Hiroshi Habe

List of Publications by Year
in descending order

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160	4,623	94433	128289
papers	citations	37 h-index	60 g-index

162	162	162	3510
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Optimal start-up conditions for the efficient treatment of acid mine drainage using sulfate-reducing bioreactors based on physicochemical and microbiome analyses. Journal of Hazardous Materials, 2022, 423, 127089.	12.4	15
2	Isolation and characterization of microorganisms capable of cleaving the ether bond of 2-phenoxyacetophenone. Scientific Reports, 2022, 12, 2874.	3.3	7
3	Evaluation of dye decolorization using anaerobic granular sludge from an expanded granular sludge bed based on spectrometric and microbiome analyses. Journal of General and Applied Microbiology, 2022, , .	0.7	0
4	Effective Se reduction by lactate-stimulated indigenous microbial communities in excavated waste rocks. Journal of Hazardous Materials, 2021, 403, 123908.	12.4	4
5	Enrichment and Isolation of Surfactin-degrading Bacteria. Journal of Oleo Science, 2021, 70, 581-587.	1.4	4
6	Naked-eye detection of specific DNA sequences amplified by the polymerase chain reaction with nanocomposite beads. Analytical Biochemistry, 2021, 617, 114114.	2.4	1
7	Efficient conversion of organic nitrogenous wastewater to nitrate solution driven by comammox Nitrospira. Water Research, 2021, 197, 117088.	11.3	19
8	Bacterial Community Coexisting with White-Rot Fungi in Decayed Wood in Nature. Current Microbiology, 2021, 78, 3212-3217.	2.2	8
9	Heterologous expression of membrane-bound alcohol dehydrogenaseâ€“encoding genes for glyceric acid production using Gluconobacter sp. CHM43 and its derivatives. Applied Microbiology and Biotechnology, 2021, 105, 6749-6758.	3.6	3
10	Combined simultaneous enzymatic saccharification and comminution (SESC) and anaerobic digestion for sustainable biomethane generation from wood lignocellulose and the biochemical characterization of residual sludge solid. Bioresource Technology, 2020, 300, 122622.	9.6	30
11	Long-term acclimatization of sludge microbiome for treatment of high-strength organic solid waste in anaerobic membrane bioreactor. Biochemical Engineering Journal, 2020, 154, 107461.	3.6	14
12	Screening and isolation of the liamocin-producing yeast Aureobasidium melanogenum using xylose as the sole carbon source. Journal of Bioscience and Bioengineering, 2020, 129, 428-434.	2.2	18
13	Transition of microbial community structures after development of membrane fouling in membrane bioreactors (MBRs). AMB Express, 2020, 10, 18.	3.0	5
14	Microbial and enzymatic conversion of levulinic acid, an alternative building block to fermentable sugars from cellulosic biomass. Applied Microbiology and Biotechnology, 2020, 104, 7767-7775.	3.6	13
15	Complete Genome Sequence of Desulfuromonas sp. Strain AOP6, an Iron(III) Reducer Isolated from Subseafloor Sediment. Microbiology Resource Announcements, 2020, 9, .	0.6	6
16	Biofilm Formation by <i>Streptococcus mutans</i> is Enhanced by Indole via the Quorum Sensing Pathway. Microbes and Environments, 2020, 35, n/a.	1.6	10
17	Design, application, and microbiome of sulfate-reducing bioreactors for treatment of mining-influenced water. Applied Microbiology and Biotechnology, 2020, 104, 6893-6903.	3.6	20
18	Unexpected diversity of acetate degraders in anaerobic membrane bioreactor treating organic solid waste revealed by high-sensitivity stable isotope probing. Water Research, 2020, 176, 115750.	11.3	21

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19	Clarifying prokaryotic and eukaryotic biofilm microbiomes in anaerobic membrane bioreactor by non-destructive microscopy and high-throughput sequencing. Chemosphere, 2020, 254, 126810.	8.2	8
20	Microbial community in an anaerobic membrane bioreactor and its performance in treating organic solid waste under controlled and deteriorated conditions. Journal of Environmental Management, 2020, 269, 110786.	7.8	18
21	Development of Organic Gas Sensor Using Quartz Crystal Microbalance Coated with Plasma-polymerized Films. Sensors and Materials, 2020, 32, 1123.	0.5	3
22	Activated sludge microbiome in a membrane bioreactor for treating Ramen noodle-soup wastewater. Journal of General and Applied Microbiology, 2020, 66, 339-343.	0.7	6
23	Activated sludge microbial communities of a chemical plant wastewater treatment facility with high-strength bromide ions and aromatic substances. Journal of General and Applied Microbiology, 2019, 65, 106-110.	0.7	7
24	Desulfosporosinus spp. were the most predominant sulfate-reducing bacteria in pilot- and laboratory-scale passive bioreactors for acid mine drainage treatment. Applied Microbiology and Biotechnology, 2019, 103, 7783-7793.	3.6	29
25	Identification and characterization of levulinyl-CoA synthetase from Pseudomonas citronellolis, which differs phylogenetically from LvaE of Pseudomonas putida. AMB Express, 2019, 9, 127.	3.0	1
26	Transcriptome analysis of activated sludge microbiomes reveals an unexpected role of minority nitrifiers in carbon metabolism. Communications Biology, 2019, 2, 179.	4.4	35
27	Synthesis and Characterization of a Novel Glycolipid with Glucosylglycerate as a Hydrophile Showing Protective Effects on Heat-induced Protein Denaturation. Journal of Oleo Science, 2019, 68, 493-499.	1.4	1
28	Evaluation of Yield and Surface Tension-lowering Activity of Iturin A Produced by <i>Bacillus subtilis</i> RB14. Journal of Oleo Science, 2019, 68, 1157-1162.	1.4	5
29	Effects of the Wastewater Flow Rate on Interactions between the Genus <i>Nitrosomonas</i> and Diverse Populations in an Activated Sludge Microbiome. Microbes and Environments, 2019, 34, 89-94.	1.6	6
30	Nitrifiers activity and community characteristics under stress conditions in partial nitrification systems treating ammonium-rich wastewater. Journal of Environmental Sciences, 2018, 73, 1-8.	6.1	19
31	Eukaryotic Microbiomes of Membrane-Attached Biofilms in Membrane Bioreactors Analyzed by High-Throughput Sequencing and Microscopic Observations. Microbes and Environments, 2018, 33, 98-101.	1.6	14
32	Depth error correction for projector-camera based consumer depth cameras. Computational Visual Media, 2018, 4, 103-111.	17.5	5
33	Revealing sludge and biofilm microbiomes in membrane bioreactor treating piggery wastewater by non-destructive microscopy and 16S rRNA gene sequencing. Chemical Engineering Journal, 2018, 331, 75-83.	12.7	25
34	Heterologous expression of Trametes versicolor laccase in Saccharomyces cerevisiae. Protein Expression and Purification, 2018, 141, 39-43.	1.3	30
35	Year-Round Performance of a Passive Sulfate-Reducing Bioreactor that Uses Rice Bran as an Organic Carbon Source to Treat Acid Mine Drainage. Mine Water and the Environment, 2018, 37, 586-594.	2.0	21
36	Draft Genome Sequence of Pseudomonas citronellolis LA18T, a Bacterium That Uses Levulinic Acid. Microbiology Resource Announcements, 2018, 7, .	0.6	3

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37	Microbiomes and chemical components of feed water and membrane-attached biofilm in reverse osmosis system to treat membrane bioreactor effluents. Scientific Reports, 2018, 8, 16805.	3.3	12
38	Application of Glycolipid Biosurfactants as Surface Modifiers in Bioplastics. Journal of Oleo Science, 2018, 67, 1609-1616.	1.4	13
39	Surface Activity and Ca²⁺-Dependent Aggregation Property of Lichenysin Produced by <i>Bacillus licheniformis</i> NBRC 104464. Journal of Oleo Science, 2018, 67, 1307-1313.	1.4	6
40	Microbial community analysis of sulfate-reducing passive bioreactor for treating acid mine drainage under failure conditions after long-term continuous operation. Journal of Environmental Chemical Engineering, 2018, 6, 5795-5800.	6.7	15
41	Identification of active and taxonomically diverse 1,4-dioxane degraders in a full-scale activated sludge system by high-sensitivity stable isotope probing. ISME Journal, 2018, 12, 2376-2388.	9.8	42
42	Electrodialytic separation of levulinic acid catalytically synthesized from woody biomass for use in microbial conversion. Biotechnology Progress, 2017, 33, 448-453.	2.6	9
43	Degradation profiles of biodegradable plastic films by biodegradable plastic-degrading enzymes from the yeast Pseudozyma antarctica and the fungus Paraphoma sp. B47-9. Polymer Degradation and Stability, 2017, 141, 26-32.	5.8	33
44	Architecture, component, and microbiome of biofilm involved in the fouling of membrane bioreactors. Npj Biofilms and Microbiomes, 2017, 3, 5.	6.4	37
45	Comparative Study of Interfacial and Biological Properties in <scp>d</scp>â€Glycerateâ€Derived Surfactants. JAOCS, Journal of the American Oil Chemists' Society, 2017, 94, 1393-1401.	1.9	2
46	Draft Genome Sequence of Geobacter pelophilus Strain Dfr2, a Ferric Ironâ€“Reducing Bacterium. Genome Announcements, 2017, 5, .	0.8	2
47	Hydraulic retention time and pH affect the performance and microbial communities of passive bioreactors for treatment of acid mine drainage. AMB Express, 2017, 7, 142.	3.0	41
48	Screening of a Bacillus subtilis Strain Producing Multiple Types of Cyclic Lipopeptides and Evaluation of Their Surface-tension-lowering Activities. Journal of Oleo Science, 2017, 66, 785-790.	1.4	5
49	Preliminary Evaluation of Glyceric Acid-producing Ability of <i>Acidomonas methanolica</i> NBRC104435 from Glycerol Containing Methanol. Journal of Oleo Science, 2017, 66, 653-658.	1.4	4
50	Synthesis and Characterization of Dioctanoyl Glycerate as Water-soluble Trypsin Inhibitor. Journal of Oleo Science, 2016, 65, 251-256.	1.4	2
51	High susceptibility of aerobic microbiota in membrane bioreactor (MBR) sludge towards olive oil as revealed by high-throughput sequencing of 16S rRNA genes. Journal of Environmental Chemical Engineering, 2016, 4, 4392-4399.	6.7	12
52	Effects of Organic-Loading-Rate Reduction on Sludge Biomass and Microbial Community in a Deteriorated Pilot-Scale Membrane Bioreactor. Microbes and Environments, 2016, 31, 361-364.	1.6	17
53	Draft Genome Sequence of Burkholderia stabilis LA20W, a Trehalose Producer That Uses Levulinic Acid as a Substrate. Genome Announcements, 2016, 4, .	0.8	1
54	Functional maintenance and structural flexibility of microbial communities perturbed by simulated intense rainfall in a pilot-scale membrane bioreactor. Applied Microbiology and Biotechnology, 2016, 100, 6447-6456.	3.6	23

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55	High-resolution phylogenetic analysis of residual bacterial species of fouled membranes after NaOCl cleaning. Water Research, 2016, 94, 166-175.	11.3	40
56	Fine-scale monitoring of shifts in microbial community composition after high organic loading in a pilot-scale membrane bioreactor. Journal of Bioscience and Bioengineering, 2016, 121, 550-556.	2.2	35
57	Bacterial production of short-chain organic acids and trehalose from levulinic acid: A potential cellulose-derived building block as a feedstock for microbial production. Bioresource Technology, 2015, 177, 381-386.	9.6	25
58	Draft Genome Sequence of the Yeast Starmerella bombicola NBRC10243, a Producer of Sophorolipids, Glycolipid Biosurfactants. Genome Announcements, 2015, 3, .	0.8	10
59	Microbial resolution of dl-glyceric acid for l-glyceric acid production with newly isolated bacterial strains. Journal of Bioscience and Bioengineering, 2015, 119, 554-557.	2.2	7
60	Isolation and characterization of bacterial strains with the ability to utilize high concentrations of levulinic acid, a platform chemical from inedible biomass. Bioscience, Biotechnology and Biochemistry, 2015, 79, 1552-1555.	1.3	11
61	Effect of a microbiota activator on accumulated ammonium and microbial community structure in a pilot-scale membrane bioreactor. Journal of General and Applied Microbiology, 2015, 61, 132-138.	0.7	7
62	Genome and Transcriptome Analysis of the Basidiomycetous Yeast Pseudozyma antarctica Producing Extracellular Glycolipids, Mannosylerythritol Lipids. PLoS ONE, 2014, 9, e86490.	2.5	45
63	Draft Genome Sequence of the Yeast Pseudozyma antarctica Type Strain JCM10317, a Producer of the Glycolipid Biosurfactants, Mannosylerythritol Lipids. Genome Announcements, 2014, 2, .	0.8	25
64	Draft Genome Sequence of Acetobacter tropicalis Type Strain NBRC16470, a Producer of Optically Pure d -Glyceric Acid. Genome Announcements, 2014, 2, .	0.8	2
65	In vitro evaluation of glyceric acid and its glucosyl derivative, Î±-glucosylglyceric acid, as cell proliferation inducers and protective solutes. Bioscience, Biotechnology and Biochemistry, 2014, 78, 1183-1186.	1.3	11
66	Structural Basis of the Divergent Oxygenation Reactions Catalyzed by the Rieske Nonheme Iron Oxygenase Carbazole 1,9a-Dioxygenase. Applied and Environmental Microbiology, 2014, 80, 2821-2832.	3.1	12
67	Production of d-arabitol from raw glycerol by Candida quercitrusa. Applied Microbiology and Biotechnology, 2014, 98, 2947-2953.	3.6	26
68	Production of mannitol from raw glycerol by Candida azyma. Journal of Bioscience and Bioengineering, 2014, 117, 725-729.	2.2	22
69	Chemical mutagenesis of Gluconobacter frateurii to construct methanol-resistant mutants showing glyceric acid production from methanol-containing glycerol. Journal of Bioscience and Bioengineering, 2014, 117, 197-199.	2.2	13
70	Separation and Functional Evaluation of Dark Brown Colorants in Distillery Wastewater from a Sugarcane-Molasses-Derived Bioethanol Production Process. Journal of Water and Environment Technology, 2014, 12, 407-420.	0.7	1
71	Effect of Membrane-bound Aldehyde Dehydrogenase-encoding Gene Disruption on Glyceric Acid Production in Gluconobacter oxydans. Journal of Oleo Science, 2014, 63, 953-957.	1.4	2
72	Change in product selectivity during the production of glyceric acid from glycerol by Gluconobacter strains in the presence of methanol. AMB Express, 2013, 3, 20.	3.0	11

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73	Cloning of dfdA genes from Terrabacter sp. strain DBF63 encoding dibenzofuran 4,4a-dioxygenase and heterologous expression in Streptomyces lividans. Applied Microbiology and Biotechnology, 2013, 97, 4485-4498.	3.6	13
74	Draft Genome Sequence of Gluconobacter frateurii NBRC 103465, a Glyceric Acid-Producing Strain. Genome Announcements, 2013, 1, .	0.8	4
75	Expression and Characterization of a Class III Alcohol Dehydrogenase Gene from Gluconobacter frateurii in the Presence of Methanol during Glyceric Acid Production from Glycerol. Journal of Oleo Science, 2013, 62, 835-842.	1.4	3
76	Biodegradation of Biodiesel Wash Water from a Biodiesel Fuel Production Plant. Journal of Oleo Science, 2013, 62, 525-532.	1.4	1
77	Chemical Analysis of Impurities in Diverse Bioethanol Samples. Journal of the Japan Petroleum Institute, 2013, 56, 414-422.	0.6	24
78	Synthesis and Interfacial Properties of Monoacyl Glyceric Acids as a New Class of Green Surfactants. Journal of Oleo Science, 2012, 61, 343-348.	1.4	17
79	Stepwise synthesis of 2,3-<i>O</i>-dipalmitoyl-D-glyceric acid and an in vitro evaluation of its cytotoxicity. Journal of Oleo Science, 2012, 61, 337-341.	1.4	5
80	Pervaporation of aqueous dilute 1-butanol, 2-propanol, ethanol and acetone using a tubular silicalite membrane. Desalination and Water Treatment, 2011, 34, 290-294.	1.0	14
81	Synthesis and Evaluation of Dioleoyl Glyceric Acids Showing Antitrypsin Activity. Journal of Oleo Science, 2011, 60, 327-331.	1.4	14
82	Effect of Glyceric Acid Calcium Salt on the Viability of Ethanol-Dosed Gastric Cells. Journal of Oleo Science, 2011, 60, 585-590.	1.4	10
83	Synthesis of Dilinoleoyl-D-Glyceric Acid and Evaluation of Its Cytotoxicity to Human Dermal Fibroblast and Endothelial Cells. Journal of Oleo Science, 2011, 60, 483-487.	1.4	8
84	Bioprocessing of Glycerol into Glyceric Acid for Use in Bioplastic Monomer. Journal of Oleo Science, 2011, 60, 369-373.	1.4	18
85	Membrane-Bound Alcohol Dehydrogenase Is Essential for Glyceric Acid Production in Acetobacter tropicalis. Journal of Oleo Science, 2011, 60, 489-494.	1.4	8
86	Two-stage electrodialytic concentration of glyceric acid from fermentation broth. Journal of Bioscience and Bioengineering, 2010, 110, 690-695.	2.2	14
87	Use of electrodialysis to separate and concentrate Î³-amino butyric acid. Desalination, 2010, 253, 101-105.	8.2	14
88	Use of a<i>Gluconobacter frateurii</i>Mutant to Prevent Dihydroxyacetone Accumulation during Glyceric Acid Production from Glycerol. Bioscience, Biotechnology and Biochemistry, 2010, 74, 2330-2332.	1.3	17
89	Disruption of the Membrane-Bound Alcohol Dehydrogenase-Encoding Gene Improved Glycerol Use and Dihydroxyacetone Productivity in<i>Gluconobacter oxydans</i>. Bioscience, Biotechnology and Biochemistry, 2010, 74, 1391-1395.	1.3	31
90	Detection of Acetyl Monoglyceride as a Metabolite of Newly Isolated Glycerol-assimilating Bacteria. Journal of Oleo Science, 2009, 58, 147-154.	1.4	5

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91	Glycerol Conversion to D-Xylulose by a Two-stage Microbial Reaction Using Candida parapsilosis and Gluconobacter oxydans. Journal of Oleo Science, 2009, 58, 595-600.	1.4	9
92	Microbial Production of Glyceric Acid, an Organic Acid That Can Be Mass Produced from Glycerol. Applied and Environmental Microbiology, 2009, 75, 7760-7766.	3.1	108
93	Application of electrodialysis to glycerate recovery from a glycerol containing model solution and culture broth. Journal of Bioscience and Bioengineering, 2009, 107, 425-428.	2.2	19
94	Biotechnological production of d-glyceric acid and its application. Applied Microbiology and Biotechnology, 2009, 84, 445-452.	3.6	70
95	Biotransformation of glycerol to d-glyceric acid by Acetobacter tropicalis. Applied Microbiology and Biotechnology, 2009, 81, 1033-1039.	3.6	56
96	Production of Glyceric Acid byGluconobactersp. NBRC3259 Using Raw Glycerol. Bioscience, Biotechnology and Biochemistry, 2009, 73, 1799-1805.	1.3	49
97	Identification of the Electron Transfer Flavoprotein as an Upregulated Enzyme in the Benzoate Utilization ofDesulfotignum balticum. Bioscience, Biotechnology and Biochemistry, 2009, 73, 1647-1652.	1.3	6
98	Subtractive hybridization and random arbitrarily primed PCR analyses of a benzoate-assimilating bacterium, Desulfotignum balticum. Applied Microbiology and Biotechnology, 2008, 79, 87-95.	3.6	6
99	Alteration of the Substrate Specificity of the Angular Dioxygenase Carbazole 1,9a-Dioxygenase. Bioscience, Biotechnology and Biochemistry, 2008, 72, 3237-3248.	1.3	9
100	Transcription Factors CysB and SfnR Constitute the Hierarchical Regulatory System for the Sulfate Starvation Response inPseudomonas putida. Journal of Bacteriology, 2008, 190, 4521-4531.	2.2	21
101	Isolation and Characterization of Thermotolerant Fungi Producing Lignoceric Acid from Glycerol. Journal of Oleo Science, 2008, 57, 251-255.	1.4	7
102	The Sphingomonas Plasmid pCAR3 Is Involved in Complete Mineralization of Carbazole. Journal of Bacteriology, 2007, 189, 2007-2020.	2.2	55
103	Transcriptional regulation of the sulfate-starvation-induced gene sfnA by a Ïƒ 54-dependent activator of Pseudomonas putida. Microbiology (United Kingdom), 2007, 153, 3091-3098.	1.8	15
104	Convenient Transformation of Anamorphic Basidiomycetous Yeasts Belonging to Genus Pseudozyma Induced by Electroporation. Journal of Bioscience and Bioengineering, 2007, 104, 517-520.	2.2	20
105	TheptsPgene encoding the PTS family protein EI^{Ntr}is essential for dimethyl sulfone utilization byPseudomonas putida. FEMS Microbiology Letters, 2007, 275, 175-181.	1.8	11
106	Detection of a Bacterial Group within the Phylum Chloroflexi and Reductive-Dehalogenase-Homologous Genes in Pentachlorobenzene-Dechlorinating Estuarine Sediment from the Arakawa River, Japan. Microbes and Environments, 2006, 21, 154-162.	1.6	3
107	Electron Transfer Complex Formation between Oxygenase and Ferredoxin Components in Rieske Nonheme Iron Oxygenase System. Structure, 2006, 14, 1779-1789.	3.3	65
108	Plasmid pCAR3 Contains Multiple Gene Sets Involved in the Conversion of Carbazole to Anthranilate. Applied and Environmental Microbiology, 2006, 72, 3198-3205.	3.1	42

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109	Characterization of Novel Carbazole Catabolism Genes from Gram-Positive Carbazole Degrader Nocardioides aromaticivorans IC177. Applied and Environmental Microbiology, 2006, 72, 3321-3329.	3.1	58
110	Characterization of the Replication, Maintenance, and Transfer Features of the IncP-7 Plasmid pCAR1, Which Carries Genes Involved in Carbazole and Dioxin Degradation. Applied and Environmental Microbiology, 2006, 72, 3206-3216.	3.1	80
111	Differentiation of Carbazole Catabolic Operons by Replacement of the Regulated Promoter via Transposition of an Insertion Sequence*. Journal of Biological Chemistry, 2006, 281, 8450-8457.	3.4	22
112	Functional and transcriptional analyses of the initial oxygenase genes for acenaphthene degradation from Sphingomonas sp. strain A4. Microbiology (United Kingdom), 2006, 152, 2455-2467.	1.8	14
113	Diversity of carbazole-degrading bacteria having thecargene cluster: Isolation of a novel gram-positive carbazole-degrading bacterium. FEMS Microbiology Letters, 2005, 245, 145-153.	1.8	56
114	Large plasmid pCAR2 and class II transposon Tn4676 are functional mobile genetic elements to distribute the carbazole/dioxin-degradative car gene cluster in different bacteria. Applied Microbiology and Biotechnology, 2005, 67, 370-382.	3.6	45
115	Characterization of [3Fe-4S] ferredoxin DbfA3, which functions in the angular dioxygenase system of Terrabacter sp. strain DBF63. Applied Microbiology and Biotechnology, 2005, 68, 336-345.	3.6	13
116	Recipient Range of IncP-7 Conjugative Plasmid pCAR2 from Pseudomonas putida HS01 is Broader than from Other Pseudomonas Strains. Biotechnology Letters, 2005, 27, 1847-1853.	2.2	57
117	Crystallization and preliminary X-ray diffraction analysis of the electron-transfer complex between the terminal oxygenase component and ferredoxin in the Rieske non-haem iron oxygenase system carbazole 1,9a-dioxygenase. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 577-580.	0.7	17
118	Crystal structure of the ferredoxin component of carbazole 1,9a-dioxygenase of Pseudomonas resinovorans strain CA10, a novel Rieske non-heme iron oxygenase system. Proteins: Structure, Function and Bioinformatics, 2005, 58, 779-789.	2.6	40
119	The fluorene catabolic linear plasmid in Terrabacter sp. strain DBF63 carries the Î²-ketoadipate pathway genes, pcaRHGBDCFIJ, also found in proteobacteria. Microbiology (United Kingdom), 2005, 151, 3713-3722.	1.8	33
120	Structure of the Terminal Oxygenase Component of Angular Dioxygenase, Carbazole 1,9a-Dioxygenase. Journal of Molecular Biology, 2005, 351, 355-370.	4.2	86
121	Divergent Structures of Carbazole DegradativecarOperons Isolated from Gram-negative Bacteria. Bioscience, Biotechnology and Biochemistry, 2004, 68, 1467-1480.	1.3	48
122	Transcriptional Regulation of the ant Operon, Encoding Two-Component Anthranilate 1,2-Dioxygenase, on the Carbazole-Degradative Plasmid pCAR1 of Pseudomonas resinovorans Strain CA10. Journal of Bacteriology, 2004, 186, 6815-6823.	2.2	66
123	Characterization of the Upper Pathway Genes for Fluorene Metabolism in Terrabacter sp. Strain DBF63. Journal of Bacteriology, 2004, 186, 5938-5944.	2.2	42
124	The Ïƒ54-dependent transcriptional activator SfnR regulates the expression of the Pseudomonas putida sfnFG operon responsible for dimethyl sulphone utilization. Molecular Microbiology, 2004, 55, 897-911.	2.5	21
125	Isolation and characterization of genes encoding polycyclic aromatic hydrocarbon dioxygenase from acenaphthene and acenaphthylene degradingSphingomonassp. strain A4. FEMS Microbiology Letters, 2004, 238, 297-305.	1.8	37
126	Isolation and characterization of an alkaliphilic bacterium utilizing pyrene as a carbon source. Journal of Bioscience and Bioengineering, 2004, 98, 306-308.	2.2	40

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127	Crystallization and preliminary crystallographic analysis of the 2â€²-aminobiphenyl-2,3-diol 1,2-dioxygenase from the carbazole-degraderPseudomonas resinovoransstrain CA10. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2340-2342.	2.5	2
128	Genetic characterization of the dibenzofuran-degrading Actinobacteria carrying thedbfA1A2gene homologues isolated from activated sludge. FEMS Microbiology Letters, 2004, 239, 147-155.	1.8	12
129	Isolation and characterization of genes encoding polycyclic aromatic hydrocarbon dioxygenase from acenaphthene and acenaphthylene degrading sp. strain A4. FEMS Microbiology Letters, 2004, 238, 297-305.	1.8	43
130	Marinobacterium sp. strain DMS-S1 uses dimethyl sulphide as a sulphur source after light-dependent transformation by excreted flavins. Environmental Microbiology, 2003, 5, 503-509.	3.8	14
131	Genetics of Polycyclic Aromatic Hydrocarbon Metabolism in Diverse Aerobic Bacteria. Bioscience, Biotechnology and Biochemistry, 2003, 67, 225-243.	1.3	370
132	Complete Nucleotide Sequence of Carbazole/Dioxin-degrading Plasmid pCAR1 in Pseudomonas resinovorans Strain CA10 Indicates its Mosaicity and the Presence of Large Catabolic Transposon Tn4676. Journal of Molecular Biology, 2003, 326, 21-33.	4.2	153
133	Identification of three novel salicylate 1-hydroxylases involved in the phenanthrene degradation of Sphingobium sp. strain P2. Biochemical and Biophysical Research Communications, 2003, 301, 350-357.	2.1	85
134	Crystal structure of a histidine-tagged serine hydrolase involved in the carbazole degradation (CarC) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.1	34
135	Purification and Characterization ofmeta-Cleavage Compound Hydrolase from a Carbazole DegraderPseudomonas resinovoransStrain CA10. Bioscience, Biotechnology and Biochemistry, 2003, 67, 36-45.	1.3	20
136	Expression, Purification, and Characterization of 2â€²-Aminobiphenyl-2,3-diol 1,2-dioxygenase from Carbazole-degraderPseudomonas resinovoransStrain CA10. Bioscience, Biotechnology and Biochemistry, 2003, 67, 300-307.	1.3	19
137	A CysB-regulated and Ïƒ54-dependent regulator, SfnR, is essential for dimethyl sulfone metabolism of Pseudomonas putida strain DS1. Microbiology (United Kingdom), 2003, 149, 991-1000.	1.8	34
138	Rhizoremediation of Dioxin-like Compounds by a RecombinantRhizobium tropiciStrain Expressing Carbazole 1,9a-Dioxygenase Constitutively. Bioscience, Biotechnology and Biochemistry, 2003, 67, 1144-1148.	1.3	19
139	The unique aromatic catabolic genes in sphingomonads degrading polycyclic aromatic hydrocarbons(PAHs).. Journal of General and Applied Microbiology, 2003, 49, 1-19.	0.7	189
140	Genes involved in the synthesis of the exopolysaccharide methanolan by the obligate methylotroph Methylobacillus sp. strain 12S. Microbiology (United Kingdom), 2003, 149, 431-444.	1.8	49
141	Purification and Characterization of Carbazole 1,9a-Dioxygenase, a Three-Component Dioxygenase System of Pseudomonas resinovorans Strain CA10. Applied and Environmental Microbiology, 2002, 68, 5882-5890.	3.1	76
142	Organization and Transcriptional Characterization of Catechol Degradation Genes Involved in Carbazole Degradation byPseudomonas resinovoransStrain CA10. Bioscience, Biotechnology and Biochemistry, 2002, 66, 897-901.	1.3	33
143	Degradation characteristics of a dibenzofuran-degrader Terrabacter sp. strain DBF63 toward chlorinated dioxins in soil. Chemosphere, 2002, 48, 201-207.	8.2	32
144	Dioxin catabolic genes are dispersed on the Terrabacter sp. DBF63 genome. Biochemical and Biophysical Research Communications, 2002, 296, 233-240.	2.1	37

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145	Crystallization and preliminary crystallographic analysis of the terminal oxygenase component of carbazole 1,9a-dioxygenase of Pseudomonas resinovorans strain CA10. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1350-1352.	2.5	8
146	Sphingomonassp. strain KA1, carrying a carbazole dioxygenase gene homologue, degrades chlorinated dibenzo-p-dioxins in soil. FEMS Microbiology Letters, 2002, 211, 43-49.	1.8	83
147	Title is missing!. Biotechnology Letters, 2002, 24, 2099-2106.	2.2	32
148	Isolation and Characterization of the Genes Encoding a Novel Oxygenase Component of Angular Dioxygenase from the Gram-Positive Dibenzofuran-Degrader Terrabacter sp. Strain DBF63. Biochemical and Biophysical Research Communications, 2001, 283, 195-204.	2.1	79
149	Bacterial degradation of aromatic compounds via angular dioxygenation.. Journal of General and Applied Microbiology, 2001, 47, 279-305.	0.7	66
150	Title is missing!. Biotechnology Letters, 2001, 23, 787-791.	2.2	3
151	Isolation of transposon Tn5 mutant affected in the metabolism of 18Î²-glycyrrhetinic acid. Biotechnology Letters, 2001, 23, 873-879.	2.2	2
152	Microbial transformation of 18Î²-glycyrrhetinic acid by Sphingomonas paucimobilis strain G5. Biotechnology Letters, 2001, 23, 1619-1624.	2.2	8
153	Quantification of the carbazole 1,9a-dioxygenase gene by real-time competitive PCR combined with co-extraction of internal standards. FEMS Microbiology Letters, 2001, 202, 51-57.	1.8	36
154	Genetic Characterization and Evolutionary Implications of a car Gene Cluster in the Carbazole Degrader Pseudomonas sp. Strain CA10. Journal of Bacteriology, 2001, 183, 3663-3679.	2.2	103
155	Degradation of Chlorinated Dibenzofurans and Dibenzo- p -Dioxins by Two Types of Bacteria Having Angular Dioxygenases with Different Features. Applied and Environmental Microbiology, 2001, 67, 3610-3617.	3.1	107
156	New Classification System for Oxygenase Components Involved in Ring-Hydroxylating Oxygenations. Bioscience, Biotechnology and Biochemistry, 2001, 65, 254-263.	1.3	91
157	Identification of novel metabolites in the degradation of phenanthrene bySphingomonassp. strain P2. FEMS Microbiology Letters, 2000, 191, 115-121.	1.8	126
158	Identification of novel metabolites in the degradation of phenanthrene by Sphingomonas sp. strain P2. FEMS Microbiology Letters, 2000, 191, 115-121.	1.8	5
159	Cloning, nucleotide sequence, and characterization of the genes encoding enzymes involved in the degradation of cumene to 2-hydroxy-6-oxo-7-methylocta-2,4-dienoic acid in Pseudomonas fluorescens IP01. Journal of Bioscience and Bioengineering, 1996, 81, 187-196.	0.9	52
160	Cloning and nucleotide sequences of the genes involved in the meta-cleavage pathway of cumene degradation in Pseudomonas fluorescens IP01. Journal of Bioscience and Bioengineering, 1996, 81, 247-254.	0.9	20