

# Hiro Takahashi

## List of Publications by Year in descending order

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Version: 2024-02-01

62  
papers

1,341  
citations

331670

21  
h-index

377865

34  
g-index

65  
all docs

65  
docs citations

65  
times ranked

1804  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene expression analysis of soft tissue sarcomas: characterization and reclassification of malignant fibrous histiocytoma. <i>Modern Pathology</i> , 2007, 20, 749-759.	5.5	155
2	Dual regulation of <i>ETTIN</i> ( <i>ARF3</i> ) gene expression by AS1-AS2, which maintains the DNA methylation level, is involved in stabilization of leaf adaxial-abaxial partitioning in <i>Arabidopsis</i> . <i>Development</i> (Cambridge), 2013, 140, 1958-1969.	2.5	91
3	The complex of <i>ASYMMETRIC LEAVES</i> ( <i>AS</i> ) proteins plays a central role in antagonistic interactions of genes for leaf polarity specification in <i>Arabidopsis</i> . <i>Wiley Interdisciplinary Reviews: Developmental Biology</i> , 2015, 4, 655-671.	5.9	68
4	Identification of novel <i>Arabidopsis thaliana</i> upstream open reading frames that control expression of the main coding sequences in a peptide sequence-dependent manner. <i>Nucleic Acids Research</i> , 2015, 43, 1562-1576.	14.5	61
5	BAIUCAS: a novel BLAST-based algorithm for the identification of upstream open reading frames with conserved amino acid sequences and its application to the <i>Arabidopsis thaliana</i> genome. <i>Bioinformatics</i> , 2012, 28, 2231-2241.	4.1	60
6	ASYMMETRIC LEAVES2 and Elongator, a Histone Acetyltransferase Complex, Mediate the Establishment of Polarity in Leaves of <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2011, 52, 1259-1273.	3.1	55
7	Changes in mRNA Stability Associated with Cold Stress in <i>Arabidopsis</i> Cells. <i>Plant and Cell Physiology</i> , 2013, 54, 180-194.	3.1	49
8	High expression of EVI1 and MEL1 is a compelling poor prognostic marker of pediatric AML. <i>Leukemia</i> , 2015, 29, 1076-1083.	7.2	42
9	A genetic link between epigenetic repressor AS1-AS2 and a putative small subunit processome in leaf polarity establishment of <i>Arabidopsis</i> . <i>Biology Open</i> , 2016, 5, 942-954.	1.2	38
10	Analysis of Gene Expression Profiles of Soft Tissue Sarcoma Using a Combination of Knowledge-Based Filtering with Integration of Multiple Statistics. <i>PLoS ONE</i> , 2014, 9, e106801.	2.5	33
11	Discovery of novel rules for G-quadruplex-forming sequences in plants by using bioinformatics methods. <i>Journal of Bioscience and Bioengineering</i> , 2012, 114, 570-575.	2.2	32
12	Patient-derived xenograft models of non-small cell lung cancer for evaluating targeted drug sensitivity and resistance. <i>Cancer Science</i> , 2019, 110, 3215-3224.	3.9	32
13	Identification of ENHANCER OF SHOOT REGENERATION 1-upregulated genes during in vitro shoot regeneration. <i>Plant Biotechnology</i> , 2009, 26, 385-393.	1.0	31
14	Identification of Alternative Splicing Events Regulated by an <i>Arabidopsis</i> Serine/Arginine-Like Protein, atSR45a, in Response to High-Light Stress using a Tiling Array. <i>Plant and Cell Physiology</i> , 2011, 52, 1786-1805.	3.1	29
15	Forkhead box A1 transcriptional pathway in KRT7-expressing esophageal squamous cell carcinomas with extensive lymph node metastasis. <i>International Journal of Oncology</i> , 2010, 36, 321-30.	3.9	29
16	Cancer diagnosis marker extraction for soft tissue sarcomas based on gene expression profiling data by using projective adaptive resonance theory (PART) filtering method. <i>BMC Bioinformatics</i> , 2006, 7, 399.	2.6	28
17	Identification of <i>Arabidopsis thaliana</i> upstream open reading frames encoding peptide sequences that cause ribosomal arrest. <i>Nucleic Acids Research</i> , 2017, 45, 8844-8858.	14.5	28
18	Construction of robust prognostic predictors by using projective adaptive resonance theory as a gene filtering method. <i>Bioinformatics</i> , 2005, 21, 179-186.	4.1	27

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19	Prognostic predictor with multiple fuzzy neural models using expression profiles from DNA microarray for metastases of breast cancer. <i>Journal of Bioscience and Bioengineering</i> , 2004, 98, 193-199.	2.2	25
20	Meta-Analyses of Microarrays of Arabidopsis asymmetric leaves1 (as1), as2 and Their Modifying Mutants Reveal a Critical Role for the ETT Pathway in Stabilization of Adaxialâ€Abaxial Patterning and Cell Division During Leaf Development. <i>Plant and Cell Physiology</i> , 2013, 54, 418-431.	3.1	24
21	Forkhead box A1 transcriptional pathway in KRT7-expressing esophageal squamous cell carcinomas with extensive lymph node metastasis. <i>International Journal of Oncology</i> , 2009, 36, .	3.3	22
22	Knowledge-based Fuzzy Adaptive Resonance Theory and Its Application to the Analysis of Gene Expression in Plants. <i>Journal of Bioscience and Bioengineering</i> , 2008, 106, 587-593.	2.2	21
23	A New Reliable Cancer Diagnosis Method Using Boosted Fuzzy Classifier with a SWEEP Operator Method. <i>Journal of Chemical Engineering of Japan</i> , 2005, 38, 763-773.	0.6	20
24	Inference of common genetic network using fuzzy adaptive resonance theory associated matrix method. <i>Journal of Bioscience and Bioengineering</i> , 2003, 96, 154-160.	2.2	19
25	Arabidopsis Zinc-Finger-Like Protein ASYMMETRIC LEAVES2 (AS2) and Two Nucleolar Proteins Maintain Gene Body DNA Methylation in the Leaf Polarity Gene ETTIN (ARF3). <i>Plant and Cell Physiology</i> , 2018, 59, 1385-1397.	3.1	19
26	Prediction of peptide binding to major histocompatibility complex class II molecules through use of boosted fuzzy classifier with SWEEP operator method. <i>Journal of Bioscience and Bioengineering</i> , 2006, 101, 137-141.	2.2	17
27	Reduced GNG2 expression levels in mouse malignant melanomas and human melanoma cell lines. <i>American Journal of Cancer Research</i> , 2012, 2, 322-9.	1.4	17
28	New cancer diagnosis modeling using boosting and projective adaptive resonance theory with improved reliable index. <i>Biochemical Engineering Journal</i> , 2007, 33, 100-109.	3.6	16
29	Berberine enhances defects in the establishment of leaf polarity in asymmetric leaves1 and asymmetric leaves2 of Arabidopsis thaliana. <i>Plant Molecular Biology</i> , 2012, 79, 569-581.	3.9	16
30	Classification of intramural metastases and lymph node metastases of esophageal cancer from gene expression based on boosting and projective adaptive resonance theory. <i>Journal of Bioscience and Bioengineering</i> , 2006, 102, 46-52.	2.2	15
31	Comprehensive genome-wide identification of angiosperm upstream ORFs with peptide sequences conserved in various taxonomic ranges using a novel pipeline, ESUCA. <i>BMC Genomics</i> , 2020, 21, 260.	2.8	14
32	Loss-of-function of an Arabidopsis NADPH pyrophosphohydrolase, AtNUDX19, impacts on the pyridine nucleotides status and confers photooxidative stress tolerance. <i>Scientific Reports</i> , 2016, 6, 37432.	3.3	13
33	Addition of ascorbic acid to the extracellular environment activates lipoplexes of a ferrocenyl lipid and promotes cell transfection. <i>Journal of Controlled Release</i> , 2012, 157, 249-259.	9.9	12
34	The formation of perinucleolar bodies is important for normal leaf development and requires the zincâ€finger DNAâ€binding motif in Arabidopsis ASYMMETRIC LEAVES2. <i>Plant Journal</i> , 2020, 101, 1118-1134.	5.7	12
35	Roles of ASYMMETRIC LEAVES2 (AS2) and Nucleolar Proteins in the Adaxialâ€Abaxial Polarity Specification at the Perinucleolar Region in Arabidopsis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7314.	4.1	12
36	Macrophage Migration Inhibitory Factor and Stearoyl-CoA Desaturase 1: Potential Prognostic Markers for Soft Tissue Sarcomas Based on Bioinformatics Analyses. <i>PLoS ONE</i> , 2013, 8, e78250.	2.5	12

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37	Construction of possible integrated predictive index based on EGFR and ANXA3 polymorphisms for chemotherapy response in fluoropyrimidine-treated Japanese gastric cancer patients using a bioinformatic method. BMC Cancer, 2015, 15, 718.	2.6	11
38	Lymphoma Prognostication from Expression Profiling Using a Combination Method of Boosting and Projective Adaptive Resonance Theory. Journal of Chemical Engineering of Japan, 2006, 39, 767-771.	0.6	11
39	Proposal of new gene filtering method, BagPART, for gene expression analysis with small sample. Journal of Bioscience and Bioengineering, 2008, 105, 81-84.	2.2	10
40	Zebrafish behavior feature recognition using three-dimensional tracking and machine learning. Scientific Reports, 2021, 11, 13492.	3.3	10
41	Modified signal-to-noise: a new simple and practical gene filtering approach based on the concept of projective adaptive resonance theory (PART) filtering method. Bioinformatics, 2006, 22, 1662-1664.	4.1	9
42	An upstream open reading frame represses expression of a tomato homologue of Arabidopsis <i>ANAC096</i> , a NAC domain transcription factor gene, in a peptide sequence-dependent manner. Plant Biotechnology, 2015, 32, 157-163.	1.0	9
43	Identification of a candidate single-nucleotide polymorphism related to chemotherapeutic response through a combination of knowledge-based algorithm and hypothesis-free genomic data. Journal of Bioscience and Bioengineering, 2013, 116, 768-773.	2.2	8
44	Excess sterols disrupt plant cellular activity by inducing stress-responsive gene expression. Journal of Plant Research, 2020, 133, 383-392.	2.4	8
45	Inference of common genetic network using fuzzy adaptive resonance theory associated matrix method. Journal of Bioscience and Bioengineering, 2003, 96, 154-60.	2.2	8
46	TBP-like Protein (TLP) Disrupts the p53-MDM2 Interaction and Induces Long-lasting p53 Activation. Journal of Biological Chemistry, 2017, 292, 3201-3212.	3.4	7
47	Control of Dual Stimuli-Responsive Vesicle Formation in Aqueous Solutions of Single-Tailed Ferrocenyl Surfactant by Varying pH and Redox Conditions. Journal of Oleo Science, 2014, 63, 239-248.	1.4	6
48	Exhaustive identification of conserved upstream open reading frames with potential translational regulatory functions from animal genomes. Scientific Reports, 2020, 10, 16289.	3.3	6
49	Predictive value of high-molecular weight adiponectin in subjects with a higher risk of the development of metabolic syndrome: From a population based 5-year follow-up data. International Journal of Cardiology, 2013, 167, 1068-1070.	1.7	5
50	Application of a Combination of a Knowledge-Based Algorithm and 2-Stage Screening to Hypothesis-Free Genomic Data on Irinotecan-Treated Patients for Identification of a Candidate Single Nucleotide Polymorphism Related to an Adverse Effect. PLoS ONE, 2014, 9, e105160.	2.5	5
51	Draft Genome Sequence of Aspergillus terreus High-Itaconic-Acid-Productivity Mutant TN-484. Microbiology Resource Announcements, 2019, 8, .	0.6	5
52	Computational studies on nonenzymatic succinimide-formation mechanisms of the aspartic acid residues catalyzed by two water molecules. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2020, 1868, 140459.	2.3	5
53	Draft Genome Sequence of the Aspergillus terreus High-Itaconic-Acid-Productivity Strain IFO6365. Microbiology Resource Announcements, 2020, 9, .	0.6	4
54	Draft Genome Sequence of Trebouxiophyceae sp. Strain KSI-1, Isolated from an Island Hot Spring. Microbiology Resource Announcements, 2018, 7, .	0.6	3

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55	Draft Genome Sequence of <i>Saccharomyces cerevisiae</i> Strain Hm-1, Isolated from Cotton Rosemallow. Microbiology Resource Announcements, 2018, 7, .	0.6	3
56	Draft Genome Sequence of Glycoside Hydrolase-Producing <i>Trichoderma asperellum</i> Strain IC-1. Microbiology Resource Announcements, 2020, 9, .	0.6	3
57	Correlated expression levels of endothelin receptor B and Plexin C1 in melanoma. American Journal of Cancer Research, 2015, 5, 1117-23.	1.4	3
58	Is chloroplastic class IIA aldolase a marine enzyme?. ISME Journal, 2016, 10, 2767-2772.	9.8	2
59	Draft Genome Sequence of <i>Saccharomyces cerevisiae</i> Strain Pf-1, Isolated from <i>Prunus mume</i> . Microbiology Resource Announcements, 2019, 8, .	0.6	2
60	SIMON: Simple methods for analyzing DNA methylation by targeted bisulfite next-generation sequencing. Plant Biotechnology, 2019, 36, 213-222.	1.0	2
61	Draft Genome Sequence of <i>Saccharomyces cerevisiae</i> Strain P-684, Isolated from <i>Prunus verecunda</i> . Microbiology Resource Announcements, 2020, 9, .	0.6	1
62	Draft Genome Sequence of NYR20, a Red Pigment-Secreting Mutant of <i>Saccharomyces cerevisiae</i> . Microbiology Resource Announcements, 2021, 10, .	0.6	0