2017, 124, 77-84.	5.3	82
26	Diverse Marinimicrobia bacteria may mediate coupled biogeochemical cycles along eco-thermodynamic gradients. <i>Nature Communications</i> , 2017, 8, 1507.	5.8	99
27	Draft Genome Sequence of <i>Syntrophomonas wolfei</i> subsp. <i>methylbutyratica</i> Strain 4J5 (JCM 14075), a Mesophilic Butyrate- and 2-Methylbutyrate-Degrading Syntroph. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
28	Comparative Genomics of Syntrophic Branched-Chain Fatty Acid Degrading Bacteria. <i>Microbes and Environments</i> , 2016, 31, 288-292.	0.7	19
29	Evaluating digestion efficiency in full-scale anaerobic digesters by identifying active microbial populations through the lens of microbial activity. <i>Scientific Reports</i> , 2016, 6, 34090.	1.6	87
30	Complete Genome Sequence of the Intracellular Bacterial Symbiont TC1 in the Anaerobic Ciliate <i>Trimyema compressum</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	6
31	Chasing the elusive Euryarchaeota class WSA2: genomes reveal a uniquely fastidious methyl-reducing methanogen. <i>ISME Journal</i> , 2016, 10, 2478-2487.	4.4	239
32	Phylogeny and physiology of candidate phylum Atribacteria (OP9/JS1) inferred from cultivation-independent genomics. <i>ISME Journal</i> , 2016, 10, 273-286.	4.4	166
33	A Single-Granule-Level Approach Reveals Ecological Heterogeneity in an Upflow Anaerobic Sludge Blanket Reactor. <i>PLoS ONE</i> , 2016, 11, e0167788.	1.1	46
34	Microbial Community Analysis of Anaerobic Reactors Treating Soft Drink Wastewater. <i>PLoS ONE</i> , 2015, 10, e0119131.	1.1	27
35	The nexus of syntrophy-associated microbiota in anaerobic digestion revealed by long-term enrichment and community survey. <i>Environmental Microbiology</i> , 2015, 17, 1707-1720.	1.8	149
36	Microbial dark matter ecogenomics reveals complex synergistic networks in a methanogenic bioreactor. <i>ISME Journal</i> , 2015, 9, 1710-1722.	4.4	360

#	ARTICLE	IF	CITATIONS
37	Microbial Community Involved in Anaerobic Purified Terephthalic Acid Treatment Process. , 2015, , 31-48.		4
38	The genome of <i>Syntrophorhabdus aromaticivorans</i> strain UI provides new insights for syntrophic aromatic compound metabolism and electron flow. Environmental Microbiology, 2015, 17, 4861-4872.	1.8	72
39	Draft Genome Sequence of <i>Syntrophorhabdus aromaticivorans</i> Strain UI, a Mesophilic Aromatic Compound-Degrading Syntroph. Genome Announcements, 2014, 2, .	0.8	23
40	Metagenomic characterization of <i>Candidatus</i> <i>Delfluviicoccus tetraformis</i> strain TFO71 <sup>TM</sup> , a tetrad-forming organism, predominant in an anaerobic-aerobic membrane bioreactor with deteriorated biological phosphorus removal. Environmental Microbiology, 2014, 16, 2739-2751.	1.8	34