

Hiroki Takahashi

List of Publications by Year in descending order

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73
papers

5,095
citations

218677

26
h-index

95266

68
g-index

83
all docs

83
docs citations

83
times ranked

8277
citing authors

#	ARTICLE	IF	CITATIONS
1	MassBank: a public repository for sharing mass spectral data for life sciences. <i>Journal of Mass Spectrometry</i> , 2010, 45, 703-714.	1.6	1,831
2	KNAPSAcK Family Databases: Integrated Metabolite-Plant Species Databases for Multifaceted Plant Research. <i>Plant and Cell Physiology</i> , 2012, 53, e1-e1.	3.1	529
3	Sequence-specific error profile of Illumina sequencers. <i>Nucleic Acids Research</i> , 2011, 39, e90-e90.	14.5	513
4	Cinnamoyl-CoA reductase, a key enzyme in lignin biosynthesis, is an effector of small GTPase Rac in defense signaling in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 230-235.	7.1	325
5	Activation of a Rac GTPase by the NLR Family Disease Resistance Protein Pit Plays a Critical Role in Rice Innate Immunity. <i>Cell Host and Microbe</i> , 2010, 7, 362-375.	11.0	138
6	Genome-wide binding profiles of the <i>Bacillus subtilis</i> transition state regulator AbrB and its homolog Abh reveals their interactive role in transcriptional regulation. <i>Nucleic Acids Research</i> , 2011, 39, 414-428.	14.5	115
7	Whole-Genome Comparison of <i>Aspergillus fumigatus</i> Strains Serially Isolated from Patients with Aspergillosis. <i>Journal of Clinical Microbiology</i> , 2014, 52, 4202-4209.	3.9	99
8	Metabolomics of Medicinal Plants: The Importance of Multivariate Analysis of Analytical Chemistry Data. <i>Current Computer-Aided Drug Design</i> , 2010, 6, 179-196.	1.2	96
9	Visualizing translocation dynamics and nascent transcript errors in paused RNA polymerases in vivo. <i>Genome Biology</i> , 2015, 16, 98.	8.8	82
10	Chromosome-level genome assembly of <i>Ophiorrhiza pumila</i> reveals the evolution of camptothecin biosynthesis. <i>Nature Communications</i> , 2021, 12, 405.	12.8	77
11	Metabolomics approach for determining growth-specific metabolites based on Fourier transform ion cyclotron resonance mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2008, 391, 2769-2782.	3.7	70
12	Non- <i>cyp51A</i> Azole-Resistant <i>Aspergillus fumigatus</i> Isolates with Mutation in HMG-CoA Reductase. <i>Emerging Infectious Diseases</i> , 2018, 24, 1889-1897.	4.3	68
13	Comparative transcriptome analysis revealing dormant conidia and germination associated genes in <i>Aspergillus</i> species: an essential role for AtfA in conidial dormancy. <i>BMC Genomics</i> , 2016, 17, 358.	2.8	67
14	RNA-seq Transcriptome Analysis of <i>Panax japonicus</i> , and Its Comparison with Other <i>Panax</i> Species to Identify Potential Genes Involved in the Saponins Biosynthesis. <i>Frontiers in Plant Science</i> , 2016, 7, 481.	3.6	62
15	<i>Staphylococcus</i> Agr virulence is critical for epidermal colonization and associates with atopic dermatitis development. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	62
16	Genome sequence comparison of <i>Aspergillus fumigatus</i> strains isolated from patients with pulmonary aspergilloma and chronic necrotizing pulmonary aspergillosis. <i>Medical Mycology</i> , 2015, 53, 353-360.	0.7	60
17	De novo transcriptome assembly and characterization of nine tissues of <i>Lonicera japonica</i> to identify potential candidate genes involved in chlorogenic acid, luteolins, and secoiridoid biosynthesis pathways. <i>Journal of Natural Medicines</i> , 2017, 71, 1-15.	2.3	60
18	Dynamic Transcriptional and Metabolic Responses in Yeast Adapting to Temperature Stress. <i>OMICS A Journal of Integrative Biology</i> , 2010, 14, 249-259.	2.0	53

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19	Nutritional Heterogeneity Among <i>Aspergillus fumigatus</i> Strains Has Consequences for Virulence in a Strain- and Host-Dependent Manner. <i>Frontiers in Microbiology</i> , 2019, 10, 854.	3.5	52
20	Functions of the Hha and YdgT Proteins in Transcriptional Silencing by the Nucleoid Proteins, H-NS and StpA, in <i>Escherichia coli</i> . <i>DNA Research</i> , 2013, 20, 263-271.	3.4	41
21	Multi-azole resistant <i>Aspergillus fumigatus</i> harboring Cyp51A TR46/Y121F/T289A isolated in Japan. <i>Journal of Infection and Chemotherapy</i> , 2016, 22, 577-579.	1.7	40
22	High-throughput sequencing and de novo transcriptome assembly of <i>Swertia japonica</i> to identify genes involved in the biosynthesis of therapeutic metabolites. <i>Plant Cell Reports</i> , 2016, 35, 2091-2111.	5.6	38
23	De Novo RNA Sequencing and Expression Analysis of <i>Aconitum carmichaelii</i> to Analyze Key Genes Involved in the Biosynthesis of Diterpene Alkaloids. <i>Molecules</i> , 2017, 22, 2155.	3.8	38
24	Transcription factor Aftmac1 controls copper import machinery in <i>Aspergillus fumigatus</i> . <i>Current Genetics</i> , 2017, 63, 777-789.	1.7	33
25	Prediction of operon-like gene clusters in the <i>Arabidopsis thaliana</i> genome based on co-expression analysis of neighboring genes. <i>Gene</i> , 2012, 503, 56-64.	2.2	30
26	Improved production of secreted heterologous enzyme in <i>Bacillus subtilis</i> strain MGB874 via modification of glutamate metabolism and growth conditions. <i>Microbial Cell Factories</i> , 2013, 12, 18.	4.0	29
27	<i>Aspergillus fumigatus</i> adhesion factors in dormant conidia revealed through comparative phenotypic and transcriptomic analyses. <i>Cellular Microbiology</i> , 2018, 20, e12802.	2.1	29
28	Dynamics of Time-Lagged Gene-to-Metabolite Networks of <i>Escherichia coli</i> Elucidated by Integrative Omics Approach. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 15-23.	2.0	28
29	Global gene expression reveals stress-responsive genes in <i>Aspergillus fumigatus</i> mycelia. <i>BMC Genomics</i> , 2017, 18, 942.	2.8	25
30	Transcriptome Analysis of Nine Tissues to Discover Genes Involved in the Biosynthesis of Active Ingredients in <i>Sophora flavescens</i> . <i>Biological and Pharmaceutical Bulletin</i> , 2015, 38, 876-883.	1.4	22
31	Fecal microbiota transplantation prevents <i>Candida albicans</i> from colonizing the gastrointestinal tract. <i>Microbiology and Immunology</i> , 2019, 63, 155-163.	1.4	22
32	Transcriptomic landscape of <i>Pueraria lobata</i> demonstrates potential for phytochemical study. <i>Frontiers in Plant Science</i> , 2015, 6, 426.	3.6	21
33	Ribosomal subunit protein typing using matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS) for the identification and discrimination of <i>Aspergillus</i> species. <i>BMC Microbiology</i> , 2017, 17, 100.	3.3	21
34	Assessment of transcriptional responses of <i>Bacillus subtilis</i> cells to the antibiotic enduracidin, which interferes with cell wall synthesis, using a high-density tiling chip. <i>Genes and Genetic Systems</i> , 2009, 84, 253-267.	0.7	20
35	Antisense Transcription Regulates the Expression of the Enterohemorrhagic <i>Escherichia coli</i> Virulence Regulatory Gene <i>ler</i> in Response to the Intracellular Iron Concentration. <i>PLoS ONE</i> , 2014, 9, e101582.	2.5	20
36	Draft Genome Sequence of the Pathogenic Filamentous Fungus <i>Aspergillus udagawae</i> Strain IFM 46973 T. <i>Genome Announcements</i> , 2015, 3, .	0.8	19

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37	The dynamic balance of import and export of zinc in <i>Escherichia coli</i> suggests a heterogeneous population response to stress. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20150069.	3.4	19
38	Clinical and Bacteriologic Analysis of Nontypeable <i>Haemophilus influenzae</i> Strains Isolated from Children with Invasive Diseases in Japan from 2008 to 2015. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	19
39	Draft Genome Sequence of the Pathogenic Filamentous Fungus <i>Aspergillus lentulus</i> IFM 54703 T. <i>Genome Announcements</i> , 2016, 4, .	0.8	18
40	Metabolomic characterization of the possible involvement of a Cytochrome P450, CYP81F4, in the biosynthesis of indolic glucosinolate in <i>Arabidopsis</i> . <i>Plant Biotechnology</i> , 2011, 28, 379-385.	1.0	17
41	AMDORAP: Non-targeted metabolic profiling based on high-resolution LC-MS. <i>BMC Bioinformatics</i> , 2011, 12, 259.	2.6	16
42	Comparative genome analysis of <i>Aspergillus flavus</i> clinically isolated in Japan. <i>DNA Research</i> , 2019, 26, 95-103.	3.4	11
43	Efficacy Prediction of Jamu Formulations by PLS Modeling. <i>Current Computer-Aided Drug Design</i> , 2013, 9, 46-59.	1.2	11
44	Genetic differences between Japan and other countries in <i>cyp51A</i> polymorphisms of <i>Aspergillus fumigatus</i> . <i>Mycoses</i> , 2021, 64, 1354-1365.	4.0	10
45	System Biology Approach for Elucidating the Relationship Between Indonesian Herbal Plants and the Efficacy of Jamu. , 2010, , .		9
46	Emerging Antifungal Drug Resistance in <i>Aspergillus fumigatus</i> and Among Other Species of <i>Aspergillus</i> . <i>Current Fungal Infection Reports</i> , 2018, 12, 105-111.	2.6	9
47	An approach to peak detection in GC-MS chromatograms and application of KNApSAcK database in prediction of candidate metabolites. <i>Plant Biotechnology</i> , 2009, 26, 167-174.	1.0	9
48	Metabolic pathway prediction based on inclusive relation between cyclic substructures. <i>Plant Biotechnology</i> , 2009, 26, 459-468.	1.0	9
49	Systems Biology Approaches and Metabolomics for Understanding Japanese Traditional Kampo Medicine. <i>Current Pharmacogenomics and Personalized Medicine</i> , 2012, 10, 111-124.	0.2	8
50	Control of transcriptional pausing by biased thermal fluctuations on repetitive genomic sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7409-E7417.	7.1	8
51	Heterogeneity in Pathogenicity-related Properties and Stress Tolerance in <i>Aspergillus fumigatus</i> Clinical Isolates. <i>Medical Mycology Journal</i> , 2018, 59, E63-E70.	1.4	7
52	Draft Genome Sequence of <i>Aspergillus tubingensis</i> WU-2223L, a Citric Acid-Producing Filamentous Fungus Belonging to <i>Aspergillus</i> Section <i>Nigri</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	7
53	Intimate genetic relationships and fungicide resistance in multiple strains of <i>Aspergillus fumigatus</i> isolated from a plant bulb. <i>Environmental Microbiology</i> , 2021, 23, 5621-5638.	3.8	7
54	Isolation of Nabscessin C from <i>Nocardia abscessus</i> IFM 10029 and a Study on Biosynthetic Pathway for Nabscessins. <i>Chemical and Pharmaceutical Bulletin</i> , 2018, 66, 976-982.	1.3	6

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55	Control of Transcription Initiation by Biased Thermal Fluctuations on Repetitive Genomic Sequences. <i>Biomolecules</i> , 2020, 10, 1299.	4.0	6
56	Identification of Novel Mutations Contributing to Azole Tolerance of <i>Aspergillus fumigatus</i> through <i>In Vitro</i> Exposure to Tebuconazole. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0265720.	3.2	6
57	MetalMine: a database of functional metal-binding sites in proteins. <i>Plant Biotechnology</i> , 2009, 26, 517-521.	1.0	5
58	Human EP2 prostanoid receptors exhibit more constraints to mutations than human DP prostanoid receptors. <i>FEBS Letters</i> , 2015, 589, 766-772.	2.8	5
59	Dlpartite: A tool for detecting bipartite motifs by considering base interdependencies. <i>PLoS ONE</i> , 2019, 14, e0220207.	2.5	5
60	Draft Genome Sequence of <i>Aspergillus awamori</i> IFM 58123 ^{NT} . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	5
61	Interspecies Genomic Variation and Transcriptional Activeness of Secondary Metabolism-Related Genes in <i>Aspergillus Section Fumigati</i> . <i>Frontiers in Fungal Biology</i> , 2021, 2, .	2.0	5
62	DrEFTIR: The data mining software for fourier transform near-infrared reflectance spectroscopy focused on food metabolic finger printing. <i>Plant Biotechnology</i> , 2009, 26, 451-457.	1.0	5
63	Draft Genome Sequences of Five <i>Cystobasidium ongulense</i> Strains Isolated from Areas near Syowa Station, East Antarctica. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.6	4
64	KNAPSAck gene classification system for <i>Arabidopsis thaliana</i> : Comparative genomic analysis of unicellular to seed plants. <i>Plant Biotechnology</i> , 2009, 26, 509-516.	1.0	3
65	Low complexity Fourier Transform using double square-waves. , 2007, , .		2
66	MEIS3 is repressed in A549 lung epithelial cells by deoxynivalenol and the repression contributes to the deleterious effect. <i>Journal of Toxicological Sciences</i> , 2016, 41, 25-31.	1.5	1
67	Discrepancy between Hepatitis C Virus Genotypes and NS4-Based Serotypes: Association with Their Subgenomic Sequences. <i>International Journal of Molecular Sciences</i> , 2017, 18, 172.	4.1	1
68	Isolation and Characterization of the Polyhexamethylene Biguanide Hydrochloride-Resistant Fungus, <i>Purpureocillium lilacinum</i> . <i>Biocontrol Science</i> , 2021, 26, 157-166.	0.8	1
69	The complete chloroplast genome of <i>Abutilon theophrasti</i> medic (Malvaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 912-913.	0.4	1
70	Predicting conformation of protein complexes by determining statistically significant domain-domain interactions. <i>Plant Biotechnology</i> , 2009, 26, 495-501.	1.0	1
71	Protein function prediction based on k-cores of interaction networks. , 2010, , .		0
72	Direct Assessment of Transcription Fidelity by RNA Sequencing. <i>Biophysical Journal</i> , 2014, 106, 486a.	0.5	0

#	ARTICLE	IF	CITATIONS
73	is conserved between and psychrophilic, polar-collected fungi. MicroPublication Biology, 2021, 2021, .	0.1	0