

# 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	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
2	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
3	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
4	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
5	Interspecies Genomic Variation and Transcriptional Activeness of Secondary Metabolism-Related Genes in <i>Aspergillus</i> Section <i>Fumigati</i> . <i>Frontiers in Fungal Biology</i> , 2021, 2, .	2.0	5
6	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
7	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
8	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
9	is conserved between and psychrophilic, polar-collected fungi. <i>MicroPublication Biology</i> , 2021, 2021, .	0.1	0
10	Control of Transcription Initiation by Biased Thermal Fluctuations on Repetitive Genomic Sequences. <i>Biomolecules</i> , 2020, 10, 1299.	4.0	6
11	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
12	<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
13	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
14	Dipartite: A tool for detecting bipartite motifs by considering base interdependencies. <i>PLoS ONE</i> , 2019, 14, e0220207.	2.5	5
15	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
16	Draft Genome Sequence of <i>Aspergillus awamori</i> IFM 58123 <sup>NT</sup> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	5
17	Comparative genome analysis of <i>Aspergillus flavus</i> clinically isolated in Japan. <i>DNA Research</i> , 2019, 26, 95-103.	3.4	11
18	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

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19	<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
20	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
21	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
22	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
23	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
24	Transcription factor Aftac1 controls copper import machinery in <i>Aspergillus fumigatus</i> . <i>Current Genetics</i> , 2017, 63, 777-789.	1.7	33
25	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
26	De novo transcriptome assembly and characterization of nine tissues of <i>Lonicera japonica</i> to identify potential candidate genes involved in chlorogenic acid, luteolosides, and secoiridoid biosynthesis pathways. <i>Journal of Natural Medicines</i> , 2017, 71, 1-15.	2.3	60
27	Global gene expression reveals stress-responsive genes in <i>Aspergillus fumigatus</i> mycelia. <i>BMC Genomics</i> , 2017, 18, 942.	2.8	25
28	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
29	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
30	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
31	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
32	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
33	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
34	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
35	Draft Genome Sequence of the Pathogenic Filamentous Fungus <i>Aspergillus lentulus</i> IFM 54703 T. <i>Genome Announcements</i> , 2016, 4, .	0.8	18
36	Multi-azole resistant <i>Aspergillus fumigatus</i> harboring <i>Cyp51A</i> TR46/Y121F/T289A isolated in Japan. <i>Journal of Infection and Chemotherapy</i> , 2016, 22, 577-579.	1.7	40

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37	Transcriptome Analysis of Nine Tissues to Discover Genes Involved in the Biosynthesis of Active Ingredients in <i>Sophora flavescens</i> . Biological and Pharmaceutical Bulletin, 2015, 38, 876-883.	1.4	22
38	Visualizing translocation dynamics and nascent transcript errors in paused RNA polymerases in vivo. Genome Biology, 2015, 16, 98.	8.8	82
39	Transcriptomic landscape of <i>Pueraria lobata</i> demonstrates potential for phytochemical study. Frontiers in Plant Science, 2015, 6, 426.	3.6	21
40	Draft Genome Sequence of the Pathogenic Filamentous Fungus <i>Aspergillus udagawae</i> Strain IFM 46973 T. Genome Announcements, 2015, 3, .	0.8	19
41	Human EP2 prostanoid receptors exhibit more constraints to mutations than human DP prostanoid receptors. FEBS Letters, 2015, 589, 766-772.	2.8	5
42	The dynamic balance of import and export of zinc in <i>Escherichia coli</i> suggests a heterogeneous population response to stress. Journal of the Royal Society Interface, 2015, 12, 20150069.	3.4	19
43	Genome sequence comparison of <i>Aspergillus fumigatus</i> strains isolated from patients with pulmonary aspergilloma and chronic necrotizing pulmonary aspergillosis. Medical Mycology, 2015, 53, 353-360.	0.7	60
44	Whole-Genome Comparison of <i>Aspergillus fumigatus</i> Strains Serially Isolated from Patients with Aspergillosis. Journal of Clinical Microbiology, 2014, 52, 4202-4209.	3.9	99
45	Direct Assessment of Transcription Fidelity by RNA Sequencing. Biophysical Journal, 2014, 106, 486a.	0.5	0
46	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. PLoS ONE, 2014, 9, e101582.	2.5	20
47	Improved production of secreted heterologous enzyme in <i>Bacillus subtilis</i> strain MGB874 via modification of glutamate metabolism and growth conditions. Microbial Cell Factories, 2013, 12, 18.	4.0	29
48	Functions of the Hha and YdgT Proteins in Transcriptional Silencing by the Nucleoid Proteins, H-NS and StpA, in <i>Escherichia coli</i> . DNA Research, 2013, 20, 263-271.	3.4	41
49	Efficacy Prediction of Jamu Formulations by PLS Modeling. Current Computer-Aided Drug Design, 2013, 9, 46-59.	1.2	11
50	KNAPSAcK Family Databases: Integrated Metabolite-Plant Species Databases for Multifaceted Plant Research. Plant and Cell Physiology, 2012, 53, e1-e1.	3.1	529
51	Systems Biology Approaches and Metabolomics for Understanding Japanese Traditional Kampo Medicine. Current Pharmacogenomics and Personalized Medicine, 2012, 10, 111-124.	0.2	8
52	Prediction of operon-like gene clusters in the <i>Arabidopsis thaliana</i> genome based on co-expression analysis of neighboring genes. Gene, 2012, 503, 56-64.	2.2	30
53	Metabolomic characterization of the possible involvement of a Cytochrome P450, CYP81F4, in the biosynthesis of indolic glucosinolate in <i>Arabidopsis</i> . Plant Biotechnology, 2011, 28, 379-385.	1.0	17
54	AMDORAP: Non-targeted metabolic profiling based on high-resolution LC-MS. BMC Bioinformatics, 2011, 12, 259.	2.6	16

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55	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
56	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
57	Sequence-specific error profile of Illumina sequencers. <i>Nucleic Acids Research</i> , 2011, 39, e90-e90.	14.5	513
58	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
59	Protein function prediction based on k-cores of interaction networks. , 2010, , .		0
60	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
61	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
62	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
63	System Biology Approach for Elucidating the Relationship Between Indonesian Herbal Plants and the Efficacy of Jamu. , 2010, , .		9
64	MetalMine: a database of functional metal-binding sites in proteins. <i>Plant Biotechnology</i> , 2009, 26, 517-521.	1.0	5
65	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
66	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
67	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
68	Metabolic pathway prediction based on inclusive relation between cyclic substructures. <i>Plant Biotechnology</i> , 2009, 26, 459-468.	1.0	9
69	Predicting conformation of protein complexes by determining statistically significant domain-domain interactions. <i>Plant Biotechnology</i> , 2009, 26, 495-501.	1.0	1
70	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
71	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
72	Low complexity Fourier Transform using double square-waves. , 2007, , .		2

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73	Cinnamoyl-CoA reductase, a key enzyme in lignin biosynthesis, is an effector of small GTPase Rac in defense signaling in rice. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 230-235.	7.1	325