

Hiro Takahashi

List of Publications by Year in descending order

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62
papers

1,341
citations

331259

21
h-index

377514

34
g-index

65
all docs

65
docs citations

65
times ranked

1804
citing authors

#	ARTICLE	IF	CITATIONS
1	Draft Genome Sequence of NYR20, a Red Pigment-Secreting Mutant of <i>Saccharomyces cerevisiae</i> . <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
2	Zebrafish behavior feature recognition using three-dimensional tracking and machine learning. <i>Scientific Reports</i> , 2021, 11, 13492.	1.6	10
3	The formation of perinucleolar bodies is important for normal leaf development and requires the zinc-finger DNA-binding motif in <i>Arabidopsis</i> ASYMMETRIC LEAVES2. <i>Plant Journal</i> , 2020, 101, 1118-1134.	2.8	12
4	Draft Genome Sequence of <i>Saccharomyces cerevisiae</i> Strain P-684, Isolated from <i>Prunus verecunda</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
5	Exhaustive identification of conserved upstream open reading frames with potential translational regulatory functions from animal genomes. <i>Scientific Reports</i> , 2020, 10, 16289.	1.6	6
6	Draft Genome Sequence of Glycoside Hydrolase-Producing <i>Trichoderma asperellum</i> Strain IC-1. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
7	Roles of ASYMMETRIC LEAVES2 (AS2) and Nucleolar Proteins in the Adaxial-Abaxial Polarity Specification at the Perinucleolar Region in <i>Arabidopsis</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 7314.	1.8	12
8	Excess sterols disrupt plant cellular activity by inducing stress-responsive gene expression. <i>Journal of Plant Research</i> , 2020, 133, 383-392.	1.2	8
9	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.	1.2	14
10	Computational studies on nonenzymatic succinimide-formation mechanisms of the aspartic acid residues catalyzed by two water molecules. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020, 1868, 140459.	1.1	5
11	Draft Genome Sequence of the <i>Aspergillus terreus</i> High-Itaconic-Acid-Productivity Strain IFO6365. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
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.	1.7	32
13	Draft Genome Sequence of <i>Saccharomyces cerevisiae</i> Strain Pf-1, Isolated from <i>Prunus mume</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
14	Draft Genome Sequence of <i>Aspergillus terreus</i> High-Itaconic-Acid-Productivity Mutant TN-484. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
15	SIMON: Simple methods for analyzing DNA methylation by targeted bisulfite next-generation sequencing. <i>Plant Biotechnology</i> , 2019, 36, 213-222.	0.5	2
16	<i>Arabidopsis</i> 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.	1.5	19
17	Draft Genome Sequence of <i>Trebouxiophyceae</i> sp. Strain KSI-1, Isolated from an Island Hot Spring. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	3
18	Draft Genome Sequence of <i>Saccharomyces cerevisiae</i> Strain Hm-1, Isolated from Cotton Rosemallow. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	3

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19	TBP-like Protein (TLP) Disrupts the p53-MDM2 Interaction and Induces Long-lasting p53 Activation. <i>Journal of Biological Chemistry</i> , 2017, 292, 3201-3212.	1.6	7
20	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.	6.5	28
21	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.	0.6	38
22	Is chloroplastic class IIA aldolase a marine enzyme?. <i>ISME Journal</i> , 2016, 10, 2767-2772.	4.4	2
23	Loss-of-function of an <i>Arabidopsis</i> NADPH pyrophosphohydrolase, AtNUDX19, impacts on the pyridine nucleotides status and confers photooxidative stress tolerance. <i>Scientific Reports</i> , 2016, 6, 37432.	1.6	13
24	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. <i>BMC Cancer</i> , 2015, 15, 718.	1.1	11
25	The complex of <sc>ASYMMETRIC LEAVES</sc> (<sc>AS</sc>) 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
26	An upstream open reading frame represses expression of a tomato homologue of <i>Arabidopsis</i> <i>ANACO96</i>, a NAC domain transcription factor gene, in a peptide sequence-dependent manner. <i>Plant Biotechnology</i> , 2015, 32, 157-163.	0.5	9
27	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.	6.5	61
28	High expression of EVI1 and MEL1 is a compelling poor prognostic marker of pediatric AML. <i>Leukemia</i> , 2015, 29, 1076-1083.	3.3	42
29	Correlated expression levels of endothelin receptor B and Plexin C1 in melanoma. <i>American Journal of Cancer Research</i> , 2015, 5, 1117-23.	1.4	3
30	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. <i>PLoS ONE</i> , 2014, 9, e105160.	1.1	5
31	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.	1.1	33
32	Control of Dual Stimuli-Responsive Vesicle Formation in Aqueous Solutions of Single-Tailed Ferrocenyl Surfactant by Varying pH and Redox Conditions. <i>Journal of Oleo Science</i> , 2014, 63, 239-248.	0.6	6
33	Identification of a candidate single-nucleotide polymorphism related to chemotherapeutic response through a combination of knowledge-based algorithm and hypothesis-free genomic data. <i>Journal of Bioscience and Bioengineering</i> , 2013, 116, 768-773.	1.1	8
34	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 (Cambridge)</i> , 2013, 140, 1958-1969.	1.2	91
35	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. <i>International Journal of Cardiology</i> , 2013, 167, 1068-1070.	0.8	5
36	Changes in mRNA Stability Associated with Cold Stress in <i>Arabidopsis</i> Cells. <i>Plant and Cell Physiology</i> , 2013, 54, 180-194.	1.5	49

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37	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.	1.5	24
38	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.	1.1	12
39	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.	1.8	60
40	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.	2.0	16
41	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.	1.1	32
42	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.	4.8	12
43	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
44	Identification of Alternative Splicing Events Regulated by an Arabidopsis 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.	1.5	29
45	ASYMMETRIC LEAVES2 and Elongator, a Histone Acetyltransferase Complex, Mediate the Establishment of Polarity in Leaves of Arabidopsis thaliana. <i>Plant and Cell Physiology</i> , 2011, 52, 1259-1273.	1.5	55
46	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
47	Identification of ENHANCER OF SHOOT REGENERATION 1-upregulated genes during in vitro shoot regeneration. <i>Plant Biotechnology</i> , 2009, 26, 385-393.	0.5	31
48	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, .	1.4	22
49	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.	1.1	21
50	Proposal of new gene filtering method, BagPART, for gene expression analysis with small sample. <i>Journal of Bioscience and Bioengineering</i> , 2008, 105, 81-84.	1.1	10
51	New cancer diagnosis modeling using boosting and projective adaptive resonance theory with improved reliable index. <i>Biochemical Engineering Journal</i> , 2007, 33, 100-109.	1.8	16
52	Gene expression analysis of soft tissue sarcomas: characterization and reclassification of malignant fibrous histiocytoma. <i>Modern Pathology</i> , 2007, 20, 749-759.	2.9	155
53	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.	1.1	17
54	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.	1.1	15

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55	Cancer diagnosis marker extraction for soft tissue sarcomas based on gene expression profiling data by using projective adaptive resonance theory (PART) filtering method. BMC Bioinformatics, 2006, 7, 399.	1.2	28
56	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.	1.8	9
57	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.	0.3	11
58	Construction of robust prognostic predictors by using projective adaptive resonance theory as a gene filtering method. Bioinformatics, 2005, 21, 179-186.	1.8	27
59	A New Reliable Cancer Diagnosis Method Using Boosted Fuzzy Classifier with a SWEEP Operator Method. Journal of Chemical Engineering of Japan, 2005, 38, 763-773.	0.3	20
60	Prognostic predictor with multiple fuzzy neural models using expression profiles from DNA microarray for metastases of breast cancer. Journal of Bioscience and Bioengineering, 2004, 98, 193-199.	1.1	25
61	Inference of common genetic network using fuzzy adaptive resonance theory associated matrix method. Journal of Bioscience and Bioengineering, 2003, 96, 154-160.	1.1	19
62	Inference of common genetic network using fuzzy adaptive resonance theory associated matrix method. Journal of Bioscience and Bioengineering, 2003, 96, 154-60.	1.1	8