

# Kentaro Miyazaki

## List of Publications by Year in descending order

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100  
papers

3,826  
citations

147801

31  
h-index

133252

59  
g-index

103  
all docs

103  
docs citations

103  
times ranked

4405  
citing authors

#	ARTICLE	IF	CITATIONS
1	How enzymes adapt: lessons from directed evolution. Trends in Biochemical Sciences, 2001, 26, 100-106.	7.5	351
2	Functional metagenomics for enzyme discovery: challenges to efficient screening. Current Opinion in Biotechnology, 2009, 20, 616-622.	6.6	294
3	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
4	A hyperthermophilic laccase from Thermus thermophilus HB27. Extremophiles, 2005, 9, 415-425.	2.3	191
5	Exploring Nonnatural Evolutionary Pathways by Saturation Mutagenesis: Rapid Improvement of Protein Function. Journal of Molecular Evolution, 1999, 49, 716-720.	1.8	187
6	Creating Random Mutagenesis Libraries Using Megaprimer PCR of Whole Plasmid. BioTechniques, 2002, 33, 1033-1038.	1.8	158
7	Functional screening of a metagenomic library for genes involved in microbial degradation of aromatic compounds. Environmental Microbiology, 2007, 9, 2289-2297.	3.8	144
8	MEGAWHOP Cloning. Methods in Enzymology, 2011, 498, 399-406.	1.0	133
9	Cold Adaptation of a Mesophilic Subtilisin-like Protease by Laboratory Evolution. Journal of Biological Chemistry, 2000, 275, 31635-31640.	3.4	128
10	Product-Induced Gene Expression, a Product-Responsive Reporter Assay Used To Screen Metagenomic Libraries for Enzyme-Encoding Genes. Applied and Environmental Microbiology, 2010, 76, 7029-7035.	3.1	114
11	Characterization of a Novel $\beta$ -Glucosidase from a Compost Microbial Metagenome with Strong Transglycosylation Activity. Journal of Biological Chemistry, 2013, 288, 18325-18334.	3.4	113
12	Thermal Stabilization of Bacillus subtilis Family-11 Xylanase by Directed Evolution. Journal of Biological Chemistry, 2006, 281, 10236-10242.	3.4	106
13	Purification, Catalytic Properties, and Thermal Stability of Threo-Ds-3-Isopropylmalate Dehydrogenase Coded by leuB Gene from an Extreme Thermophile, Thermus thermophilus Strain HB81. Journal of Biochemistry, 1990, 108, 449-456.	1.7	103
14	Cloning, Expression and Characteristics of a Novel Alkalistable and Thermostable Xylanase Encoding Gene (Mxyl) Retrieved from Compost-Soil Metagenome. PLoS ONE, 2013, 8, e52459.	2.5	82
15	Novel organization of aromatic degradation pathway genes in a microbial community as revealed by metagenomic analysis. ISME Journal, 2009, 3, 1335-1348.	9.8	80
16	Metagenomic Screening for Bleomycin Resistance Genes. Applied and Environmental Microbiology, 2008, 74, 6803-6805.	3.1	60
17	Creating Random Mutagenesis Libraries by Megaprimer PCR of Whole Plasmid (MEGAWHOP). , 2003, 231, 23-28.		54
18	X-ray structure of a two-domain type laccase: A missing link in the evolution of multi-copper proteins. FEBS Letters, 2009, 583, 1189-1195.	2.8	53

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19	Crystal structure and identification of a key amino acid for glucose tolerance, substrate specificity, and transglycosylation activity of metagenomic Î²-D-glucosidase Td2F2. <i>FEBS Journal</i> , 2016, 283, 2340-2353.	4.7	53
20	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
21	Revisiting bacterial phylogeny. <i>Mobile Genetic Elements</i> , 2013, 3, e24210.	1.8	52
22	Patterns of adaptation in a laboratory evolved thermophilic enzyme. <i>BBA - Proteins and Proteomics</i> , 2001, 1549, 1-8.	2.1	50
23	Molecular engineering of a PheS counterselection marker for improved operating efficiency in <i>Escherichia coli</i> . <i>BioTechniques</i> , 2015, 58, 86-88.	1.8	49
24	Glucose-tolerant Î²-D-glucosidase retrieved from a Kusaya gravy metagenome. <i>Frontiers in Microbiology</i> , 2015, 6, 548.	3.5	48
25	Accurate high-throughput screening based on digital protein synthesis in a massively parallel femtoliter droplet array. <i>Science Advances</i> , 2019, 5, eaav8185.	10.3	48
26	Bacterial Cellular Engineering by Genome Editing and Gene Silencing. <i>International Journal of Molecular Sciences</i> , 2014, 15, 2773-2793.	4.1	42
27	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
28	Conversion of the Coenzyme Specificity of Isocitrate Dehydrogenase by Module Replacement. <i>Journal of Biochemistry</i> , 1996, 119, 1014-1018.	1.7	36
29	Hyperthermophilic Î±-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
30	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
31	Random DNA fragmentation with endonuclease V: application to DNA shuffling. <i>Nucleic Acids Research</i> , 2002, 30, 139e-139.	14.5	33
32	Kinetic analysis on the substrate specificity of 3-isopropylmalate dehydrogenase. <i>FEBS Letters</i> , 1993, 332, 35-36.	2.8	32
33	Directed Evolution of Mesophilic Enzymes into Their Thermophilic Counterparts. <i>Annals of the New York Academy of Sciences</i> , 1999, 870, 400-403.	3.8	29
34	Specific inhibition of bacterial RNase T2 by helix 41 of 16S ribosomal RNA. <i>Nature Communications</i> , 2011, 2, 549.	12.8	28
35	Comparative RNA function analysis reveals high functional similarity between distantly related bacterial 16 S rRNAs. <i>Scientific Reports</i> , 2017, 7, 9993.	3.3	28
36	The crystal structure of a xyloglucan-specific endo-1,4-Î²-D-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

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37	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
38	Metagenomic Screening for Aromatic Compound-Responsive Transcriptional Regulators. <i>PLoS ONE</i> , 2013, 8, e75795.	2.5	23
39	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
40	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
41	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.	2.1	21
42	Co-enzyme specificity of 3-isopropylmalate dehydrogenase from <i>Thermits thermophilus</i> HB8. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 401-403.	2.1	19
43	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.	3.5	19
44	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
45	Crystal Structures of Glycoside Hydrolase Family 51 Î±-Arabinofuranosidase from <i>Thermotoga maritima</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2012, 76, 423-428.	1.3	17
46	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.	3.1	17
47	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
48	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
49	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
50	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
51	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.	3.3	14
52	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
53	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
54	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.	1.3	12

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55	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
56	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.	2.7	12
57	Activity–stability relationships revisited in blue oxidases catalyzing electron transfer at extreme temperatures. <i>Extremophiles</i> , 2016, 20, 621-629.	2.3	12
58	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.	4.1	12
59	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.	2.1	11
60	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
61	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.	2.2	10
62	Functional metagenomic approach to identify overlooked antibiotic resistance mutations in bacterial rRNA. <i>Scientific Reports</i> , 2018, 8, 5179.	3.3	9
63	Substrate specificity analysis and inhibitor design of homoisocitrate dehydrogenase. <i>Bioorganic and Medicinal Chemistry</i> , 2007, 15, 1346-1355.	3.0	8
64	DNA fragmentation caused by an overdose of Zeocin. <i>Journal of Bioscience and Bioengineering</i> , 2013, 116, 644-646.	2.2	8
65	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, .	0.6	8
66	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
67	Substrate Recognition of Isocitrate Dehydrogenase and 3-Isopropylmalate Dehydrogenase from <i>Thermus thermophilus</i> HB8. <i>Journal of Biochemistry</i> , 1997, 121, 77-81.	1.7	7
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	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.	2.2	7
70	Complete Genome Sequencing of <i>Thermus thermophilus</i> Strain HC11, Isolated from Mine Geyser in Japan. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	7
71	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
72	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.	2.2	5

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73	Complete Genome Sequence of <i>Staphylococcus arlettae</i> Strain P2, Isolated from a Laboratory Environment. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	5
74	Complete Genome Sequence of <i>Thermus thermophilus</i> Strain HB5018, Isolated from Mine Hot Spring in Japan. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	5
75	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
76	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.	2.5	4
77	Complete Genome Sequence of <i>Pseudomonas otitidis</i> Strain MrB4, Isolated from Lake Biwa in Japan. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	4
78	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, .	0.6	3
79	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.	0.6	3
80	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
81	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
82	Intramolecular Electron Transfer in the Bacterial Two-Domain Multicopper Oxidase mgLAC. <i>Biochemistry</i> , 2016, 55, 2960-2966.	2.5	2
83	Complete Genome Sequence of <i>Rubrobacter xylanophilus</i> Strain AA3-22, Isolated from Arima Onsen in Japan. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
84	Complete Genome Sequence of <i>Bacillus cereus</i> Strain PL1, Isolated from Soil in Japan. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
85	Complete Genome Sequence of <i>Vibrio rotiferianus</i> Strain AM7. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
86	Complete Genome Sequences of <i>Thermus</i> Strains Isolated from Senami Hot Spring in Japan. <i>Microbiology Resource Announcements</i> , 0, , .	0.6	2
87	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.	2.1	1
88	<i>Journal of Chemical Information and Modeling</i> , 2010, 10, 2066-2074. Kagaku. To Seibutsu, 2010,		
89	Complete Genome Sequence of <i>Geobacillus</i> sp. Strain E55-1, Isolated from Mine Geysir in Japan. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
90	Complete Genome Sequences of Four <i>Parageobacillus</i> Strains Isolated from Soil in Japan. <i>Microbiology Resource Announcements</i> , 2022, 11, e0020422.	0.6	1

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91	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.	0.1	0
92	2P076 Exapnsin activity observed by FTIR(01D. Protein: Function,Poster,The 52nd Annual Meeting of the) Tj ETQq0,0,0 rgBT (Overlock 1	0.1	0
93	Complete Genome Sequence of <i>Alteromonas</i> sp. Strain I4, Isolated from the Japan Sea. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	0
94	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, .	0.6	0
95	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, .	0.6	0
96	Extradiol Dioxygenases Retrieved from the Metagenome. , 2013, , 1-5.		0
97	Extradiol Dioxygenases Retrieved from the Metagenome. , 2015, , 167-171.		0
98	Constructing Mutant Ribosomes Containing Mutant Ribosomal RNAs. , 2018, , 17-32.		0
99	Development of an electroplated polishing tape applying electrodeposited nickel foil method. , 2008, , 459-462.		0
100	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.	0.6	0