

# Hideto Takami

## List of Publications by Year in descending order

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108  
papers

7,099  
citations

87843

38  
h-index

60583

81  
g-index

111  
all docs

111  
docs citations

111  
times ranked

7496  
citing authors

#	ARTICLE	IF	CITATIONS
1	Community structure and metabolic potentials of the traditional rice beer starter "emao"™. Scientific Reports, 2021, 11, 14628.	1.6	3
2	Metabolic potential of the imperfect denitrifier <i>Candidatus</i> Desulfobacillus denitrificans in an anammox bioreactor. MicrobiologyOpen, 2021, 10, e1227.	1.2	4
3	The physiological potential of anammox bacteria as revealed by their core genome structure. DNA Research, 2021, 28, .	1.5	21
4	Comprehensive Comparative Genomics and Phenotyping of Methylobacterium Species. Frontiers in Microbiology, 2021, 12, 740610.	1.5	20
5	Diversity of <i>Bradyrhizobium</i> in Non-Leguminous Sorghum Plants: <i>B. ottawaense</i> Isolates Unique in Genes for N <sub>2</sub> O Reductase and Lack of the Type VI Secretion System. Microbes and Environments, 2020, 35, n/a.	0.7	16
6	MAPLE Enables Functional Assessment of Microbiota in Various Environments. , 2019, , 85-119.		4
7	An aluminum shield enables the amphipod <i>Hirondellea gigas</i> to inhabit deep-sea environments. PLoS ONE, 2019, 14, e0206710.	1.1	10
8	Molecular Tools in Microbial Diversity. , 2019, , 117-136.		0
9	Functional Microbial Diversity. , 2019, , 427-449.		1
10	Polysaccharide hydrolase of the hadal zone amphipods <i>Hirondellea gigas</i> . Bioscience, Biotechnology and Biochemistry, 2018, 82, 1123-1133.	0.6	10
11	MAPLE 2.3.0: an improved system for evaluating the functionomes of genomes and metagenomes. Bioscience, Biotechnology and Biochemistry, 2018, 82, 1515-1517.	0.6	80
12	d-Lactate electrochemical biosensor prepared by immobilization of thermostable dye-linked d-lactate dehydrogenase from <i>Candidatus</i> <i>Caldiarchaeum</i> <i>subterraneum</i> . Journal of Bioscience and Bioengineering, 2018, 126, 425-430.	1.1	15
13	Complete Genome Sequence of <i>Altererythrobacter</i> sp. Strain B11, an Aromatic Monomer-Degrading Bacterium, Isolated from Deep-Sea Sediment under the Seabed off Kashima, Japan. Genome Announcements, 2018, 6, .	0.8	4
14	<i>Amylibacter kogurei</i> sp. nov., a novel marine alphaproteobacterium isolated from the coastal sea surface microlayer of a marine inlet. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2872-2877.	0.8	10
15	An acid-tolerant ammonia-oxidizing $\beta$ -proteobacterium from soil. ISME Journal, 2017, 11, 1130-1141.	4.4	123
16	Complete genome sequence and expression profile of the commercial lytic enzyme producer <i>Lysobacter</i> <i>enzymogenes</i> M497-1. DNA Research, 2017, 24, dsw055.	1.5	12
17	Biochemical characterization of a new nicotinamidase from an unclassified bacterium thriving in a geothermal water stream microbial mat community. PLoS ONE, 2017, 12, e0181561.	1.1	2
18	An automated system for evaluation of the potential functionome: MAPLE version 2.1.0. DNA Research, 2016, 23, 467-475.	1.5	66

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19	Low frequency of endospore-specific genes in subseafloor sedimentary metagenomes. <i>Environmental Microbiology Reports</i> , 2015, 7, 341-350.	1.0	11
20	Functional Classification of Uncultured "Candidatus Caldiarchaeum subterraneum" Using the Maple System. <i>PLoS ONE</i> , 2015, 10, e0132994.	1.1	29
21	High frequency of phylogenetically diverse reductive dehalogenase-homologous genes in deep subseafloor sedimentary metagenomes. <i>Frontiers in Microbiology</i> , 2014, 5, 80.	1.5	61
22	Structural and functional characterization of the <i>Geobacillus</i> copper nitrite reductase: Involvement of the unique N-terminal region in the interprotein electron transfer with its redox partner. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, 396-405.	0.5	14
23	Structural insights into the function of a thermostable copper-containing nitrite reductase. <i>Journal of Biochemistry</i> , 2014, 155, 123-135.	0.9	21
24	New Method for Comparative Functional Genomics and Metagenomics Using KEGG MODULE. , 2014, , 1-15.		6
25	Active Bacterial Flora Surrounding Foraminifera ( <i>Xenophyophorea</i> ) Living on the Deep-Sea Floor. <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 381-384.	0.6	13
26	Biochemical and Mutational Analysis of a Novel Nicotinamidase from <i>Oceanobacillus iheyensis</i> HTE831. <i>PLoS ONE</i> , 2013, 8, e56727.	1.1	16
27	New Insights into the Phylogeny and Molecular Classification of Nicotinamide Mononucleotide Deamidases. <i>PLoS ONE</i> , 2013, 8, e82705.	1.1	7
28	Unique substrate specificity of a thermostable glycosyl hydrolase from an uncultured <i>Anaerolinea</i> , derived from bacterial mat on a subsurface geothermal water stream. <i>Biotechnology Letters</i> , 2012, 34, 1887-1893.	1.1	1
29	Evaluation method for the potential functionome harbored in the genome and metagenome. <i>BMC Genomics</i> , 2012, 13, 699.	1.2	65
30	Three inositol dehydrogenases involved in utilization and interconversion of inositol stereoisomers in a thermophile, <i>Geobacillus kaustophilus</i> HTA426. <i>Microbiology (United Kingdom)</i> , 2012, 158, 1942-1952.	0.7	19
31	A Deeply Branching Thermophilic Bacterium with an Ancient Acetyl-CoA Pathway Dominates a Subsurface Ecosystem. <i>PLoS ONE</i> , 2012, 7, e30559.	1.1	161
32	The Hadal Amphipod <i>Hirondellea gigas</i> Possessing a Unique Cellulase for Digesting Wooden Debris Buried in the Deepest Seafloor. <i>PLoS ONE</i> , 2012, 7, e42727.	1.1	67
33	Genomic Heterogeneity in a Natural Archaeal Population Suggests a Model of tRNA Gene Disruption. <i>PLoS ONE</i> , 2012, 7, e32504.	1.1	9
34	Genomics and Evolution of Alkaliphilic <i>Bacillus</i> Species. , 2011, , 183-211.		3
35	I-2. Extreme environments from metagenomic point of view. <i>Nippon Suisan Gakkaishi</i> , 2011, 77, 248.	0.0	0
36	Alternative Splicing by Participation of the Group II Intron ORF in Extremely Halotolerant and Alkaliphilic <i>Oceanobacillus iheyensis</i> . <i>Microbes and Environments</i> , 2011, 26, 54-60.	0.7	4

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37	Branched fatty acids inhibit the biosynthesis of menaquinone in <i>Helicobacter pylori</i> . <i>Journal of Antibiotics</i> , 2011, 64, 151-153.	1.0	23
38	Cloning, expression, purification, crystallization and preliminary X-ray crystallographic study of GK0767, the copper-containing nitrite reductase from <i>Geobacillus kaustophilus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 692-695.	0.7	9
39	<i>Bifidobacterium kashiwanohense</i> sp. nov., isolated from healthy infant faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 2610-2615.	0.8	40
40	Insights into the evolution of Archaea and eukaryotic protein modifier systems revealed by the genome of a novel archaeal group. <i>Nucleic Acids Research</i> , 2011, 39, 3204-3223.	6.5	303
41	<i>Lactobacillus equicursoris</i> sp. nov., isolated from the faeces of a thoroughbred racehorse. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010, 60, 109-112.	0.8	19
42	Bacterial Lifestyle in a Deep-sea Hydrothermal Vent Chimney Revealed by the Genome Sequence of the Thermophilic Bacterium <i>Deferribacter desulfuricans</i> SSM1. <i>DNA Research</i> , 2010, 17, 123-137.	1.5	41
43	Fungal diversity in deep-sea sediments – the presence of novel fungal groups. <i>Fungal Ecology</i> , 2010, 3, 316-325.	0.7	139
44	Characterization of a Novel Thermostable Carboxylesterase from <i>Geobacillus kaustophilus</i> HTA426 Shows the Existence of a New Carboxylesterase Family. <i>Journal of Bacteriology</i> , 2009, 191, 3076-3085.	1.0	50
45	<i>Lactobacillus hayakitensis</i> , <i>L. equigenosus</i> and <i>L. equi</i> , predominant lactobacilli in the intestinal flora of healthy thoroughbreds. <i>Animal Science Journal</i> , 2009, 80, 339-346.	0.6	23
46	Characterization and structural modeling of a novel thermostable glycine oxidase from <i>Geobacillus kaustophilus</i> HTA426. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 1429-1441.	1.5	18
47	Characterization of a New Rhamnogalacturonan Acetyl Esterase from <i>Bacillus halodurans</i> C-125 with a New Putative Carbohydrate Binding Domain. <i>Journal of Bacteriology</i> , 2008, 190, 1375-1382.	1.0	30
48	<i>Sharpea azabuensis</i> gen. nov., sp. nov., a Gram-positive, strictly anaerobic bacterium isolated from the faeces of thoroughbred horses. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 2682-2686.	0.8	36
49	An Improved DNA Isolation Method for Metagenomic Analysis of the Microbial Flora of the Human Intestine. <i>Microbes and Environments</i> , 2007, 22, 214-222.	0.7	95
50	ç°äçfæ©ÿèf1/2ã,2ãfŽãfÿã,ã,1ç”ç©¶ã®ãÿ°ç,ã*ãã,ãfjã,ã,2ãfŽãfè\$£æž. <i>Kagaku To Seibutsu</i> , 2007, 45, 330-339. 0		1
51	Comparative Metagenomics Revealed Commonly Enriched Gene Sets in Human Gut Microbiomes. <i>DNA Research</i> , 2007, 14, 169-181.	1.5	760
52	<i>Lactobacillus hayakitensis</i> sp. nov., isolated from intestines of healthy thoroughbreds. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 2836-2839.	0.8	30
53	Microbial flora in the deepest sea mud of the Mariana Trench. <i>FEMS Microbiology Letters</i> , 2006, 152, 279-285.	0.7	251
54	Genetic and functional properties of uncultivated thermophilic crenarchaeotes from a subsurface gold mine as revealed by analysis of genome fragments. <i>Environmental Microbiology</i> , 2005, 7, 1967-1984.	1.8	119

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55	An Alkali-Inducible Flotillin-like Protein from <i>Bacillus halodurans</i> C-125. <i>Protein Journal</i> , 2005, 24, 125-131.	0.7	21
56	Characterization of alkaliphilic <i>Bacillus</i> strains used in industry: proposal of five novel species. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005, 55, 2309-2315.	0.8	105
57	Housekeeping <i>recA</i> gene interrupted by group II intron in the thermophilic <i>Geobacillus kaustophilus</i> . <i>Gene</i> , 2005, 363, 211-220.	1.0	17
58	The BH1999 Protein of <i>Bacillus halodurans</i> C-125 Is Gentsyl-Coenzyme A Thioesterase. <i>Journal of Bacteriology</i> , 2004, 186, 393-399.	1.0	19
59	Wide-Range Distribution of Insertion Sequences Identified in <i>B. halodurans</i> among Bacilli and a New Transposon Disseminated in Alkaliphilic and Thermophilic Bacilli. <i>DNA Research</i> , 2004, 11, 153-162.	1.5	6
60	Identification and Distribution of New Insertion Sequences in the Genome of the Extremely Halotolerant and Alkaliphilic <i>Oceanobacillus iheyensis</i> HTE831. <i>DNA Research</i> , 2004, 11, 233-245.	1.5	8
61	Thermoadaptation trait revealed by the genome sequence of thermophilic <i>Geobacillus kaustophilus</i> . <i>Nucleic Acids Research</i> , 2004, 32, 6292-6303.	6.5	186
62	Genomic characterization of thermophilic <i>Geobacillus</i> species isolated from the deepest sea mud of the Mariana Trench. <i>Extremophiles</i> , 2004, 8, 351-356.	0.9	68
63	Role of Arginine Residues on the S4 Segment of the <i>Bacillus halodurans</i> Na <sup>+</sup> Channel in Voltage-sensing. <i>Journal of Membrane Biology</i> , 2004, 201, 9-24.	1.0	35
64	Characterization of Endo- $\beta$ -N-acetylglucosaminidase from Alkaliphilic <i>Bacillus halodurans</i> C-125. <i>Bioscience, Biotechnology and Biochemistry</i> , 2004, 68, 1059-1066.	0.6	25
65	Genome sequence of <i>Oceanobacillus iheyensis</i> isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments. <i>Nucleic Acids Research</i> , 2002, 30, 3927-3935.	6.5	175
66	Complete Genome Sequence of Enterohemorrhagic <i>Escherichia coli</i> O157:H7 and Genomic Comparison with a Laboratory Strain K-12. <i>DNA Research</i> , 2001, 8, 11-22.	1.5	1,190
67	A globin-coupled oxygen sensor from the facultatively alkaliphilic <i>Bacillus halodurans</i> C-125. <i>Extremophiles</i> , 2001, 5, 351-354.	0.9	25
68	Distribution and identification of red yeasts in deep-sea environments around the northwest Pacific Ocean. <i>Antonie Van Leeuwenhoek</i> , 2001, 80, 101-110.	0.7	99
69	<i>Oceanobacillus iheyensis</i> gen. nov., sp. nov., a deep-sea extremely halotolerant and alkaliphilic species isolated from a depth of 1050 m on the Iheya Ridge. <i>FEMS Microbiology Letters</i> , 2001, 205, 291-297.	0.7	204
70	Identification and Distribution of New Insertion Sequences in the Genome of Alkaliphilic <i>Bacillus halodurans</i> C-125. <i>Journal of Bacteriology</i> , 2001, 183, 4345-4356.	1.0	26
71	Complete Nucleotide Sequence of a <i>Staphylococcus aureus</i> Exfoliative Toxin B Plasmid and Identification of a Novel ADP-Ribosyltransferase, EDIN-C. <i>Infection and Immunity</i> , 2001, 69, 7760-7771.	1.0	127
72	Phage conversion of exfoliative toxin A production in <i>Staphylococcus aureus</i> . <i>Molecular Microbiology</i> , 2000, 38, 694-705.	1.2	146

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73	Characterization and comparative study of the <i>rrn</i> operons of alkaliphilic <i>Bacillus halodurans</i> C-125. <i>Extremophiles</i> , 2000, 4, 209-214.	0.9	14
74	Reidentification of facultatively alkaliphilic <i>Bacillus firmus</i> OF4 as <i>Bacillus pseudofirmus</i> OF4. <i>Extremophiles</i> , 2000, 4, 19-22.	0.9	22
75	Analysis of the genome of an alkaliphilic <i>Bacillus</i> strain from an industrial point of view. <i>Extremophiles</i> , 2000, 4, 99-108.	0.9	71
76	Effects of Hydrostatic Pressure and Temperature on Growth and Lipid Composition of the Inner Membrane of Barotolerant <i>Pseudomonas</i> sp. BT1 Isolated from the Deep-sea. <i>Bioscience, Biotechnology and Biochemistry</i> , 2000, 64, 72-79.	0.6	35
77	Novel Oxidatively Stable Subtilisin-like Serine Proteases from Alkaliphilic <i>Bacillus</i> spp.: Enzymatic Properties, Sequences, and Evolutionary Relationships. <i>Biochemical and Biophysical Research Communications</i> , 2000, 279, 313-319.	1.0	40
78	Complete genome sequence of the alkaliphilic bacterium <i>Bacillus halodurans</i> and genomic sequence comparison with <i>Bacillus subtilis</i> . <i>Nucleic Acids Research</i> , 2000, 28, 4317-4331.	6.5	495
79	An Automated System for Genome Analysis to Support Microbial Whole-genome Shotgun Sequencing. <i>Bioscience, Biotechnology and Biochemistry</i> , 2000, 64, 670-673.	0.6	38
80	Genome Analysis of Facultatively Alkaliphilic <i>Bacillus halodurans</i> C-125. , 1999, , 249-284.		1
81	Sequence Analysis of a 32-kb Region Including the Major Ribosomal Protein Gene Clusters from Alkaliphilic <i>Bacillus</i> sp. Strain C-125. <i>Bioscience, Biotechnology and Biochemistry</i> , 1999, 63, 452-455.	0.6	16
82	An improved physical and genetic map of the genome of alkaliphilic <i>Bacillus</i> sp. C-125. <i>Extremophiles</i> , 1999, 3, 21-28.	0.9	47
83	Sequencing of three lambda clones from the genome of alkaliphilic <i>Bacillus</i> sp. strain C-125. <i>Extremophiles</i> , 1999, 3, 29-34.	0.9	33
84	Biodiversity in deep-sea sites located near the south part of Japan. <i>Extremophiles</i> , 1999, 3, 97-102.	0.9	92
85	Genetic analysis of the chromosome of alkaliphilic <i>Bacillus halodurans</i> C-125. <i>Extremophiles</i> , 1999, 3, 227-233.	0.9	21
86	Reidentification of the keratinase-producing facultatively alkaliphilic <i>Bacillus</i> sp. AH-101 as <i>Bacillus halodurans</i> . <i>Extremophiles</i> , 1999, 3, 293-296.	0.9	48
87	Replication Origin Region of the Chromosome of Alkaliphilic <i>Bacillus halodurans</i> C-125. <i>Bioscience, Biotechnology and Biochemistry</i> , 1999, 63, 1134-1137.	0.6	11
88	Reidentification of Facultatively Alkaliphilic <i>Bacillus</i> sp. C-125 to <i>Bacillus halodurans</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 1999, 63, 943-945.	0.6	55
89	Isolation and Characterization of Microorganisms from Deep-Sea Mud. , 1999, , 3-26.		14
90	Outer Membrane Changes in a Toluene-Sensitive Mutant of Toluene-Tolerant <i>Pseudomonas putida</i> IH-2000. <i>Journal of Bacteriology</i> , 1999, 181, 4493-4498.	1.0	46

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91	Cloning and expression of the gene encoding RNA polymerase $\beta$ subunit from alkaliphilic <i>Bacillus</i> sp. strain C-125. <i>FEMS Microbiology Letters</i> , 1998, 168, 269-276.	0.7	5
92	Isolation and characterization of toluene-sensitive mutants from <i>Pseudomonas putida</i> IH-2000. <i>FEMS Microbiology Letters</i> , 1998, 169, 219-225.	0.7	11
93	Isolation and transposon mutagenesis of a <i>Pseudomonas putida</i> KT2442 toluene-resistant variant: involvement of an efflux system in solvent resistance. <i>Extremophiles</i> , 1998, 2, 395-400.	0.9	61
94	Characterization of $\alpha$ -maltotetrahydrolase produced by <i>Pseudomonas</i> sp. MS300 isolated from the deepest site of the Mariana Trench. <i>Extremophiles</i> , 1998, 2, 401-407.	0.9	26
95	Cloning and expression of the gene encoding RNA polymerase $\beta$ subunit from alkaliphilic <i>Bacillus</i> sp. strain C-125. <i>FEMS Microbiology Letters</i> , 1998, 168, 269-276.	0.7	3
96	Deep-sea, new resource for screening of biocatalysts. <i>Studies in Organic Chemistry</i> , 1998, 53, 259-263.	0.2	1
97	Isolation of Extradiol Dioxygenase Genes That Are Phylogenetically Distant from Other meta-Cleavage Dioxygenase Genes. <i>Bioscience, Biotechnology and Biochemistry</i> , 1997, 61, 530-532.	0.6	12
98	Microbial flora in the deepest sea mud of the Mariana Trench. <i>FEMS Microbiology Letters</i> , 1997, 152, 279-285.	0.7	17
99	Pristine environments harbor a new group of oligotrophic 2,4-dichlorophenoxyacetic acid-degrading bacteria. <i>Applied and Environmental Microbiology</i> , 1997, 63, 2266-2272.	1.4	144
100	Cloning, Expression, and Characterization of a Minor Alkaline Protease from <i>Bacillus</i> sp. No. AH-101. <i>Bioscience, Biotechnology and Biochemistry</i> , 1992, 56, 510-511.	0.6	3
101	Degradation of Human Hair by a Thermostable Alkaline Protease from Alkaliphilic <i>Bacillus</i> sp. No. AH-101. <i>Bioscience, Biotechnology and Biochemistry</i> , 1992, 56, 1667-1669.	0.6	56
102	Molecular Cloning, Nucleotide Sequence, and Expression of the Structural Gene for Alkaline Serine Protease from Alkaliphilic <i>Bacillus</i> sp. 221. <i>Bioscience, Biotechnology and Biochemistry</i> , 1992, 56, 1455-1460.	0.6	17
103	Substrate Specificity of Thermostable Alkaline Protease from <i>Bacillus</i> sp. No. AH-101. <i>Bioscience, Biotechnology and Biochemistry</i> , 1992, 56, 333-334.	0.6	25
104	Molecular cloning, nucleotide sequence and expression of the structural gene for a thermostable alkaline protease from <i>Bacillus</i> sp. no. AH-101. <i>Applied Microbiology and Biotechnology</i> , 1992, 38, 101-8.	1.7	22
105	Characterization of an alkaline protease from <i>Bacillus</i> sp. no. AH-101. <i>Applied Microbiology and Biotechnology</i> , 1990, 33, 519-23.	1.7	56
106	Production of extremely thermostable alkaline protease from <i>Bacillus</i> sp. no. AH-101. <i>Applied Microbiology and Biotechnology</i> , 1989, 30, 120.	1.7	139
107	Classification of ascoideaceous yeasts based on the electrophoretic comparison of enzymes and coenzymes Q systems. <i>Journal of General and Applied Microbiology</i> , 1986, 32, 271-282.	0.4	9
108	Isolation and characterization of toluene-sensitive mutants from <i>Pseudomonas putida</i> IH-2000. , 0, .		1