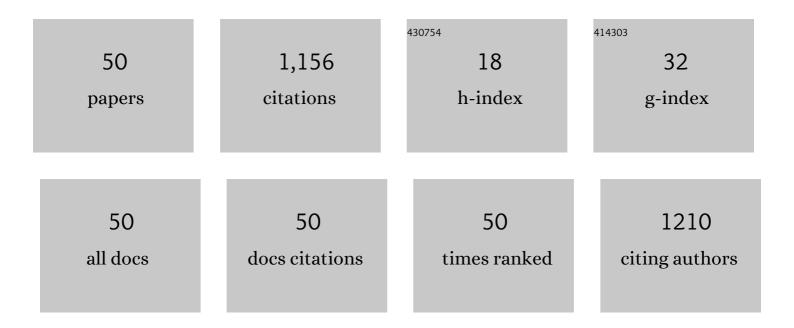
Masao Fukuda

List of Publications by Year in descending order

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Μλέλο Ειικίισλ

#	Article	IF	CITATIONS
1	Identification and transcriptional analysis of poly(cis-1,4-isoprene) degradation gene in Rhodococcus sp. strain RDE2. Journal of Bioscience and Bioengineering, 2022, 133, 452-458.	1.1	3
2	Characterization of the genes responsible for rubber degradation in Actinoplanes sp. strain OR16. Applied Microbiology and Biotechnology, 2020, 104, 7367-7376.	1.7	6
3	Biodegradation of natural rubber and deproteinized natural rubber by enrichment bacterial consortia. Biodegradation, 2020, 31, 303-317.	1.5	19
4	Ecological impact assessment of a bioaugmentation site on remediation of chlorinated ethylenes by multi-omics analysis. Journal of General and Applied Microbiology, 2019, 65, 225-233.	0.4	6
5	Complete genome sequence of natural rubber-degrading, gram-negative bacterium, Rhizobacter gummiphilus strain NS21T. Biotechnology Reports (Amsterdam, Netherlands), 2019, 22, e00332.	2.1	6
6	2,3-Dihydroxybenzoate meta-Cleavage Pathway is Involved in o-Phthalate Utilization in Pseudomonas sp. strain PTH10. Scientific Reports, 2019, 9, 1253.	1.6	8
7	Characterization and Transcriptional Regulation of n-Alkane Hydroxylase Gene Cluster of Rhodococcus jostii RHA1. Microorganisms, 2019, 7, 479.	1.6	14
8	Regulation of vanillate and syringate catabolism by a MarR-type transcriptional regulator DesR in Sphingobium sp. SYK-6. Scientific Reports, 2019, 9, 18036.	1.6	16
9	Characteristics of greenhouse gas emissions from an anaerobic wastewater treatment system in a natural rubber processing factory. Environmental Technology (United Kingdom), 2019, 40, 2954-2961.	1.2	5
10	Biphenyl degradation by recombinant photosynthetic cyanobacterium Synechocystis sp. PCC6803 in an oligotrophic environment using unphysiological electron transfer. Biochemical Journal, 2019, 476, 3615-3630.	1.7	2
11	Development of downflow hanging sponge (DHS) reactor as post treatment of existing combined anaerobic tank treating natural rubber processing wastewater. Water Science and Technology, 2017, 75, 57-68.	1.2	38
12	Characterization and functional expression of a rubber degradation gene of a Nocardia degrader from a rubber-processing factory. Journal of Bioscience and Bioengineering, 2017, 123, 412-418.	1.1	31
13	Identification of natural rubber degradation gene in <i>Rhizobacter gummiphilus</i> NS21. Bioscience, Biotechnology and Biochemistry, 2017, 81, 614-620.	0.6	31
14	Thermodynamics of the Thermal Denaturation of Acid Molten Globule State of Cytochrome <i>c</i> Indicate a Reversible High-Temperature Oligomerization Process. Biochemistry, 2017, 56, 2372-2378.	1.2	8
15	Performance evaluation of the pilot scale upflow anaerobic sludge blanket – Downflow hanging sponge system for natural rubber processing wastewater treatment in South Vietnam. Bioresource Technology, 2017, 237, 204-212.	4.8	36
16	A bacterial aromatic aldehyde dehydrogenase critical for the efficient catabolism of syringaldehyde. Scientific Reports, 2017, 7, 44422.	1.6	43
17	Amino acid residues critical for DNA binding and inducer recognition in CbnR, a LysR-type transcriptional regulator from <i>Cupriavidus necator</i> NH9. Bioscience, Biotechnology and Biochemistry, 2017, 81, 2119-2129.	0.6	13
18	Common origin of methylenedioxy ring degradation and demethylation in bacteria. Scientific Reports, 2017, 7, 7422.	1.6	6

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19	Impact of aluminum chloride on process performance and microbial community structure of granular sludge in an upflow anaerobic sludge blanket reactor for natural rubber processing wastewater treatment. Water Science and Technology, 2016, 74, 500-507.	1.2	10
20	Draft Genome Sequences of <i>Sphingobium</i> sp. Strain TCM1 and <i>Sphingomonas</i> sp. Strain TDK1, Haloalkyl Phosphate Flame Retardant- and Plasticizer-Degrading Bacteria. Genome Announcements, 2016, 4, .	0.8	8
21	Ammonia Stripping from High Ammonia-Containing Wastewater by Downflow Hanging Sponge (DHS) Reactor. Journal of Water and Environment Technology, 2016, 14, 303-307.	0.3	7
22	Draft Genome Sequence of Comamonas thiooxydans Strain PHE2-6 (NBRC 110656), a Chlorinated-Ethene-Degrading Bacterium. Genome Announcements, 2016, 4, .	0.8	5
23	Draft Genome Sequence of a Chlorinated-Ethene Degrader, <i>Cupriavidus necator</i> Strain PHE3-6 (NBRC 110655). Genome Announcements, 2016, 4, .	0.8	3
24	Identification of novel extracellular protein for PCB/biphenyl metabolism in Rhodococcus jostii RHA1. Bioscience, Biotechnology and Biochemistry, 2016, 80, 1012-1019.	0.6	10
25	Development of a BR–UASB–DHS system for natural rubber processing wastewater treatment. Environmental Technology (United Kingdom), 2016, 37, 459-465.	1.2	21
26	11-Hydroxylation of Protoberberine by the Novel Berberine-Utilizing Aerobic Bacterium <i>Sphingobium</i> sp. Strain BD3100. Journal of Natural Products, 2015, 78, 2880-2886.	1.5	12
27	Introduction of chemically labile substructures into <i>Arabidopsis</i> lignin through the use of LigD, the Cαâ€dehydrogenase from <i>Sphingobium</i> sp. strain <scp>SYK</scp> â€6. Plant Biotechnology Journal, 2015, 13, 821-832.	4.1	45
28	Membrane-Associated Glucose-Methanol-Choline Oxidoreductase Family Enzymes PhcC and PhcD Are Essential for Enantioselective Catabolism of Dehydrodiconiferyl Alcohol. Applied and Environmental Microbiology, 2015, 81, 8022-8036.	1.4	20
29	Î ³ -Resorcylate Catabolic-Pathway Genes in the Soil Actinomycete Rhodococcus jostii RHA1. Applied and Environmental Microbiology, 2015, 81, 7656-7665.	1.4	11
30	Differentiation of industrial sake yeast strains by a loop-mediated isothermal amplification method that targets the PHO3 gene. Journal of Bioscience and Bioengineering, 2014, 118, 661-664.	1.1	2
31	Three-Component <i>O</i> -Demethylase System Essential for Catabolism of a Lignin-Derived Biphenyl Compound in Sphingobium sp. Strain SYK-6. Applied and Environmental Microbiology, 2014, 80, 7142-7153.	1.4	35
32	Molecular Mechanism of Strict Substrate Specificity of an Extradiol Dioxygenase, DesB, Derived from Sphingobium sp. SYK-6. PLoS ONE, 2014, 9, e92249.	1.1	19
33	Rhizobacter gummiphilus sp. nov., a rubber-degrading bacterium isolated from the soil of a botanical garden in Japan. Journal of General and Applied Microbiology, 2013, 59, 199-205.	0.4	39
34	Isolation and characterization of Streptomyces, Actinoplanes, and Methylibium strains that are involved in degradation of natural rubber and synthetic poly(cis-1,4-isoprene). Enzyme and Microbial Technology, 2011, 49, 526-531.	1.6	60
35	Identification and Characterization of Uptake Systems for Glucose and Fructose in <i>Rhodococcus jostii</i> RHA1. Journal of Molecular Microbiology and Biotechnology, 2011, 20, 125-136.	1.0	12
36	Uncovering the Protocatechuate 2,3-Cleavage Pathway Genes. Journal of Bacteriology, 2009, 191, 6758-6768.	1.0	84

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37	Molecular Mechanism of the Redox-dependent Interaction between NADH-dependent Ferredoxin Reductase and Rieske-type Ferredoxin. Nihon Kessho Gakkaishi, 2008, 50, 341-347.	0.0	Ο
38	Multiplicity of Aromatic Ring Hydroxylation Dioxygenase Genes in a Strong PCB Degrader, Rhodococcus sp. Strain RHA1 Demonstrated by Denaturing Gradient Gel Electrophoresis. Bioscience, Biotechnology and Biochemistry, 2001, 65, 1907-1911.	0.6	49
39	Characterization of the 450-kb Linear Plasmid in a Polychlorinated Biphenyl Degrader, Rhodococcus sp. Strain RHA1. Applied and Environmental Microbiology, 2001, 67, 2021-2028.	1.4	90
40	Genetic and Biochemical Characterization of 4-Carboxy-2-Hydroxymuconate-6-Semialdehyde Dehydrogenase and Its Role in the Protocatechuate 4,5-Cleavage Pathway inSphingomonas paucimobilis SYK-6. Journal of Bacteriology, 2000, 182, 6651-6658.	1.0	57
41	The 4-Oxalomesaconate Hydratase Gene, Involved in the Protocatechuate 4,5-Cleavage Pathway, Is Essential to Vanillate and Syringate Degradation in Sphingomonas paucimobilisSYK-6. Journal of Bacteriology, 2000, 182, 6950-6957.	1.0	71
42	Degradation of polychlorinated biphenyls by a â€~Maitake' mushroom, Grifola frondosa. Biotechnology Letters, 1999, 21, 27-31.	1.1	19
43	Degradation of anaerobic reductive dechlorination products of Aroclor 1242 by four aerobic bacteria. Biodegradation, 1999, 10, 363-371.	1.5	70
44	Structural alteration of linear plasmids encoding the genes for polychlorinated biphenyl degradation in Rhodococcus strain RHA1. Antonie Van Leeuwenhoek, 1998, 74, 169-173.	0.7	17
45	Characterization of polychlorinated biphenyl degradation in a fermentor by Comamonas testosteroni strain TK102 Japanese Journal of Water Treatment Biology, 1998, 34, 57-65.	0.2	8
46	Three-dimensional Structure of Microbial 2-Hydroxyl-6-oxo-6-phenylhexa-2,4-dienoic Acid (HPDA) Hydrolase (BphD Enzyme) from Rhodococcus sp. Strain RHA1, in the PCB Degradation Pathway Proceedings of the Japan Academy Series B: Physical and Biological Sciences, 1997, 73, 154-157.	1.6	14
47	Growth inhibition of Rhodococcus sp. strain RHA1 in the course of PCB transformation. Biotechnology Letters, 1996, 18, 1193-1198.	1.1	11
48	Catabolic potential of multiple PCB transformation systems in Rhodococcus sp. strain RHA1. Biotechnology Letters, 1996, 18, 1305-1308.	1.1	9
49	Three-dimensional Structure of 2,3-Dihydroxybiphenyl Dioxygenase (BphC enzyme) from Pseudomonas sp. Strain KKS102 Having Polychlorinated Biphenyl (PCB)-Degrading Activity Proceedings of the Japan Academy Series B: Physical and Biological Sciences, 1995, 71, 32-35.	1.6	31
50	Crystallization and preliminary crystallographic analysis of a 2,3-dihydroxybiphenyl dioxygenase fromPseudomonas sp. strain KKS102 having polychlorinated biphenyl (PCB)-degrading activity. Proteins: Structure, Function and Bioinformatics, 1995, 22, 284-286.	1.5	16