

Sanjay Kapoor

List of Publications by Year in descending order

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70
papers

4,842
citations

126907

33
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102487

66
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71
all docs

71
docs citations

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times ranked

6089
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of Transcription Regulatory Domains of OsMADS29: Identification of Proximal Auxin-Responsive Domains and a Strong Distal Negative Element. <i>Frontiers in Plant Science</i> , 2022, 13, 850956.	3.6	1
2	OsCPK29 Interacts with MADS68 to Regulate Pollen Development in Rice. <i>Plant Science</i> , 2022, , 111297.	3.6	4
3	The DEAD-box RNA helicase eIF4A1 interacts with the SWI2/SNF2-related chromatin remodelling ATPase DDM1 in the moss <i>Physcomitrella</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021, 1869, 140592.	2.3	4
4	A comprehensive transcriptome analysis of contrasting rice cultivars highlights the role of auxin and ABA responsive genes in heat stress response. <i>Genomics</i> , 2021, 113, 1247-1261.	2.9	24
5	Determination of Tripartite Interaction between Two Monomers of a MADS-box Transcription Factor and a Calcium Sensor Protein by BiFC-FRET-FLIM Assay. <i>Journal of Visualized Experiments</i> , 2021, , .	0.3	0
6	The DEAD-box RNA helicase eIF4A regulates plant development and interacts with the hnRNP LIF2L1 in <i>Physcomitrella patens</i> . <i>Molecular Genetics and Genomics</i> , 2020, 295, 373-389.	2.1	12
7	Transcriptome Analysis of <i>ppdnmt2</i> and Identification of Superoxide Dismutase as a Novel Interactor of DNMT2 in the Moss <i>Physcomitrella patens</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 1185.	3.6	7
8	The Arabidopsis Hypoxia Inducible AtR8 Long Non-Coding RNA also Contributes to Plant Defense and Root Elongation Coordinating with WRKY Genes under Low Levels of Salicylic Acid. <i>Non-coding RNA</i> , 2020, 6, 8.	2.6	14
9	Functional characterization of LIKE HETEROCHROMATIN PROTEIN 1 in the moss <i>Physcomitrella patens</i> : its conserved protein interactions in land plants. <i>Plant Journal</i> , 2019, 97, 221-239.	5.7	21
10	Decrease in DNA methylation 1 interacts with chromomethylase and like heterochromatin protein 1 in <i>Physcomitrella patens</i> . <i>FEBS Letters</i> , 2019, 593, 2686-2697.	2.8	3
11	Evolvement of transgenic male-sterility and fertility-restoration system in rice for production of hybrid varieties. <i>Plant Molecular Biology</i> , 2018, 96, 35-51.	3.9	14
12	Analysis of drought-responsive signalling network in two contrasting rice cultivars using transcriptome-based approach. <i>Scientific Reports</i> , 2017, 7, 42131.	3.3	50
13	bHLH142 regulates various metabolic pathway-related genes to affect pollen development and anther dehiscence in rice. <i>Scientific Reports</i> , 2017, 7, 43397.	3.3	34
14	A temperature-responsive gene in sorghum encodes a glycine-rich protein that interacts with calmodulin. <i>Biochimie</i> , 2017, 137, 115-123.	2.6	7
15	A novel application of periodic acid-Schiff (PAS) staining and fluorescence imaging for analysing tapetum and microspore development. <i>Histochemistry and Cell Biology</i> , 2017, 147, 103-110.	1.7	10
16	<i>Physcomitrella patens</i> DNA methyltransferase 2 is required for recovery from salt and osmotic stress. <i>FEBS Journal</i> , 2016, 283, 556-570.	4.7	29
17	Rice Improvement Through Genome-Based Functional Analysis and Molecular Breeding in India. <i>Rice</i> , 2016, 9, 1.	4.0	111
18	Characterization of Peptidyl-Prolyl Cis-Trans Isomerase- and Calmodulin-Binding Activity of a Cytosolic Arabidopsis thaliana Cyclophilin AtCyp19-3. <i>PLoS ONE</i> , 2015, 10, e0136692.	2.5	28

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19	The <i>PpCMT</i> chromomethylase affects cell growth and interacts with the homolog of LIKE HETEROCHROMATIN PROTEIN-1 in the moss <i>Physcomitrella patens</i> . <i>Plant Journal</i> , 2014, 77, 589-603.	5.7	19
20	Post-translational regulation of rice MADS29 function: homodimerization or binary interactions with other seed-expressed MADS proteins modulate its translocation into the nucleus. <i>Journal of Experimental Botany</i> , 2014, 65, 5339-5350.	4.8	26
21	Genome-wide expressional and functional analysis of calcium transport elements during abiotic stress and development in rice. <i>FEBS Journal</i> , 2014, 281, 894-915.	4.7	92
22	Comprehensive Expression Analysis of Rice Armadillo Gene Family During Abiotic Stress and Development. <i>DNA Research</i> , 2014, 21, 267-283.	3.4	66
23	Comprehensive structural, interaction and expression analysis of CBL and CIPK complement during abiotic stresses and development in rice. <i>Cell Calcium</i> , 2014, 56, 81-95.	2.4	136
24	A 286bp upstream regulatory region of a rice anther-specific gene, OSIPP3, confers pollen-specific expression in Arabidopsis. <i>Biotechnology Letters</i> , 2013, 35, 455-462.	2.2	11
25	De Novo Methyltransferase, OsDRM2, Interacts with the ATP-Dependent RNA Helicase, OsEIF4A, in Rice. <i>Journal of Molecular Biology</i> , 2013, 425, 2853-2866.	4.2	22
26	Plant Omics: Genome-Wide Analysis of ABA Repressor1 (<i>ABR1</i>) Related Genes in Rice During Abiotic Stress and Development. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 439-450.	2.0	25
27	Spatial and temporal activity of upstream regulatory regions of rice anther-specific genes in transgenic rice and Arabidopsis. <i>Transgenic Research</i> , 2013, 22, 31-46.	2.4	21
28	Functional delineation of rice MADS29 reveals its role in embryo and endosperm development by affecting hormone homeostasis. <i>Journal of Experimental Botany</i> , 2013, 64, 4239-4253.	4.8	61
29	Comprehensive Genomic Analysis and Expression Profiling of Phospholipase C Gene Family during Abiotic Stresses and Development in Rice. <i>PLoS ONE</i> , 2013, 8, e62494.	2.5	62
30	Gene Expression Analysis of Rice Seedling under Potassium Deprivation Reveals Major Changes in Metabolism and Signaling Components. <i>PLoS ONE</i> , 2013, 8, e70321.	2.5	51
31	Rice Phospholipase A Superfamily: Organization, Phylogenetic and Expression Analysis during Abiotic Stresses and Development. <i>PLoS ONE</i> , 2012, 7, e30947.	2.5	60
32	Comprehensive expression analysis of rice phospholipase D gene family during abiotic stresses and development. <i>Plant Signaling and Behavior</i> , 2012, 7, 847-855.	2.4	55
33	Heterosis: emerging ideas about hybrid vigour. <i>Journal of Experimental Botany</i> , 2012, 63, 6309-6314.	4.8	117
34	Screening and isolation of halophilic bacteria producing industrially important enzymes. <i>Brazilian Journal of Microbiology</i> , 2012, 43, 1595-1603.	2.0	111
35	Role of DNA methylation in growth and differentiation in <i>Physcomitrella patens</i> and characterization of cytosine DNA methyltransferases. <i>FEBS Journal</i> , 2012, 279, 4081-4094.	4.7	42
36	Anthology of Anther/Pollen-Specific Promoters and Transcription Factors. <i>Critical Reviews in Plant Sciences</i> , 2012, 31, 359-390.	5.7	21

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37	Analysis of transcriptional and upstream regulatory sequence activity of two environmental stress-inducible genes, NBS-Str1 and BLEC-Str8, of rice. <i>Transgenic Research</i> , 2012, 21, 351-366.	2.4	14
38	Transcriptome analysis of rin mutant fruit and in silico analysis of promoters of differentially regulated genes provides insight into LeMADS-RIN-regulated ethylene-dependent as well as ethylene-independent aspects of ripening in tomato. <i>Molecular Genetics and Genomics</i> , 2012, 287, 189-203.	2.1	42
39	Expression dynamics of metabolic and regulatory components across stages of panicle and seed development in indica rice. <i>Functional and Integrative Genomics</i> , 2012, 12, 229-248.	3.5	66
40	Screening and isolation of halophilic bacteria producing industrially important enzymes. <i>Brazilian Journal of Microbiology</i> , 2012, 43, 1595-603.	2.0	40
41	Modulation of transcription factor and metabolic pathway genes in response to water-deficit stress in rice. <i>Functional and Integrative Genomics</i> , 2011, 11, 157-178.	3.5	78
42	Analysis of anther transcriptomes to identify genes contributing to meiosis and male gametophyte development in rice. <i>BMC Plant Biology</i> , 2011, 11, 78.	3.6	115
43	Transcription factors regulating the progression of monocot and dicot seed development. <i>BioEssays</i> , 2011, 33, 189-202.	2.5	138
44	A novel organic solvent tolerant protease from a newly isolated <i>Geomicrobium</i> sp. EMB2 (MTCC 10310): production optimization by response surface methodology. <i>New Biotechnology</i> , 2011, 28, 136-145.	4.4	40
45	The Mediator Complex in Plants: Structure, Phylogeny, and Expression Profiling of Representative Genes in a Dicot (<i>Arabidopsis</i>) and a Monocot (Rice) during Reproduction and Abiotic Stress. <i>Plant Physiology</i> , 2011, 157, 1609-1627.	4.8	158
46	Comparative Transcriptomics Reveals 129 Transcripts That Are Temporally Regulated during Anther Development and Meiotic Progression in Both Bread Wheat (<i>Triticum aestivum</i>) and Rice (<i>Oryza sativa</i>). <i>International Journal of Plant Genomics</i> , 2011, 2011, 1-9.	2.2	5
47	Gene Identification and Molecular Characterization of Solvent Stable Protease from A Moderately Haloalkaliphilic Bacterium, <i>Geomicrobium</i> sp. EMB2. <i>Journal of Microbiology and Biotechnology</i> , 2011, 21, 129-135.	2.1	19
48	Epigenome and Abiotic Stress Tolerance in Plants. , 2011, , 121-127.		0
49	Rice genomics moves ahead. <i>Molecular Breeding</i> , 2010, 26, 257-273.	2.1	7
50	Protein phosphatase complement in rice: genome-wide identification and transcriptional analysis under abiotic stress conditions and reproductive development. <i>BMC Genomics</i> , 2010, 11, 435.	2.8	158
51	Purification and characterization of a solvent stable aminopeptidase from <i>Pseudomonas aeruginosa</i> : Cloning and analysis of aminopeptidase gene conferring solvent stability. <i>Process Biochemistry</i> , 2010, 45, 757-764.	3.7	19
52	Whole genome approaches to identify early meiotic gene candidates in cereals. <i>Functional and Integrative Genomics</i> , 2009, 9, 219-229.	3.5	11
53	Rice cytosine DNA methyltransferases " gene expression profiling during reproductive development and abiotic stress. <i>FEBS Journal</i> , 2009, 276, 6301-6311.	4.7	85
54	Expression and functional analysis of rice genes involved in reproductive development and stress response. <i>International Rice Research Notes</i> , 2009, 31, .	0.0	0

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55	Genome-wide identification, organization and phylogenetic analysis of Dicer-like, Argonaute and RNA-dependent RNA Polymerase gene families and their expression analysis during reproductive development and stress in rice. <i>BMC Genomics</i> , 2008, 9, 451.	2.8	262
56	The Receptor-Like Cytoplasmic Kinase (OsRLCK) Gene Family in Rice: Organization, Phylogenetic Relationship, and Expression during Development and Stress. <i>Molecular Plant</i> , 2008, 1, 732-750.	8.3	158
57	Solvent-Stable &Pseudomonas aeruginosa&PseA Protease Gene: Identification, Molecular Characterization, Phylogenetic and Bioinformatic Analysis to Study Reasons for Solvent Stability. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2008, 15, 234-243.	1.0	14
58	F-Box Proteins in Rice. Genome-Wide Analysis, Classification, Temporal and Spatial Gene Expression during Panicle and Seed Development, and Regulation by Light and Abiotic Stress. <i>Plant Physiology</i> , 2007, 143, 1467-1483.	4.8	580
59	MADS-box gene family in rice: genome-wide identification, organization and expression profiling during reproductive development and stress. <i>BMC Genomics</i> , 2007, 8, 242.	2.8	545
60	Genome-wide identification of C2H2 zinc-finger gene family in rice and their phylogeny and expression analysis. <i>Plant Molecular Biology</i> , 2007, 65, 467-485.	3.9	227
61	Expression analysis of calcium-dependent protein kinase gene family during reproductive development and abiotic stress conditions in rice (<i>Oryza sativa</i> L. ssp. indica). <i>Molecular Genetics and Genomics</i> , 2007, 278, 493-505.	2.1	216
62	Silencing of an Anther-specific Zinc-finger Gene, MEZ1, Causes Aberrant Meiosis and Pollen Abortion in Petunia. <i>Plant Molecular Biology</i> , 2006, 61, 415-430.	3.9	32
63	Silencing of the Tapetum-Specific Zinc Finger Gene TAZ1 Causes Premature Degeneration of Tapetum and Pollen Abortion in Petunia. <i>Plant Cell</i> , 2002, 14, 2353-2367.	6.6	136
64	Identification of Two Essential Sequence Elements in the Nonconsensus Type II PatpB-290 Plastid Promoter by Using Plastid Transcription Extracts from Cultured Tobacco BY-2 Cells. <i>Plant Cell</i> , 1999, 11, 1799-1810.	6.6	68
65	Identification of Two Essential Sequence Elements in the Nonconsensus Type II PatpB-290 Plastid Promoter by Using Plastid Transcription Extracts from Cultured Tobacco BY-2 Cells. <i>Plant Cell</i> , 1999, 11, 1799.	6.6	2
66	Transcript analysis of the tobacco plastid operon rps2/atpl/H/F/A reveals the existence of a non-consensus type II (NCII) promoter upstream of the atpl coding sequence. <i>Molecular Genetics and Genomics</i> , 1998, 257, 299-307.	2.4	51
67	Identification and functional significance of a new class of non-consensus-type plastid promoters. <i>Plant Journal</i> , 1997, 11, 327-337.	5.7	126
68	An atpE-specific promoter within the coding region of the atpB gene in tobacco chloroplast DNA. <i>Current Genetics</i> , 1994, 26, 263-268.	1.7	29
69	Developmental and light-dependent cues interact to establish steady-state levels of transcripts for photosynthesis-related genes (psbA, psbD, psaA and rbcL) in rice (<i>Oryza sativa</i> L.). <i>Current Genetics</i> , 1994, 25, 362-366.	1.7	23
70	Organ-Specific Expression of Plastid-Encoded Genes in Rice Involves both Quantitative and Qualitative Changes in mRNAs. <i>Plant and Cell Physiology</i> , 0, , .	3.1	3