

Hideo Matsumura

List of Publications by Year in descending order

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82
papers

5,957
citations

94269

37
h-index

79541

73
g-index

88
all docs

88
docs citations

88
times ranked

6775
citing authors

#	ARTICLE	IF	CITATIONS
1	Development of PCR-based marker for resistance to Fusarium wilt race 2 in lettuce (<i>Lactuca sativa</i> L.). <i>Euphytica</i> , 2021, 217, 1.	0.6	3
2	Genomic characterization of a rare <i>Carica papaya</i> X chromosome mutant reveals a candidate monodehydroascorbate reductase 4 gene involved in all-hermaphrodite phenomenon. <i>Molecular Genetics and Genomics</i> , 2021, 296, 1323-1335.	1.0	2
3	Reply to Renner: Meticulous investigation, not sequencing effort, leads to robust conclusion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 24632-24633.	3.3	0
4	Identification of two QTLs for resistance to Fusarium wilt race 1 in lettuce (<i>Lactuca sativa</i> L.). <i>Euphytica</i> , 2020, 216, 1.	0.6	7
5	Long-read bitter gourd (<i>Momordica charantia</i>) genome and the genomic architecture of nonclassic domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 14543-14551.	3.3	43
6	A CIN-like TCP transcription factor (LsTCP4) having retrotransposon insertion associates with a shift from Salinas type to Empire type in crisphead lettuce (<i>Lactuca sativa</i> L.). <i>Horticulture Research</i> , 2020, 7, 15.	2.9	30
7	Glimpse on Genomics and Breeding in Bitter Gourd: A Crop of the Future for Food, Nutrition and Health Security. <i>Compendium of Plant Genomes</i> , 2020, , 1-6.	0.3	0
8	Future Prospects of Genomics and Breeding in Bitter Gourd. <i>Compendium of Plant Genomes</i> , 2020, , 133-135.	0.3	0
9	Genome Sequence of Bitter Gourd and Its Comparative Study with Other Cucurbitaceae Genomes. <i>Compendium of Plant Genomes</i> , 2020, , 113-123.	0.3	3
10	Molecular Linkage Mapping in Bitter Gourd. <i>Compendium of Plant Genomes</i> , 2020, , 105-111.	0.3	0
11	Identification of dominant genetic markers relevant to male sex determination in mulberry (<i>Morus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	0.6	0
12	Identification of candidate flowering and sex genes in white Guinea yam (<i>D. rotundata</i> Poir.) by SuperSAGE transcriptome profiling. <i>PLoS ONE</i> , 2019, 14, e0216912.	1.1	16
13	Dissecting the all-hermaphrodite phenomenon of a rare X chromosome mutant in papaya (<i>Carica papaya</i>) Tj ETQq1 1 0.784314 rgBT /	1.0	6
14	HTâ€SuperSAGE of the gut tissue of a Vip3Aaâ€resistant <i>Heliothis virescens</i> (Lepidoptera: Noctuidae) strain provides insights into the basis of resistance. <i>Insect Science</i> , 2019, 26, 479-498.	1.5	5
15	Production of backcross plants between intergeneric hybrids (<i>Carica papaya</i> /â€†â€† <i>Vasconcellea</i>) Tj ETQq1 1 0.784314 rgBT / mosaic virus resistance. <i>Ikushugaku Kenkyu</i> , 2018, 20, 115-123.	0.1	1
16	Draft genome sequence of bitter gourd (<i>Momordica charantia</i>), a vegetable and medicinal plant in tropical and subtropical regions. <i>DNA Research</i> , 2017, 24, dsw047.	1.5	93
17	OsHKT1;5 mediates Na ⁺ exclusion in the vasculature to protect leaf blades and reproductive tissues from salt toxicity in rice. <i>Plant Journal</i> , 2017, 91, 657-670.	2.8	210
18	Genome sequencing of the staple food crop white Guinea yam enables the development of a molecular marker for sex determination. <i>BMC Biology</i> , 2017, 15, 86.	1.7	114

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19	Development of plants resistant to <i>Papaya leaf distortion mosaic virus</i> by intergeneric hybridization between <i>Carica papaya</i> and <i>Vasconcellea cundinamaricensis</i> . <i>Breeding Science</i> , 2016, 66, 734-741.	0.9	4
20	Expression of a <i>Nicotiana tabacum</i> pathogen-induced gene is involved in the susceptibility to black shank. <i>Functional Plant Biology</i> , 2016, 43, 534.	1.1	3
21	â€Candidatus <i>Liberibacter asiaticus</i> â€™™, Causal Agent of Citrus Huanglongbing, Is Reduced by Treatment with Brassinosteroids. <i>PLoS ONE</i> , 2016, 11, e0146223.	1.1	51
22	<i>Magnaporthe oryzae</i> Glycine-Rich Secretion Protein, Rbf1 Critically Participates in Pathogenicity through the Focal Formation of the Biotrophic Interfacial Complex. <i>PLoS Pathogens</i> , 2016, 12, e1005921.	2.1	33
23	Leaf margin phenotype-specific restriction-site-associated DNA-derived markers for pineapple (<i>Ananas comosus</i> L.). <i>Breeding Science</i> , 2015, 65, 276-284.	0.9	12
24	MutMap accelerates breeding of a salt-tolerant rice cultivar. <i>Nature Biotechnology</i> , 2015, 33, 445-449.	9.4	265
25	A cytochrome P450, OsDSS1, is involved in growth and drought stress responses in rice (<i>Oryza sativa</i>) Tj ETQq1 1 0.784314 191 / Over	2.0	191
26	Genome sequence comparison reveals a candidate gene involved in maleâ€“hermaphrodite differentiation in papaya (<i>Carica papaya</i>) trees. <i>Molecular Genetics and Genomics</i> , 2015, 290, 661-670.	1.0	26
27	SuperSAGE as an Analytical Tool for Host and Viral Gene Expression. <i>Methods in Molecular Biology</i> , 2015, 1236, 181-195.	0.4	4
28	Mapping of the Gynoecy in Bitter Gourd (<i>Momordica charantia</i>) Using RAD-Seq Analysis. <i>PLoS ONE</i> , 2014, 9, e87138.	1.1	65
29	Functional characterization of a new grapevine MYB transcription factor and regulation of proanthocyanidin biosynthesis in grapes. <i>Journal of Experimental Botany</i> , 2014, 65, 4433-4449.	2.4	87
30	Rice alcohol dehydrogenase 1 promotes survival and has a major impact on carbohydrate metabolism in the embryo and endosperm when seeds are germinated in partially oxygenated water. <i>Annals of Botany</i> , 2014, 113, 851-859.	1.4	45
31	Whole-genome resequencing of mutant progeny bulk combined with <i>de novo</i> assembly of gap regions identifies the rice blast resistance gene <i>Pii</i> . <i>New Phytologist</i> , 2013, 200, 276-283.	3.5	196
32	Expression of a microbial serine proteinase inhibitor gene enhances the tobacco defense against oomycete pathogens. <i>Physiological and Molecular Plant Pathology</i> , 2013, 84, 99-106.	1.3	7
33	Deep sequencing uncovers commonality in small RNA profiles between transgene-induced and naturally occurring RNA silencing of chalcone synthase-A gene in petunia. <i>BMC Genomics</i> , 2013, 14, 63.	1.2	23
34	MutMap+: Genetic Mapping and Mutant Identification without Crossing in Rice. <i>PLoS ONE</i> , 2013, 8, e68529.	1.1	267
35	Distribution of CRa in clubroot resistance (CR) cultivars of Chinese cabbage. <i>Plant Biotechnology</i> , 2013, 30, 393-397.	0.5	5
36	Large-Scale Gene Disruption in <i>Magnaporthe oryzae</i> Identifies MC69, a Secreted Protein Required for Infection by Monocot and Dicot Fungal Pathogens. <i>PLoS Pathogens</i> , 2012, 8, e1002711.	2.1	150

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37	Analysis of RAPD and AFLP markers linked to resistance to <i>Fusarium oxysporum</i> f. sp. <i>lactucae</i> race 2 in lettuce (<i>Lactuca sativa</i> L.). <i>Euphytica</i> , 2012, 187, 1-9.	0.6	17
38	Molecular characterization of the CRa gene conferring clubroot resistance in <i>Brassica rapa</i> . <i>Plant Molecular Biology</i> , 2012, 80, 621-629.	2.0	173
39	Whole genome sequencing and future breeding of rice. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2012, 21, 10-14.	0.9	2
40	Genome sequencing reveals agronomically important loci in rice using MutMap. <i>Nature Biotechnology</i> , 2012, 30, 174-178.	9.4	1,087
41	SuperSAGE: Powerful Serial Analysis of Gene Expression. <i>Methods in Molecular Biology</i> , 2012, 883, 1-17.	0.4	16
42	Digital Transcriptome Analysis of Putative Sex-Determination Genes in Papaya (<i>Carica papaya</i>). <i>PLoS ONE</i> , 2012, 7, e40904.	1.1	46
43	The gene expression landscape of thermogenic skunk cabbage suggests critical roles for mitochondrial and vacuolar metabolic pathways in the regulation of thermogenesis. <i>Plant, Cell and Environment</i> , 2012, 35, 554-566.	2.8	12
44	A multifaceted genomics approach allows the isolation of the rice <i>Pia</i> blast resistance gene consisting of two adjacent NBS-LRR protein genes. <i>Plant Journal</i> , 2011, 66, 467-479.	2.8	287
45	Cell division and cell elongation in the coleoptile of rice alcohol dehydrogenase 1-deficient mutant are reduced under complete submergence. <i>Annals of Botany</i> , 2011, 108, 253-261.	1.4	40
46	High-Throughput SuperSAGE. <i>Methods in Molecular Biology</i> , 2011, 687, 135-146.	0.4	10
47	Cloning of a heat stress transcription factor, CphsfB1, that is constitutively expressed in radicles and is heat-inducible in the leaves of <i>Carica papaya</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2010, 102, 69-77.	1.2	5
48	Gill transcriptome response to changes in environmental calcium in the green spotted puffer fish. <i>BMC Genomics</i> , 2010, 11, 476.	1.2	39
49	High-Throughput SuperSAGE for Digital Gene Expression Analysis of Multiple Samples Using Next Generation Sequencing. <i>PLoS ONE</i> , 2010, 5, e12010.	1.1	98
50	Metabolome Analysis of Response to Oxidative Stress in Rice Suspension Cells Overexpressing Cell Death Suppressor Bax Inhibitor-1. <i>Plant and Cell Physiology</i> , 2010, 51, 9-20.	1.5	86
51	Association Genetics Reveals Three Novel Avirulence Genes from the Rice Blast Fungal Pathogen <i>Magnaporthe oryzae</i> . <i>Plant Cell</i> , 2009, 21, 1573-1591.	3.1	410
52	Unraveling the roles of sphingolipids in plant innate immunity. <i>Plant Signaling and Behavior</i> , 2009, 4, 536-538.	1.2	6
53	Unravelling the interaction of human cytomegalovirus with dendritic cells by using SuperSAGE. <i>Journal of General Virology</i> , 2009, 90, 2221-2233.	1.3	12
54	Coordination of Plastid Protein Import and Nuclear Gene Expression by Plastid-to-Nucleus Retrograde Signaling. <i>Plant Physiology</i> , 2009, 151, 1339-1353.	2.3	152

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55	Spermine signaling plays a significant role in the defense response of <i>Arabidopsis thaliana</i> to cucumber mosaic virus. <i>Journal of Plant Physiology</i> , 2009, 166, 626-643.	1.6	107
56	Functional Characterization and Modulation of the DNA Cleavage Efficiency of Type III Restriction Endonuclease EcoP15I in Its Interaction with Two Sites in the DNA Target. <i>Journal of Molecular Biology</i> , 2009, 387, 1309-1319.	2.0	21
57	Serine Palmitoyltransferase, the First Step Enzyme in Sphingolipid Biosynthesis, Is Involved in Nonhost Resistance. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 31-38.	1.4	37
58	High-throughput <i>in planta</i> expression screening identifies an ADP-ribosylation factor (<i>ARF1</i>) involved in non-host resistance and <i>R</i> gene-mediated resistance. <i>Molecular Plant Pathology</i> , 2008, 9, 25-36.	2.0	38
59	SuperSAGE revealed different classes of early resistance response genes in <i>Capsicum chinense</i> plants harboring L3-resistance gene infected with Pepper mild mottle virus. <i>Journal of General Plant Pathology</i> , 2008, 74, 313-321.	0.6	18
60	Functional genomics in a non-model crop: transcriptomics or proteomics?. <i>Physiologia Plantarum</i> , 2008, 133, 117-130.	2.6	50
61	SuperSAGE: the drought stress-responsive transcriptome of chickpea roots. <i>BMC Genomics</i> , 2008, 9, 553.	1.2	209
62	The cell death factor, cell wall elicitor of rice blast fungus (<i>Magnaporthe grisea</i>) causes metabolic alterations including GABA shunt in rice cultured cells. <i>Plant Signaling and Behavior</i> , 2008, 3, 945-953.	1.2	28
63	SuperSAGE: A Modern Platform for Genome-Wide Quantitative Transcript Profiling. <i>Current Pharmaceutical Biotechnology</i> , 2008, 9, 368-374.	0.9	46
64	SuperSAGE. <i>Methods in Molecular Biology</i> , 2008, 387, 55-70.	0.4	12
65	A Novel MAPKK Involved in Cell Death and Defense Signaling. <i>Plant Signaling and Behavior</i> , 2007, 2, 396-398.	1.2	3
66	A high-throughput screen of cell-death-inducing factors in <i>Nicotiana benthamiana</i> identifies a novel MAPKK that mediates INF1-induced cell death signaling and non-host resistance to <i>Pseudomonas cichorii</i> . <i>Plant Journal</i> , 2007, 49, 1030-1040.	2.8	86
67	Large-scale DNA polymorphism study of <i>Oryza sativa</i> and <i>O. rufipogon</i> reveals the origin and divergence of Asian rice. <i>Theoretical and Applied Genetics</i> , 2007, 114, 731-743.	1.8	98
68	Use of Serial Analysis of Gene Expression (Sage) for Transcript Profiling in Plants. , 2007, , 227-244.		1
69	A Point Mutation of <i>Adh1</i> Gene is Involved in the Repression of Coleoptile Elongation under Submergence in Rice. <i>Breeding Science</i> , 2006, 56, 69-74.	0.9	45
70	SuperSAGE array: the direct use of 26-base-pair transcript tags in oligonucleotide arrays. <i>Nature Methods</i> , 2006, 3, 469-474.	9.0	57
71	Regulatory Mechanisms of ROI Generation are Affected by Rice <i>spl</i> Mutations. <i>Plant and Cell Physiology</i> , 2006, 47, 1035-1044.	1.5	39
72	High-throughput <i>in planta</i> expression screening identifies a class II ethylene-responsive element binding factor-like protein that regulates plant cell death and non-host resistance. <i>Plant Journal</i> , 2005, 43, 491-505.	2.8	71

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73	SuperSAGE combined with PCR walking allows global gene expression profiling of banana (Musa) Tj ETQq1 1 0.784314 rgBT /Overloc	1.8	41
74	SuperSAGE. Cellular Microbiology, 2004, 7, 11-18.	1.1	79
75	SAGE (Serial Analysis of Gene Expression) in Magnaporthe Grisea. , 2004, , 23-28.		0
76	Gene expression analysis of plant host-pathogen interactions by SuperSAGE. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 15718-15723.	3.3	273
77	Transcript profiling in rice (Oryza sativa L.) seedlings using serial analysis of gene expression (SAGE). Plant Journal, 1999, 20, 719-726.	2.8	162
78	A Rice Mutant Lacking Alcohol Dehydrogenase.. Breeding Science, 1995, 45, 365-367.	0.2	16
79	Molecular Cloning of Rice Lactate Dehydrogenase cDNA.. Breeding Science, 1993, 43, 129-133.	0.2	2
80	SuperSAGE: The Most Advanced Transcriptome Technology for Functional Genomics. , 0, , 37-54.		4
81	Use of TILLING for Reverse and Forward Genetics of Rice. , 0, , 185-197.		9
82	SuperSAGE: A complete genome-wide quantitative expression profiling platform. , 0, 2008, .		0