

Kentaro Miyazaki

List of Publications by Year in descending order

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100
papers

3,826
citations

168829

31
h-index

150775

59
g-index

103
all docs

103
docs citations

103
times ranked

4884
citing authors

#	ARTICLE	IF	CITATIONS
1	Complete Genome Sequences of Four <i>Parageobacillus</i> Strains Isolated from Soil in Japan. <i>Microbiology Resource Announcements</i> , 2022, 11, e0020422.	0.3	1
2	Complete Genome Sequence of <i>Thiohalobacter</i> sp. Strain COW1, Isolated from Activated Sludge Treating Coke Oven Wastewater. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
3	Complete Genome Sequence of <i>Thermus thermophilus</i> Strain HB5018, Isolated from Mine Hot Spring in Japan. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	5
4	Complete Genome Sequences of <i>Thermus thermophilus</i> Strains HB5002 and HB5008, Isolated from Mine Hot Spring in Japan. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	3
5	Complete Genome Sequences of Four Halophilic <i>Thermus thermophilus</i> Strains Isolated from Arima Hot Spring in Japan. <i>Microbiology Resource Announcements</i> , 2021, 10, e0087421.	0.3	3
6	Complete Genome Resequencing of <i>Thermus thermophilus</i> Strain TMY by Hybrid Assembly of Long- and Short-Read Sequencing Technologies. <i>Microbiology Resource Announcements</i> , 2021, 10, e0097921.	0.3	0
7	Complete Genome Sequence of <i>Bacillus cereus</i> Strain PL1, Isolated from Soil in Japan. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
8	Complete Genome Sequence of <i>Pseudomonas otitidis</i> Strain MrB4, Isolated from Lake Biwa in Japan. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
9	Complete Genome Sequences of <i>Rhodothermus marinus</i> Strains AA2-13 and AA3-38, Isolated from Arima Onsen Hot Spring in Japan. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
10	Complete Genome Sequence of <i>Geobacillus</i> sp. Strain E55-1, Isolated from Mine Geysers in Japan. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
11	Complete Genome Sequence of <i>Vibrio rotiferianus</i> Strain AM7. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
12	Occurrence of randomly recombined functional 16S rRNA genes in <i>Thermus thermophilus</i> suggests genetic interoperability and promiscuity of bacterial 16S rRNAs. <i>Scientific Reports</i> , 2019, 9, 11233.	1.6	14
13	Accurate high-throughput screening based on digital protein synthesis in a massively parallel femtoliter droplet array. <i>Science Advances</i> , 2019, 5, eaav8185.	4.7	48
14	Complete Genome Sequences of <i>Thermus thermophilus</i> Strains AA2-20 and AA2-29, Isolated from Arima Onsen in Japan. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	8
15	Complete Genome Sequence of <i>Alteromonas</i> sp. Strain I4, Isolated from the Japan Sea. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
16	Complete Genome Sequence of <i>Staphylococcus arlettae</i> Strain P2, Isolated from a Laboratory Environment. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
17	Complete Genome Sequence of <i>Rubrobacter xylanophilus</i> Strain AA3-22, Isolated from Arima Onsen in Japan. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
18	Complete Genome Sequencing of <i>Thermus thermophilus</i> Strain HC11, Isolated from Mine Geysers in Japan. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	7

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19	Functional metagenomic approach to identify overlooked antibiotic resistance mutations in bacterial rRNA. <i>Scientific Reports</i> , 2018, 8, 5179.	1.6	9
20	Molecular engineering of the salicylate-inducible transcription factor Sal7AR for orthogonal and high gene expression in <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2018, 13, e0194090.	1.1	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. <i>Scientific Reports</i> , 2017, 7, 9993.	1.6	28
23	PCR Primer Design for 16S rRNAs for Experimental Horizontal Gene Transfer Test in <i>Escherichia coli</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , 2017, 5, 14.	2.0	12
24	Phylogenetic Network Analysis Revealed the Occurrence of Horizontal Gene Transfer of 16S rRNA in the Genus <i>Enterobacter</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2225.	1.5	19
25	Crystal structure and identification of a key amino acid for glucose tolerance, substrate specificity, and transglycosylation activity of metagenomic β -glucosidase Td2F2. <i>FEBS Journal</i> , 2016, 283, 2340-2353.	2.2	53
26	Intramolecular Electron Transfer in the Bacterial Two-Domain Multicopper Oxidase mgLAC. <i>Biochemistry</i> , 2016, 55, 2960-2966.	1.2	2
27	Activity-stability relationships revisited in blue oxidases catalyzing electron transfer at extreme temperatures. <i>Extremophiles</i> , 2016, 20, 621-629.	0.9	12
28	Molecular engineering of a PheS counterselection marker for improved operating efficiency in <i>Escherichia coli</i> . <i>BioTechniques</i> , 2015, 58, 86-88.	0.8	49
29	Glucose-tolerant β -glucosidase retrieved from a Kusaya gray metagenome. <i>Frontiers in Microbiology</i> , 2015, 6, 548.	1.5	48
30	Counterselection method based on conditional silencing of antitoxin genes in <i>Escherichia coli</i> . <i>Journal of Bioscience and Bioengineering</i> , 2015, 120, 591-595.	1.1	5
31	Extradiol Dioxygenases Retrieved from the Metagenome. , 2015, , 167-171.		0
32	Bacterial Cellular Engineering by Genome Editing and Gene Silencing. <i>International Journal of Molecular Sciences</i> , 2014, 15, 2773-2793.	1.8	42
33	Diversity of extradiol dioxygenases in aromatic-degrading microbial community explored using both culture-dependent and culture-independent approaches. <i>FEMS Microbiology Ecology</i> , 2014, 90, n/a-n/a.	1.3	12
34	New insights into the catalytic active-site structure of multicopper oxidases. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 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_1_0.784314 rgBT 0.0	0.0	0
36	Directed evolution study unveiling key sequence factors that affect translation efficiency in <i>Escherichia coli</i> . <i>Journal of Bioscience and Bioengineering</i> , 2013, 116, 540-545.	1.1	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.	1.3	12
38	DNA fragmentation caused by an overdose of Zeocin. <i>Journal of Bioscience and Bioengineering</i> , 2013, 116, 644-646.	1.1	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.	1.6	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.	1.1	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.	1.1	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.	3.3	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.	0.6	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.	0.3	13
48	MEGAWHOP Cloning. <i>Methods in Enzymology</i> , 2011, 498, 399-406.	0.4	133
49	Specific inhibition of bacterial RNase T2 by helix 41 of 16S ribosomal RNA. <i>Nature Communications</i> , 2011, 2, 549.	5.8	28
50	ãfjã,jã,²ãfZãfèšŁæžã,ã,šæ~žã,%ãããã,CEãÿç'°ãcfããèš³é ™æ—ãCE—ããç%ãã^tèšŁéãã/4ãç³/4ãããš¿. Kagaku. To Seibutsu, 2010,		
51	Lethal <i>ccdB</i> gene-based zero-background vector for construction of shotgun libraries. <i>Journal of Bioscience and Bioengineering</i> , 2010, 110, 372-373.	1.1	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.	1.4	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.	0.4	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.	1.3	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.	4.4	80
57	The crystal structure of a xyloglucan-specific endo- α -1,4-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.	2.2	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.	1.3	22
59	Functional metagenomics for enzyme discovery: challenges to efficient screening. <i>Current Opinion in Biotechnology</i> , 2009, 20, 616-622.	3.3	294
60	Directed Evolution of the Actinomycete Cytochrome P450 MoxA (CYP105) for Enhanced Activity. <i>Bioscience, Biotechnology and Biochemistry</i> , 2009, 73, 1922-1927.	0.6	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.	0.6	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.	0.6	11
63	Metagenomic Screening for Bleomycin Resistance Genes. <i>Applied and Environmental Microbiology</i> , 2008, 74, 6803-6805.	1.4	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 Butsurei</i> , 2008, 48, S33.	0.0	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.	2.0	52
67	Substrate specificity analysis and inhibitor design of homoisocitrate dehydrogenase. <i>Bioorganic and Medicinal Chemistry</i> , 2007, 15, 1346-1355.	1.4	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.	1.6	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.	1.8	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.	1.6	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.	0.9	36
72	A hyperthermophilic laccase from <i>Thermus thermophilus</i> HB27. <i>Extremophiles</i> , 2005, 9, 415-425.	0.9	191

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73	Bifunctional isocitrateâ€“homoisocitrate dehydrogenase: A missing link in the evolution of Î²-decarboxylating dehydrogenase. <i>Biochemical and Biophysical Research Communications</i> , 2005, 331, 341-346.	1.0	21
74	Identification of a novel trifunctional homoisocitrate dehydrogenase and modulation of the broad substrate specificity through site-directed mutagenesis. <i>Biochemical and Biophysical Research Communications</i> , 2005, 336, 596-602.	1.0	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. <i>Nucleic Acids Research</i> , 2002, 30, 139e-139.	6.5	33
77	Creating Random Mutagenesis Libraries Using Megaprimer PCR of Whole Plasmid. <i>BioTechniques</i> , 2002, 33, 1033-1038.	0.8	158
78	Patterns of adaptation in a laboratory evolved thermophilic enzyme. <i>BBA - Proteins and Proteomics</i> , 2001, 1549, 1-8.	2.1	50
79	How enzymes adapt: lessons from directed evolution. <i>Trends in Biochemical Sciences</i> , 2001, 26, 100-106.	3.7	351
80	Development of a high-resolution x-ray imaging system with a charge-coupled-device detector coupled with crystal x-ray magnifiers. <i>Review of Scientific Instruments</i> , 2000, 71, 4449.	0.6	12
81	Cold Adaptation of a Mesophilic Subtilisin-like Protease by Laboratory Evolution. <i>Journal of Biological Chemistry</i> , 2000, 275, 31635-31640.	1.6	128
82	Directed evolution study of temperature adaptation in a psychrophilic enzyme 1 Edited by J. A. Wells. <i>Journal of Molecular Biology</i> , 2000, 297, 1015-1026.	2.0	243
83	Directed Evolution of Mesophilic Enzymes into Their Thermophilic Counterparts. <i>Annals of the New York Academy of Sciences</i> , 1999, 870, 400-403.	1.8	29
84	Exploring Nonnatural Evolutionary Pathways by Saturation Mutagenesis: Rapid Improvement of Protein Function. <i>Journal of Molecular Evolution</i> , 1999, 49, 716-720.	0.8	187
85	Substrate Recognition of Isocitrate Dehydrogenase and 3-Isopropylmalate Dehydrogenase from <i>Thermus thermophilus</i> HB8. <i>Journal of Biochemistry</i> , 1997, 121, 77-81.	0.9	7
86	Conversion of the Coenzyme Specificity of Isocitrate Dehydrogenase by Module Replacement. <i>Journal of Biochemistry</i> , 1996, 119, 1014-1018.	0.9	36
87	Structure of a loop-deleted variant of 3-isopropylmalate dehydrogenase from <i>Thermus thermophilus</i> : an internal relieve tolerance mechanism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996, 52, 124-128.	2.5	4
88	Isocitrate dehydrogenase from <i>Thermus aquaticus</i> YT1: purification of the enzyme and cloning, sequencing, and expression of the gene. <i>Applied and Environmental Microbiology</i> , 1996, 62, 4627-4631.	1.4	17
89	His273 of 3-Isopropylmalate Dehydrogenase from <i>Thermus thermophilus</i> HB8 Is Involved in the Coenzyme Binding. <i>Biochemical and Biophysical Research Communications</i> , 1995, 210, 733-737.	1.0	1
90	Co-enzyme specificity of 3-isopropylmalate dehydrogenase from <i>Thermits thermophilus</i> HB8. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 401-403.	1.0	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.	1.0	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.	0.6	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.	1.3	7
95	Kinetic analysis on the substrate specificity of 3-isopropylmalate dehydrogenase. <i>FEBS Letters</i> , 1993, 332, 35-36.	1.3	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.	1.3	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.	0.6	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.	1.4	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.	0.9	103
100	Complete Genome Sequences of <i>Thermus</i> Strains Isolated from Senami Hot Spring in Japan. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	2