

# Hideki Takanashi

## List of Publications by Year in descending order

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Version: 2024-02-01

25  
papers

599  
citations

840776

11  
h-index

794594

19  
g-index

26  
all docs

26  
docs citations

26  
times ranked

873  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic Prediction of Green Fraction Dynamics in Soybean Using Unmanned Aerial Vehicles Observations. <i>Frontiers in Plant Science</i> , 2022, 13, 828864.	3.6	9
2	Sorghum Ionomics Reveals the Functional <i>SbHMA3a</i> Allele that Limits Excess Cadmium Accumulation in Grains. <i>Plant and Cell Physiology</i> , 2022, 63, 713-728.	3.1	6
3	<i>DOMINANT AWN INHIBITOR</i> Encodes the ALOG Protein Originating from Gene Duplication and Inhibits AWN Elongation by Suppressing Cell Proliferation and Elongation in Sorghum. <i>Plant and Cell Physiology</i> , 2022, 63, 901-918.	3.1	6
4	Spatial kernel models capturing field heterogeneity for accurate estimation of genetic potential. <i>Breeding Science</i> , 2021, 71, 444-455.	1.9	0
5	Genetic dissection of QTLs associated with spikelet-related traits and grain size in sorghum. <i>Scientific Reports</i> , 2021, 11, 9398.	3.3	8
6	Targeted base editing in the plastid genome of <i>Arabidopsis thaliana</i> . <i>Nature Plants</i> , 2021, 7, 906-913.	9.3	62
7	NB-LRR-encoding genes conferring susceptibility to organophosphate pesticides in sorghum. <i>Scientific Reports</i> , 2021, 11, 19828.	3.3	5
8	Targeted gene disruption of <i>ATP synthases 6â€1</i> and <i>6â€2</i> in the mitochondrial genome of <i>Arabidopsis thaliana</i> by mitoTALENs. <i>Plant Journal</i> , 2020, 104, 1459-1471.	5.7	57
9	Dissecting the Genetic Architecture of Biofuel-Related Traits in a Sorghum Breeding Population. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 4565-4577.	1.8	2
10	RAD-seq-Based High-Density Linkage Map Construction and QTL Mapping of Biomass-Related Traits in Sorghum using the Japanese Landrace Takakibi NOG. <i>Plant and Cell Physiology</i> , 2020, 61, 1262-1272.	3.1	25
11	Effect of salt tolerance on biomass production in a large population of sorghum accessions. <i>Breeding Science</i> , 2020, 70, 167-175.	1.9	13
12	Impacts of dominance effects on genomic prediction of sorghum hybrid performance. <i>Breeding Science</i> , 2020, 70, 605-616.	1.9	5
13	Comparison of shape quantification methods for genomic prediction, and genome-wide association study of sorghum seed morphology. <i>PLoS ONE</i> , 2019, 14, e0224695.	2.5	13
14	Title is missing!. , 2019, 14, e0224695.		0
15	Title is missing!. , 2019, 14, e0224695.		0
16	Title is missing!. , 2019, 14, e0224695.		0
17	Title is missing!. , 2019, 14, e0224695.		0
18	miRNAs control HAM1 functions at the single-cell-layer level and are essential for normal embryogenesis in <i>Arabidopsis</i> . <i>Plant Molecular Biology</i> , 2018, 96, 627-640.	3.9	22

#	ARTICLE	IF	CITATIONS
19	Transcriptional switch for programmed cell death in pith parenchyma of sorghum stems. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8783-E8792.	7.1	30
20	Heap: a highly sensitive and accurate SNP detection tool for low-coverage high-throughput sequencing data. DNA Research, 2017, 24, 397-405.	3.4	19
21	High-Throughput Phenotyping of Sorghum Plant Height Using an Unmanned Aerial Vehicle and Its Application to Genomic Prediction Modeling. Frontiers in Plant Science, 2017, 8, 421.	3.6	198
22	Functional analysis of the promoter of a rice 18â€‰kDa oleosin gene. Plant Biotechnology, 2016, 33, 195-200.	1.0	3
23	Distinct Gene Expression Profiles in Egg and Synergid Cells of Rice as Revealed by Cell Type-Specific Microarrays. Plant Physiology, 2011, 155, 881-891.	4.8	58
24	Studies of mitochondrial morphology and DNA amount in the rice egg cell. Current Genetics, 2010, 56, 33-41.	1.7	23
25	Different amounts of DNA in each mitochondrion in rice root. Genes and Genetic Systems, 2006, 81, 215-218.	0.7	32