

Kentaro Miyazaki

List of Publications by Year in descending order

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100
papers

3,826
citations

147801

31
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133252

59
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103
all docs

103
docs citations

103
times ranked

4405
citing authors

#	ARTICLE	IF	CITATIONS
1	Complete Genome Sequences of Four <i>Parageobacillus</i> Strains Isolated from Soil in Japan. Microbiology Resource Announcements, 2022, 11, e0020422.	0.6	1
2	Complete Genome Sequence of <i>Thiohalobacter</i> sp. Strain COW1, Isolated from Activated Sludge Treating Coke Oven Wastewater. Microbiology Resource Announcements, 2021, 10, .	0.6	0
3	Complete Genome Sequence of <i>Thermus thermophilus</i> Strain HB5018, Isolated from Mine Hot Spring in Japan. Microbiology Resource Announcements, 2021, 10, .	0.6	5
4	Complete Genome Sequences of <i>Thermus thermophilus</i> Strains HB5002 and HB5008, Isolated from Mine Hot Spring in Japan. Microbiology Resource Announcements, 2021, 10, .	0.6	3
5	Complete Genome Sequences of Four Halophilic <i>Thermus thermophilus</i> Strains Isolated from Arima Hot Spring in Japan. Microbiology Resource Announcements, 2021, 10, e0087421.	0.6	3
6	Complete Genome Resequencing of <i>Thermus thermophilus</i> Strain TMY by Hybrid Assembly of Long- and Short-Read Sequencing Technologies. Microbiology Resource Announcements, 2021, 10, e0097921.	0.6	0
7	Complete Genome Sequence of <i>Bacillus cereus</i> Strain PL1, Isolated from Soil in Japan. Microbiology Resource Announcements, 2020, 9, .	0.6	2
8	Complete Genome Sequence of <i>Pseudomonas otitidis</i> Strain MrB4, Isolated from Lake Biwa in Japan. Microbiology Resource Announcements, 2020, 9, .	0.6	4
9	Complete Genome Sequences of <i>Rhodothermus marinus</i> Strains AA2-13 and AA3-38, Isolated from Arima Onsen Hot Spring in Japan. Microbiology Resource Announcements, 2020, 9, .	0.6	0
10	Complete Genome Sequence of <i>Geobacillus</i> sp. Strain E55-1, Isolated from Mine Geyser in Japan. Microbiology Resource Announcements, 2020, 9, .	0.6	1
11	Complete Genome Sequence of <i>Vibrio rotiferianus</i> Strain AM7. Microbiology Resource Announcements, 2020, 9, .	0.6	2
12	Occurrence of randomly recombined functional 16S rRNA genes in <i>Thermus thermophilus</i> suggests genetic interoperability and promiscuity of bacterial 16S rRNAs. Scientific Reports, 2019, 9, 11233.	3.3	14
13	Accurate high-throughput screening based on digital protein synthesis in a massively parallel femtoliter droplet array. Science Advances, 2019, 5, eaav8185.	10.3	48
14	Complete Genome Sequences of <i>Thermus thermophilus</i> Strains AA2-20 and AA2-29, Isolated from Arima Onsen in Japan. Microbiology Resource Announcements, 2019, 8, .	0.6	8
15	Complete Genome Sequence of <i>Alteromonas</i> sp. Strain I4, Isolated from the Japan Sea. Microbiology Resource Announcements, 2019, 8, .	0.6	0
16	Complete Genome Sequence of <i>Staphylococcus arlettae</i> Strain P2, Isolated from a Laboratory Environment. Microbiology Resource Announcements, 2019, 8, .	0.6	5
17	Complete Genome Sequence of <i>Rubrobacter xylanophilus</i> Strain AA3-22, Isolated from Arima Onsen in Japan. Microbiology Resource Announcements, 2019, 8, .	0.6	2
18	Complete Genome Sequencing of <i>Thermus thermophilus</i> Strain HC11, Isolated from Mine Geyser in Japan. Microbiology Resource Announcements, 2019, 8, .	0.6	7

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19	Functional metagenomic approach to identify overlooked antibiotic resistance mutations in bacterial rRNA. Scientific Reports, 2018, 8, 5179.	3.3	9
20	Molecular engineering of the salicylate-inducible transcription factor Sal7AR for orthogonal and high gene expression in Escherichia coli. PLoS ONE, 2018, 13, e0194090.	2.5	4
21	Constructing Mutant Ribosomes Containing Mutant Ribosomal RNAs. , 2018, , 17-32.		0
22	Comparative RNA function analysis reveals high functional similarity between distantly related bacterial 16 S rRNAs. Scientific Reports, 2017, 7, 9993.	3.3	28
23	PCR Primer Design for 16S rRNAs for Experimental Horizontal Gene Transfer Test in Escherichia coli. Frontiers in Bioengineering and Biotechnology, 2017, 5, 14.	4.1	12
24	Phylogenetic Network Analysis Revealed the Occurrence of Horizontal Gene Transfer of 16S rRNA in the Genus Enterobacter. Frontiers in Microbiology, 2017, 8, 2225.	3.5	19
25	Crystal structure and identification of a key amino acid for glucose tolerance, substrate specificity, and transglycosylation activity of metagenomic α -glucosidase Td2F2. FEBS Journal, 2016, 283, 2340-2353.	4.7	53
26	Intramolecular Electron Transfer in the Bacterial Two-Domain Multicopper Oxidase mgLAC. Biochemistry, 2016, 55, 2960-2966.	2.5	2
27	Activity–stability relationships revisited in blue oxidases catalyzing electron transfer at extreme temperatures. Extremophiles, 2016, 20, 621-629.	2.3	12
28	Molecular engineering of a PheS counterselection marker for improved operating efficiency in <i>Escherichia coli</i> . BioTechniques, 2015, 58, 86-88.	1.8	49
29	Glucose-tolerant α -glucosidase retrieved from a Kusaya gravy metagenome. Frontiers in Microbiology, 2015, 6, 548.	3.5	48
30	Counterselection method based on conditional silencing of antitoxin genes in Escherichia coli. Journal of Bioscience and Bioengineering, 2015, 120, 591-595.	2.2	5
31	Extradiol Dioxygenases Retrieved from the Metagenome. , 2015, , 167-171.		0
32	Bacterial Cellular Engineering by Genome Editing and Gene Silencing. International Journal of Molecular Sciences, 2014, 15, 2773-2793.	4.1	42
33	Diversity of extradiol dioxygenases in aromatic-degrading microbial community explored using both culture-dependent and culture-independent approaches. FEMS Microbiology Ecology, 2014, 90, n/a-n/a.	2.7	12
34	New insights into the catalytic active-site structure of multicopper oxidases. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 772-779.	2.5	23
35	2P076 Exapnsin activity observed by FTIR(01D. Protein: Function,Poster,The 52nd Annual Meeting of the) Tj ETQq1_10.784314 rgBT 0.1	0.1	0
36	Directed evolution study unveiling key sequence factors that affect translation efficiency in Escherichia coli. Journal of Bioscience and Bioengineering, 2013, 116, 540-545.	2.2	7

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37	Direct electron transfer to a metagenome-derived laccase fused to affinity tags near the electroactive copper site. <i>Physical Chemistry Chemical Physics</i> , 2013, 15, 20585.	2.8	12
38	DNA fragmentation caused by an overdose of Zeocin. <i>Journal of Bioscience and Bioengineering</i> , 2013, 116, 644-646.	2.2	8
39	Characterization of a Novel β -Glucosidase from a Compost Microbial Metagenome with Strong Transglycosylation Activity. <i>Journal of Biological Chemistry</i> , 2013, 288, 18325-18334.	3.4	113
40	Cloning, Expression and Characteristics of a Novel Alkalistable and Thermostable Xylanase Encoding Gene (Mxyl) Retrieved from Compost-Soil Metagenome. <i>PLoS ONE</i> , 2013, 8, e52459.	2.5	82
41	Revisiting bacterial phylogeny. <i>Mobile Genetic Elements</i> , 2013, 3, e24210.	1.8	52
42	Meeting Report: 1st International Functional Metagenomics Workshop May 7-8, 2012, St. Jacobs, Ontario, Canada.. <i>Standards in Genomic Sciences</i> , 2013, 8, 106-111.	1.5	2
43	Metagenomic Screening for Aromatic Compound-Responsive Transcriptional Regulators. <i>PLoS ONE</i> , 2013, 8, e75795.	2.5	23
44	Extradiol Dioxygenases Retrieved from the Metagenome. , 2013, , 1-5.		0
45	Mutational robustness of 16S ribosomal RNA, shown by experimental horizontal gene transfer in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19220-19225.	7.1	35
46	Crystal Structures of Glycoside Hydrolase Family 51 α -Arabinofuranosidase from <i>Thermotoga maritima</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2012, 76, 423-428.	1.3	17
47	Cloning and Expression of Isoprimeverose-producing Oligoxyloglucan Hydrolase from Actinomycetes Species, <i>Oerskovia</i> sp. Y1. <i>Journal of Applied Glycoscience</i> (1999), 2012, 59, 83-88.	0.7	13
48	MEGAWHOP Cloning. <i>Methods in Enzymology</i> , 2011, 498, 399-406.	1.0	133
49	Specific inhibition of bacterial RNase T2 by helix 41 of 16S ribosomal RNA. <i>Nature Communications</i> , 2011, 2, 549.	12.8	28
50	ãfjã,ã,²ãfZãfèSŁæžã,ã,Šæ~Žã,%ã•ã•ã,ÇãŸç'ãçfããðèŠ³é ™æ—ãÇ—ã•ç%ã©ã^tèSŁéã1/4ãç³/4ãðãS¿. <i>Kagaku To Seibutsu</i> , 2010,		
51	Lethal ccdB gene-based zero-background vector for construction of shotgun libraries. <i>Journal of Bioscience and Bioengineering</i> , 2010, 110, 372-373.	2.2	10
52	Product-Induced Gene Expression, a Product-Responsive Reporter Assay Used To Screen Metagenomic Libraries for Enzyme-Encoding Genes. <i>Applied and Environmental Microbiology</i> , 2010, 76, 7029-7035.	3.1	114
53	Substrate-Induced Gene Expression Screening: A Method for High-Throughput Screening of Metagenome Libraries. <i>Methods in Molecular Biology</i> , 2010, 668, 153-168.	0.9	15
54	X-ray structure of a two-domain type laccase: A missing link in the evolution of multi-copper proteins. <i>FEBS Letters</i> , 2009, 583, 1189-1195.	2.8	53

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55	Crystallization and preliminary X-ray diffraction analysis of a putative two-domain-type laccase from a metagenome. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 264-266.	0.7	15
56	Novel organization of aromatic degradation pathway genes in a microbial community as revealed by metagenomic analysis. <i>ISME Journal</i> , 2009, 3, 1335-1348.	9.8	80
57	The crystal structure of a xyloglucanâ€specific endoâ€1,4â€glucanase from <i>Geotrichum</i> sp. M128 xyloglucanase reveals a key amino acid residue for substrate specificity. <i>FEBS Journal</i> , 2009, 276, 5094-5100.	4.7	24
58	The molecular basis for adaptive evolution in novel extradiol dioxygenases retrieved from the metagenome. <i>FEMS Microbiology Ecology</i> , 2009, 69, 472-480.	2.7	22
59	Functional metagenomics for enzyme discovery: challenges to efficient screening. <i>Current Opinion in Biotechnology</i> , 2009, 20, 616-622.	6.6	294
60	Directed Evolution of the Actinomycete Cytochrome P450 MoxA (CYP105) for Enhanced Activity. <i>Bioscience, Biotechnology and Biochemistry</i> , 2009, 73, 1922-1927.	1.3	24
61	Supramolecular Complex Formation and Crystallization of Isocitrate Dehydrogenase from <i>Thermus thermophilus</i> HB8: Preliminary Studies with X-Ray Crystallography and Atomic Force Microscopy. <i>Bioscience, Biotechnology and Biochemistry</i> , 2008, 72, 2369-2376.	1.3	2
62	A Metagenomic Approach to the Identification of UDP-Glucose 4-Epimerase as a Menadione Resistance Protein. <i>Bioscience, Biotechnology and Biochemistry</i> , 2008, 72, 1611-1614.	1.3	11
63	Metagenomic Screening for Bleomycin Resistance Genes. <i>Applied and Environmental Microbiology</i> , 2008, 74, 6803-6805.	3.1	60
64	1P-080 Supramolecular complex formation and crystallization of isocitrate dehydrogenase from <i>Thermus thermophilus</i> HB8 (The 46th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2008, 48, S33.	0.1	0
65	Development of an electroplated polishing tape applying electrodeposited nickel foil method. , 2008, , 459-462.		0
66	The Structural Basis for the Exo-mode of Action in GH74 Oligoxyloglucan Reducing End-specific Cellobiohydrolase. <i>Journal of Molecular Biology</i> , 2007, 370, 53-62.	4.2	52
67	Substrate specificity analysis and inhibitor design of homoisocitrate dehydrogenase. <i>Bioorganic and Medicinal Chemistry</i> , 2007, 15, 1346-1355.	3.0	8
68	Microbial resolution of dl-homoserine for the production of d-homoserine using a novel isolate, <i>Arthrobacter nicotinovorans</i> strain 2-3. <i>Enzyme and Microbial Technology</i> , 2007, 41, 318-321.	3.2	7
69	Functional screening of a metagenomic library for genes involved in microbial degradation of aromatic compounds. <i>Environmental Microbiology</i> , 2007, 9, 2289-2297.	3.8	144
70	Thermal Stabilization of <i>Bacillus subtilis</i> Family-11 Xylanase by Directed Evolution. <i>Journal of Biological Chemistry</i> , 2006, 281, 10236-10242.	3.4	106
71	Hyperthermophilic α -L-arabinofuranosidase from <i>Thermotoga maritima</i> MSB8: molecular cloning, gene expression, and characterization of the recombinant protein. <i>Extremophiles</i> , 2005, 9, 399-406.	2.3	36
72	A hyperthermophilic laccase from <i>Thermus thermophilus</i> HB27. <i>Extremophiles</i> , 2005, 9, 415-425.	2.3	191

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73	Bifunctional isocitrateâ€“homoisocitrate dehydrogenase: A missing link in the evolution of Î²-decarboxylating dehydrogenase. Biochemical and Biophysical Research Communications, 2005, 331, 341-346.	2.1	21
74	Identification of a novel trifunctional homoisocitrate dehydrogenase and modulation of the broad substrate specificity through site-directed mutagenesis. Biochemical and Biophysical Research Communications, 2005, 336, 596-602.	2.1	11
75	Creating Random Mutagenesis Libraries by Megaprimer PCR of Whole Plasmid (MEGAWHOP). , 2003, 231, 23-28.		54
76	Random DNA fragmentation with endonuclease V: application to DNA shuffling. Nucleic Acids Research, 2002, 30, 139e-139.	14.5	33
77	Creating Random Mutagenesis Libraries Using Megaprimer PCR of Whole Plasmid. BioTechniques, 2002, 33, 1033-1038.	1.8	158
78	Patterns of adaptation in a laboratory evolved thermophilic enzyme. BBA - Proteins and Proteomics, 2001, 1549, 1-8.	2.1	50
79	How enzymes adapt: lessons from directed evolution. Trends in Biochemical Sciences, 2001, 26, 100-106.	7.5	351
80	Development of a high-resolution x-ray imaging system with a charge-coupled-device detector coupled with crystal x-ray magnifiers. Review of Scientific Instruments, 2000, 71, 4449.	1.3	12
81	Cold Adaptation of a Mesophilic Subtilisin-like Protease by Laboratory Evolution. Journal of Biological Chemistry, 2000, 275, 31635-31640.	3.4	128
82	Directed evolution study of temperature adaptation in a psychrophilic enzyme 1 Edited by J. A. Wells. Journal of Molecular Biology, 2000, 297, 1015-1026.	4.2	243
83	Directed Evolution of Mesophilic Enzymes into Their Thermophilic Counterparts. Annals of the New York Academy of Sciences, 1999, 870, 400-403.	3.8	29
84	Exploring Nonnatural Evolutionary Pathways by Saturation Mutagenesis: Rapid Improvement of Protein Function. Journal of Molecular Evolution, 1999, 49, 716-720.	1.8	187
85	Substrate Recognition of Isocitrate Dehydrogenase and 3-Isopropylmalate Dehydrogenase from Thermus thermophilus HB8. Journal of Biochemistry, 1997, 121, 77-81.	1.7	7
86	Conversion of the Coenzyme Specificity of Isocitrate Dehydrogenase by Module Replacement. Journal of Biochemistry, 1996, 119, 1014-1018.	1.7	36
87	Structure of a loop-deleted variant of 3-isopropylmalate dehydrogenase from Thermus thermophilus: an internal relieve tolerance mechanism. Acta Crystallographica Section D: Biological Crystallography, 1996, 52, 124-128.	2.5	4
88	Isocitrate dehydrogenase from Thermus aquaticus YT1: purification of the enzyme and cloning, sequencing, and expression of the gene. Applied and Environmental Microbiology, 1996, 62, 4627-4631.	3.1	17
89	His273 of 3-Isopropylmalate Dehydrogenase from Thermus thermophilus HB8 Is Involved in the Coenzyme Binding. Biochemical and Biophysical Research Communications, 1995, 210, 733-737.	2.1	1
90	Co-enzyme specificity of 3-isopropylmalate dehydrogenase from Thermits thermophilus HB8. Protein Engineering, Design and Selection, 1994, 7, 401-403.	2.1	19

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91	Chemical modification and site-directed mutagenesis of Tyr36 of 3-isopropylmalate dehydrogenase from <i>Thermus thermophilus</i> HB8. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 99-102.	2.1	5
92	Synthesis of 2-O-Methyl Ether and 1-Carboxamide Derivatives of (2R,3S)-3-Isopropylmalic Acid and Their Interaction with Thermophilic 3-Isopropylmalate Dehydrogenase. <i>Bioscience, Biotechnology and Biochemistry</i> , 1994, 58, 870-873.	1.3	12
93	Expression, purification, and substrate specificity of isocitrate dehydrogenase from <i>Thermus thermophilus</i> HB8. <i>FEBS Journal</i> , 1994, 221, 899-903.	0.2	15
94	Roles of Arg231 and Tyr284 of <i>Thermus thermophilus</i> isocitrate dehydrogenase in the coenzyme specificity. <i>FEBS Letters</i> , 1994, 355, 171-172.	2.8	7
95	Kinetic analysis on the substrate specificity of 3-isopropylmalate dehydrogenase. <i>FEBS Letters</i> , 1993, 332, 35-36.	2.8	32
96	Tyr-139 in <i>Thermus thermophilus</i> 3-isopropylmalate dehydrogenase is involved in catalytic function. <i>FEBS Letters</i> , 1993, 332, 37-38.	2.8	14
97	Enantioselective Synthesis of (2R,3S)-3-Alkylmalic Acids, Competent Substrates for 3-Isopropylmalate Dehydrogenase. <i>Bioscience, Biotechnology and Biochemistry</i> , 1993, 57, 1916-1923.	1.3	17
98	Molecular cloning of the isocitrate dehydrogenase gene of an extreme thermophile, <i>Thermus thermophilus</i> HB8. <i>Applied and Environmental Microbiology</i> , 1992, 58, 93-98.	3.1	41
99	Purification, Catalytic Properties, and Thermal Stability of Threo-Ds-3-Isopropylmalate Dehydrogenase Coded by <i>leuB</i> Gene from an Extreme Thermophile, <i>Thermus thermophilus</i> Strain HB81. <i>Journal of Biochemistry</i> , 1990, 108, 449-456.	1.7	103
100	Complete Genome Sequences of <i>Thermus</i> Strains Isolated from Senami Hot Spring in Japan. <i>Microbiology Resource Announcements</i> , 0, , .	0.6	2