Manoj Prasad

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7511570/publications.pdf

Version: 2024-02-01

173	9,769	30068 54	45310 90
papers	citations	h-index	g-index

183	183	183	8701
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Recent advancements and future perspectives of foxtail millet genomics. Plant Growth Regulation, 2023, 99, 11-23.	3.4	7
2	Regulation of small RNA-mediated high temperature stress responses in crop plants. Plant Cell Reports, 2022, 41, 765-773.	5.6	19
3	<scp>OsPSKR15</scp>, a phytosulfokine receptor from rice enhances abscisic acid response and drought stress tolerance. Physiologia Plantarum, 2022, 174, .	5.2	12
4	The sly-miR166-SlyHB module acts as a susceptibility factor during ToLCNDV infection. Theoretical and Applied Genetics, 2022, 135, 233-242.	3.6	13
5	Role of the Sw5 Gene Cluster in the Fight against Plant Viruses. Journal of Virology, 2022, 96, jvi0208421.	3.4	4
6	GWAS identifies genetic loci underlying nitrogen responsiveness in the climate resilient C4 model Setaria italica (L.). Journal of Advanced Research, 2022, 42, 249-261.	9.5	6
7	Nutritional improvement of cereal crops to combat hidden hunger during COVID-19 pandemic: Progress and prospects. Advances in Food Security and Sustainability, 2022, , .	1.4	0
8	Combining speed breeding with traditional and genomicsâ€assisted breeding for crop improvement. Plant Breeding, 2022, 141, 301-313.	1.9	18
9	Plant-virus-abiotic stress interactions: A complex interplay. Environmental and Experimental Botany, 2022, 199, 104869.	4.2	10
10	De novo transcriptome analysis identifies key genes involved in dehydration stress response in kodo millet (Paspalum scrobiculatum L.). Genomics, 2022, 114, 110347.	2.9	8
11	Interaction of ToLCNDV TrAP with SlATG8f marks it susceptible to degradation by autophagy. Cellular and Molecular Life Sciences, 2022, 79, 241.	5.4	4
12	Genomic Tools and Proteomic Determinants for Abiotic Stress Tolerance in Pearl Millet (Pennisetum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1	
13	DNA methylation dynamics in response to abiotic and pathogen stress in plants. Plant Cell Reports, 2022, 41, 1931-1944.	5.6	16
14	IRONing out stress problems in crops: a homeostatic perspective. Physiologia Plantarum, 2021, 171, 559-577.	5.2	8
15	Small Millets for Enduring Food Security Amidst Pandemics. Trends in Plant Science, 2021, 26, 33-40.	8.8	87
16	Noncoding but Coding: Pri-miRNA into the Action. Trends in Plant Science, 2021, 26, 204-206.	8.8	21
17	A comprehensive study on core enzymes involved in starch metabolism in the model nutricereal, foxtail millet (Setaria italica L.). Journal of Cereal Science, 2021, 97, 103153.	3.7	5
18	Genetics and Genomics Interventions for Promoting Millets as Functional Foods. Current Genomics, 2021, 22, 154-163.	1.6	4

#	Article	IF	Citations
19	Molecular characterization of SlATG18f in response to Tomato leaf curl New Delhi virus infection in tomato and development of a CAPS marker for leaf curl disease tolerance. Theoretical and Applied Genetics, 2021, 134, 1463-1474.	3.6	14
20	Biotechnological approaches to dissect climate-resilient traits in millets and their application in crop improvement. Journal of Biotechnology, 2021, 327, 64-73.	3.8	25
21	Histone acetylation dynamics regulating plant development and stress responses. Cellular and Molecular Life Sciences, 2021, 78, 4467-4486.	5.4	76
22	Genomic dissection of ROS detoxifying enzyme encoding genes for their role in antioxidative defense mechanism against Tomato leaf curl New Delhi virus infection in tomato. Genomics, 2021, 113, 889-899.	2.9	12
23	Role of ubiquitination enzymes in abiotic environmental interactions with plants. International Journal of Biological Macromolecules, 2021, 181, 494-507.	7.5	18
24	Host-virus interactions mediated by long non-coding RNAs. Virus Research, 2021, 298, 198402.	2.2	13
25	Genetic determinants of micronutrient traits in graminaceous crops to combat hidden hunger. Theoretical and Applied Genetics, 2021, 134, 3147-3165.	3.6	9
26	Big genomic data analysis leads to more accurate trait prediction in hybrid breeding for yield enhancement in crop plants. Plant Cell Reports, 2021, 40, 2009-2011.	5.6	1
27	Delineating the epigenetic regulation of heat and drought response in plants. Critical Reviews in Biotechnology, 2021, , 1-14.	9.0	15
28	Insect herbivores benefit from horizontal gene transfer. Trends in Plant Science, 2021, 26, 1096-1097.	8.8	8
29	Advances in omics technology for improving crop yield and stress resilience. Plant Breeding, 2021, 140, 719-731.	1.9	13
30	The Sw5a gene confers resistance to ToLCNDV and triggers an HR response after direct AC4 effector recognition. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	28
31	Research and leaders: a twisted tale!. Trends in Genetics, 2021, 37, 863-864.	6.7	2
32	Complex molecular mechanisms determine fitness of plants to biotic and abiotic stresses. Journal of Plant Biochemistry and Biotechnology, 2021, 30, 633-635.	1.7	6
33	Genome-wide investigation of GRAM-domain containing genes in rice reveals their role in plant-rhizobacteria interactions and abiotic stress responses. International Journal of Biological Macromolecules, 2020, 156, 1243-1257.	7.5	18
34	Omics of neglected and underutilized crop species: one small step for NUCS, one giant leap for addressing global hunger. Nucleus (India), 2020, 63, 213-215.	2.2	5
35	Linking the plant stress responses with RNA helicases. Plant Science, 2020, 299, 110607.	3.6	24
36	Single Virus Targeting Multiple Organs: What We Know and Where We Are Heading?. Frontiers in Medicine, 2020, 7, 370.	2.6	31

#	Article	IF	Citations
37	Genomics approaches to synthesize plant-based biomolecules for therapeutic applications to combat SARS-CoV-2. Genomics, 2020, 112, 4322-4331.	2.9	14
38	Transcriptional regulators of nitrate metabolism: Key players in improving nitrogen use in crops. Journal of Biotechnology, 2020, 324, 121-133.	3.8	8
39	Breeding and biotechnological interventions for trait improvement: status and prospects. Planta, 2020, 252, 54.	3.2	48
40	Silencing AC1 of Tomato leaf curl virus using artificial microRNA confers resistance to leaf curl disease in transgenic tomato. Plant Cell Reports, 2020, 39, 1565-1579.	5.6	31
41	Tomato Yellow Leaf Curl Virus: Impact, Challenges, and Management. Trends in Plant Science, 2020, 25, 897-911.	8.8	74
42	Synergistic antiviral effects against SARS-CoV-2 by plant-based molecules. Plant Cell Reports, 2020, 39, 1109-1114.	5.6	48
43	Versatile roles of aquaporin in physiological processes and stress tolerance in plants. Plant Physiology and Biochemistry, 2020, 149, 178-189.	5.8	76
44	Induced Mutagenesis Enhances Lodging Resistance and Photosynthetic Efficiency of Kodomillet (Paspalum Scrobiculatum). Agronomy, 2020, 10, 227.	3.0	14
45	An efficient Agrobacterium-mediated genetic transformation method for foxtail millet (Setaria italica) Tj ETQq1 1 0.784314 rgBT /Ove	5.6	32
46	SARS-CoV-2: the emergence of a viral pathogen causing havoc on human existence. Journal of Genetics, 2020, 99, 1.	0.7	31
47	Genomic dissection and expression analysis of stress-responsive genes in C4 panicoid models, Setaria italica and Setaria viridis. Journal of Biotechnology, 2020, 318, 57-67.	3.8	5
48	Whole Genome Re-sequencing of Soybean Accession EC241780 Providing Genomic Landscape of Candidate Genes Involved in Rust Resistance. Current Genomics, 2020, 21, 504-511.	1.6	8
49	Chilli leaf curl virus infection downregulates the expression of the genes encoding chloroplast proteins and stress-related proteins. Physiology and Molecular Biology of Plants, 2019, 25, 1185-1196.	3.1	9
50	Genome-Wide Association Study of Major Agronomic Traits in Foxtail Millet (Setaria italica L.) Using ddRAD Sequencing. Scientific Reports, 2019, 9, 5020.	3.3	64
51	Recent advances in small RNA mediated plant-virus interactions. Critical Reviews in Biotechnology, 2019, 39, 587-601.	9.0	66
52	Millets genetic engineering: the progress made and prospects for the future. Plant Cell, Tissue and Organ Culture, 2019, 137, 421-439.	2.3	16
53	Study on aquaporins of Setaria italica suggests the involvement of SiPIP3;1 and SiSIP1;1 in abiotic stress response. Functional and Integrative Genomics, 2019, 19, 587-596.	3.5	23
54	Multi-omics approaches for strategic improvement of stress tolerance in underutilized crop species: A climate change perspective. Advances in Genetics, 2019, 103, 1-38.	1.8	71

#	Article	IF	Citations
55	Characterization of DEAD-box family of RNA helicases in tomato provides insights into their roles in biotic and abiotic stresses. Environmental and Experimental Botany, 2019, 158, 107-116.	4.2	23
56	Genome-wide association study (GWAS) delineates genomic loci for ten nutritional elements in foxtail millet (Setaria italica L.). Journal of Cereal Science, 2019, 85, 48-55.	3.7	53
57	Epigenetics and Epigenomics of Plants. Advances in Biochemical Engineering/Biotechnology, 2018, 164, 237-261.	1.1	11
58	Identification, characterization, expression profiling, and virus-induced gene silencing of armadillo repeat-containing proteins in tomato suggest their involvement in tomato leaf curl New Delhi virus resistance. Functional and Integrative Genomics, 2018, 18, 101-111.	3.5	8
59	Ubiquitination: a tool for plant adaptation to changing environments. Nucleus (India), 2018, 61, 253-260.	2.2	8
60	CRISPR/Cas9: A Novel Weapon in the Arsenal to Combat Plant Diseases. Frontiers in Plant Science, 2018, 9, 2008.	3.6	42
61	Genome-wide Characterization of Major Intrinsic Protein (MIP) Gene Family in Brachypodium distachyon. Current Bioinformatics, 2018, 13, 536-552.	1.5	9
62	Salinity induced differential methylation patterns in contrasting cultivars of foxtail millet (Setaria) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	5.6	45
63	An insight into plantâ€“Tomato leaf curl New Delhi virus interaction. Nucleus (India), 2017, 60, 335-348.	2.2	13
64	Foxtail Millet: An Introduction. Compendium of Plant Genomes, 2017, , 1-9.	0.5	5
65	Nutrition Potential of Foxtail Millet in Comparison to Other Millets and Major Cereals. Compendium of Plant Genomes, 2017, , 123-135.	0.5	10
66	Genome-Wide Association Studies for Improving Agronomic Traits in Foxtail Millet. Compendium of Plant Genomes, 2017, , 63-75.	0.5	3
67	Exploiting Genome Sequence Information to Develop Genomic Resources for Foxtail Millet Improvement. Compendium of Plant Genomes, 2017, , 37-51.	0.5	1
68	Regulation of Development and Stress Response by miRNAs. Compendium of Plant Genomes, 2017, , 137-152.	0.5	0
69	Foxtail Millet Genome Sequencing, Assembly, Annotation, and Application. Compendium of Plant Genomes, 2017, , 11-22.	0.5	3
70	Transposable Elements in Setaria Genomes. Compendium of Plant Genomes, 2017, , 23-35.	0.5	0
71	Genetic Transformation of Setaria: A New Perspective. Compendium of Plant Genomes, 2017, , 105-121.	0.5	6
72	Millets for Next Generation Climate-Smart Agriculture. Frontiers in Plant Science, 2017, 8, 1266.	3.6	95

#	Article	IF	Citations
73	Geminiviruses and Plant Hosts: A Closer Examination of the Molecular Arms Race. Viruses, 2017, 9, 256.	3.3	80
74	Genetic Determinants of Drought Stress Tolerance in Setaria. Plant Genetics and Genomics: Crops and Models, 2017, , 267-289.	0.3	10
75	Genomics-Assisted Breeding for Improving Stress Tolerance of Graminaceous Crops to Biotic and Abiotic Stresses: Progress and Prospects. , 2017, , 59-81.		6
76	A Functional Genomic Perspective on Drought Signalling and its Crosstalk with Phytohormone-mediated Signalling Pathways in Plants. Current Genomics, 2017, 18, 469-482.	1.6	123
77	Editorial: Abiotic Stress Signaling in Plants: Functional Genomic Intervention. Frontiers in Plant Science, 2016, 7, 681.	3.6	25
78	Structure, organization and evolution of ADP-ribosylation factors in rice and foxtail millet and their expression in rice. Scientific Reports, 2016, 6, 24008.	3.3	42
79	Tomato 26S Proteasome subunit RPT4a regulates ToLCNDV transcription and activates hypersensitive response in tomato. Scientific Reports, 2016, 6, 27078.	3.3	22
80	Role of Genomics in Enhancing Nutrition Content of Cereals. , 2016, , 77-96.		1
81	Comprehensive analysis of SET domain gene family in foxtail millet identifies the putative role of SiSET14 in abiotic stress tolerance. Scientific Reports, 2016, 6, 32621.	3.3	50
82	Genome-wide analysis of heat shock proteins in C4 model, foxtail millet identifies potential candidates for crop improvement under abiotic stress. Scientific Reports, 2016, 6, 32641.	3.3	79
83	Leaf crinkle disease in urdbean (Vigna mungo L. Hepper): An overview on causal agent, vector and host. Protoplasma, 2016, 253, 729-746.	2.1	20
84	Advances in Agrobacterium tumefaciens-mediated genetic transformation of graminaceous crops. Protoplasma, 2016, 253, 691-707.	2.1	59
85	Dehydration-responsive miRNAs in foxtail millet: genome-wide identification, characterization and expression profiling. Planta, 2016, 243, 749-766.	3.2	35
86	Exploration of millet models for developing nutrient rich graminaceous crops. Plant Science, 2016, 242, 89-97.	3.6	133
87	Chromatin-Based Epigenetic Regulation of Plant Abiotic Stress Response. Current Genomics, 2016, 17, 490-498.	1.6	64
88	Application of genomics-assisted breeding for generation of climate resilient crops: progress and prospects. Frontiers in Plant Science, 2015, 6, 563.	3.6	243
89	Genome-Wide SNP Identification and Characterization in Two Soybean Cultivars with Contrasting Mungbean Yellow Mosaic India Virus Disease Resistance Traits. PLoS ONE, 2015, 10, e0123897.	2.5	34
90	Global analysis of WRKY transcription factor superfamily in Setaria identifies potential candidates involved in abiotic stress signaling. Frontiers in Plant Science, 2015, 6, 910.	3.6	96

#	Article	IF	Citations
91	Integrative analysis and expression profiling of secondary cell wall genes in C4 biofuel model Setaria italica reveals targets for lignocellulose bioengineering. Frontiers in Plant Science, 2015, 6, 965.	3.6	33
92	Chilli leaf curl virus infection highlights the differential expression of genes involved in protein homeostasis and defense in resistant chilli plants. Applied Microbiology and Biotechnology, 2015, 99, 4757-4770.	3.6	29
93	Advances inÂSetariaÂgenomics for genetic improvement of cereals and bioenergy grasses. Theoretical and Applied Genetics, 2015, 128, 1-14.	3.6	190
94	Application of molecular antiviral compounds: novel approach for durable resistance against geminiviruses. Molecular Biology Reports, 2015, 42, 1157-1162.	2.3	12
95	Drought Stress Responses and Signal Transduction in Plants. , 2015, , 195-225.		56
96	Genome-wide development of transposable elements-based markers in foxtail millet and construction of an integrated database. DNA Research, 2015, 22, 79-90.	3.4	71
97	Review on different mechanisms of sex determination and sex-linked molecular markers in dioecious crops: a current update. Euphytica, 2015, 201, 161-194.	1.2	47
98	Identification, Characterization and Expression Profiling of Dicer-Like, Argonaute and RNA-Dependent RNA Polymerase Gene Families in Foxtail Millet. Plant Molecular Biology Reporter, 2015, 33, 43-55.	1.8	54
99	Unraveling 14-3-3 Proteins in C4 Panicoids with Emphasis on Model Plant Setaria italica Reveals Phosphorylation-Dependent Subcellular Localization of RS Splicing Factor. PLoS ONE, 2015, 10, e0123236.	2.5	37
100	Identification and Molecular Characterization of MYB Transcription Factor Superfamily in C4 Model Plant Foxtail Millet (Setaria italica L.). PLoS ONE, 2014, 9, e109920.	2.5	105
101	An overview of wheat genome sequencing and its implications for crop improvement. Journal of Genetics, 2014, 93, 619-622.	0.7	6
102	Development of novel microRNA-based genetic markers in foxtail millet for genotyping applications in related grass species. Molecular Breeding, 2014, 34, 2219-2224.	2.1	61
103	Genetic diversity of the conserved motifs of six bacterial leaf blight resistance genes in a set of rice landraces. BMC Genetics, 2014, 15, 82.	2.7	26
104	Genetic diversity analysis in a set of Caricaceae accessions using resistance gene analogues. BMC Genetics, 2014, 15, 137.	2.7	2
105	Association of an allele-specific marker with dehydration stress tolerance in foxtail millet suggests SiDREB2 to be an important QTL. Journal of Plant Biochemistry and Biotechnology, 2014, 23, 119-122.	1.7	23
106	Population structure and association mapping of yield contributing agronomic traits in foxtail millet. Plant Cell Reports, 2014, 33, 881-893.	5.6	71
107	Post-transcriptional and Epigenetic Arms of RNA Silencing: A Defense Machinery of Naturally Tolerant Tomato Plant Against Tomato Leaf Curl New Delhi Virus. Plant Molecular Biology Reporter, 2014, 32, 1015-1029.	1.8	28
108	FmTFDb: a foxtail millet transcription factors database for expediting functional genomics in millets. Molecular Biology Reports, 2014, 41, 6343-6348.	2.3	23

#	Article	IF	Citations
109	Differential expression of peroxidase and ABC transporter as the key regulatory components for degradation of azo dyes by Penicillium oxalicum SAR-3. Functional and Integrative Genomics, 2014, 14, 631-642.	3.5	8
110	Involvement of host regulatory pathways during geminivirus infection: a novel platform for generating durable resistance. Functional and Integrative Genomics, 2014, 14, 47-58.	3.5	39
111	C2H2 type of zinc finger transcription factors in foxtail millet define response to abiotic stresses. Functional and Integrative Genomics, 2014, 14, 531-543.	3.5	120
112	Comprehensive genome-wide identification and expression profiling of foxtail millet [Setaria italica (L.)] miRNAs in response to abiotic stress and development of miRNA database. Plant Cell, Tissue and Organ Culture, 2014, 118, 279-292.	2.3	56
113	Development of 5123 Intron-Length Polymorphic Markers for Large-Scale Genotyping Applications in Foxtail Millet. DNA Research, 2014, 21, 41-52.	3.4	109
114	Genome-Wide Investigation and Expression Analyses of WD40 Protein Family in the Model Plant Foxtail Millet (Setaria italica L.). PLoS ONE, 2014, 9, e86852.	2.5	100
115	Genome-Wide Investigation and Expression Profiling of AP2/ERF Transcription Factor Superfamily in Foxtail Millet (Setaria italica L.). PLoS ONE, 2014, 9, e113092.	2.5	148
116	Validation of an alleleâ€specific marker associated with dehydration stress tolerance in a core set of foxtail millet accessions. Plant Breeding, 2013, 132, 496-499.	1.9	17
117	Setaria genome sequencing: an overview. Journal of Plant Biochemistry and Biotechnology, 2013, 22, 257-260.	1.7	22
118	Reference genes for quantitative real-time PCR analysis in the model plant foxtail millet (Setaria) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	2.3	64
119	9th Solanaceae Conference 2012. The National Academy of Sciences, India, 2013, 36, 111-114.	1.3	0
120	Genetic diversity and population structure of rice landraces from Eastern and North Eastern States of India. BMC Genetics, 2013, 14, 71.	2.7	99
121	A comparative survey of genetic diversity among a set of Caricaceae accessions using microsatellite markers. SpringerPlus, 2013, 2, 345.	1.2	8
122	Development and utilization of novel <scp>SSR</scp>s in foxtail millet [<scp>S</scp>etaria italica (L.) P. Beauv.]. Plant Breeding, 2013, 132, 367-374.	1.9	25
123	Plant innate immunity: An updated insight into defense mechanism. Journal of Biosciences, 2013, 38, 433-449.	1.1	215
124	Recent Advances in Plantâ€"Virus Interaction with Emphasis on Small Interfering RNAs (siRNAs). Molecular Biotechnology, 2013, 55, 63-77.	2.4	47
125	Epigenetic mechanisms of plant stress responses and adaptation. Plant Cell Reports, 2013, 32, 1151-1159.	5.6	205
126	Genome-Wide Development and Use of Microsatellite Markers for Large-Scale Genotyping Applications in Foxtail Millet [Setaria italica (L.)]. DNA Research, 2013, 20, 197-207.	3.4	149

#	Article	IF	Citations
127	Foxtail millet: a model crop for genetic and genomic studies in bioenergy grasses. Critical Reviews in Biotechnology, 2013, 33, 328-343.	9.0	235
128	Comprehensive Genome-Wide Survey, Genomic Constitution and Expression Profiling of the NAC Transcription Factor Family in Foxtail Millet (Setaria italica L.). PLoS ONE, 2013, 8, e64594.	2.5	148
129	Development of eSSR-Markers in Setaria italica and Their Applicability in Studying Genetic Diversity, Cross-Transferability and Comparative Mapping in Millet and Non-Millet Species. PLoS ONE, 2013, 8, e67742.	2.5	121
130	FmMDb: A Versatile Database of Foxtail Millet Markers for Millets and Bioenergy Grasses Research. PLoS ONE, 2013, 8, e71418.	2.5	38
131	Recent advances in tomato functional genomics: utilization of VIGS. Protoplasma, 2012, 249, 1017-1027.	2.1	32
132	The DNA-binding activity of an AP2 protein is involved in transcriptional regulation of a stress-responsive gene, SiWD40, in foxtail millet. Genomics, 2012, 100, 252-263.	2.9	48
133	NAC proteins: regulation and role in stress tolerance. Trends in Plant Science, 2012, 17, 369-381.	8.8	890
134	Structure and regulatory networks of WD40 protein in plants. Journal of Plant Biochemistry and Biotechnology, 2012, 21, 32-39.	1.7	46
135	Dynamics of Defense-Related Components in Two Contrasting Genotypes of Tomato Upon Infection with Tomato Leaf Curl New Delhi Virus. Molecular Biotechnology, 2012, 52, 140-150.	2.4	16
136	A study of the role of gene TaMYB2 and an associated SNP in dehydration tolerance in common wheat. Molecular Biology Reports, 2012, 39, 10865-10871.	2.3	29
137	Genetic dissection of grain weight in bread wheat through quantitative trait locus interval and association mapping. Molecular Breeding, 2012, 29, 963-972.	2.1	92
138	Transcriptome Analysis of Differentially Expressed Genes During Embryo Sac Development in Apomeiotic Non-Parthenogenetic Interspecific Hybrid of Pennisetum glaucum. Molecular Biotechnology, 2012, 51, 262-271.	2.4	15
139	A comprehensive study on dehydration-induced antioxidative responses during germination of Indian bread wheat (Triticum aestivum L. em Thell) cultivars collected from different agroclimatic zones. Physiology and Molecular Biology of Plants, 2012, 18, 217-228.	3.1	38
140	Sequence-based novel genomic microsatellite markers for robust genotyping purposes in foxtail millet [Setaria italica (L.) P. Beauv.]. Plant Cell Reports, 2012, 31, 323-337.	5.6	78
141	Comparative transcriptome analysis of contrasting foxtail millet cultivars in response to short-term salinity stress. Journal of Plant Physiology, 2011, 168, 280-287.	3.5	79
142	Characterization and genetic linkage mapping of the horticulturally important mutation leafless inflorescence (lli) in periwinkle Catharanthus roseus. Scientia Horticulturae, 2011, 129, 142-153.	3.6	16
143	Development and utilization of novel intron length polymorphic markers in foxtail millet (<i>Setaria) Tj ETQq1 1 0.784314 rgBT /Over	2.0	52
144	Role of DREBs in regulation of abiotic stress responses in plants. Journal of Experimental Botany, 2011, 62, 4731-4748.	4.8	816

#	Article	IF	Citations
145	Differential antioxidative responses to dehydration-induced oxidative stress in core set of foxtail millet cultivars [Setaria italica (L.)]. Protoplasma, 2011, 248, 817-828.	2.1	95
146	Molecular Cloning and Characterization of a Membrane Associated NAC Family Gene, SiNAC from Foxtail Millet [Setaria italica (L.) P. Beauv.]. Molecular Biotechnology, 2011, 49, 138-150.	2.4	87
147	Association of an SNP in a novel DREB2-like gene SiDREB2 with stress tolerance in foxtail millet [Setaria italica (L.)]. Journal of Experimental Botany, 2011, 62, 3387-3401.	4.8	124
148	Electrophoretic mobility shift assay reveals a novel recognition sequence forSetaria italicaNAC protein. Plant Signaling and Behavior, 2011, 6, 1588-1590.	2.4	14
149	Variability in Indian bread wheat (Triticum aestivum L.) varieties differing in nitrogen efficiency as assessed by microsatellite markers. Protoplasma, 2010, 242, 55-67.	2.1	15
150	Tomato cultivar tolerant to Tomato leaf curl New Delhi virus infection induces virusâ€specific short interfering RNA accumulation and defenceâ€associated host gene expression. Molecular Plant Pathology, 2010, 11, 531-544.	4.2	63
151	Comparative transcriptome analysis of differentially expressed genes in foxtail millet (Setaria italica) Tj ETQq1 1 0.784314 rgBT /Overl 720-727.	2.1	107
152	Genome-wide QTL analysis for pre-harvest sprouting tolerance in bread wheat. Euphytica, 2009, 168, 319-329.	1.2	86
153	Development and characterization of genic SSR markers in Medicago truncatula and their transferability in leguminous and non-leguminous species. Genome, 2009, 52, 761-771.	2.0	59
154	ISSR marker-assisted selection of male and female plants in a promising dioecious crop: jojoba (Simmondsia chinensis). Plant Biotechnology Reports, 2008, 2, 239-243.	1.5	54
155	cDNA-AFLP Analysis Reveals Differential Gene Expression in Response to Salt Stress in Foxtail Millet (Setaria italica L.). Molecular Biotechnology, 2008, 40, 241-251.	2.4	72
156	EST-derived single nucleotide polymorphism markers for assembling genetic and physical maps of the barley genome. Functional and Integrative Genomics, 2008, 8, 223-233.	3.5	87
157	Crop Breeding Prospects in the Genomics Era. Journal of New Seeds, 2007, 8, 29-49.	0.3	0
158	A 1,000-loci transcript map of the barley genome: new anchoring points for integrative grass genomics. Theoretical and Applied Genetics, 2007, 114, 823-839.	3.6	239
159	Identification of sex in Simmondsia chinensis (Jojoba) using RAPD markers. Plant Biotechnology Reports, 2007, 1, 207-210.	1.5	54
160	Construction of genetic linkage map of the medicinal and ornamental plant Catharanthus roseus. Journal of Genetics, 2007, 86, 259-268.	0.7	33
161	MappedDs/T-DNA launch pads for functional genomics in barley. Plant Journal, 2006, 47, 811-826.	5.7	36
162	Expression genetics and haplotype analysis reveal cis regulation of serine carboxypeptidase I (Cxp1), a candidate gene for malting quality in barley (Hordeum vulgare L.). Functional and Integrative Genomics, 2006, 6, 25-35.	3.5	44

#	Article	IF	Citations
163	Genetic mapping and BAC assignment of EST-derived SSR markers shows non-uniform distribution of genes in the barley genome. Theoretical and Applied Genetics, 2006, 113, 239-250.	3.6	107
164	Genetic Relatedness among Indian Litchi Accessions (Litchi chinensis Sonn.) By RAPD Markers. International Journal of Agricultural Research, 2006, 1, 390-400.	0.1	14
165	Functional association between malting quality trait components and cDNA array based expression patterns in barley (Hordeum vulgare L.). Molecular Breeding, 2004, 14, 153-170.	2.1	72
166	An integrated approach for comparative mapping in rice and barley with special reference to the Rph16 resistance locus. Functional and Integrative Genomics, 2004, 4, 74-83.	3.5	55
167	The allene oxide cyclase of barley (Hordeum vulgare L.)â€"cloning and organ-specific expression. Phytochemistry, 2004, 65, 801-811.	2.9	39
168	Molecular Markers: Principles and Methodology. , 2002, , 9-54.		23
169	Use of SAMPL for a study of DNA polymorphism, genetic diversity and possible gene tagging in bread wheat. Theoretical and Applied Genetics, 2002, 104, 465-472.	3.6	32
170	Identification of eight chromosomes and a microsatellite marker on 1AS associated with QTL for grain weight in bread wheat. Theoretical and Applied Genetics, 2000, 100, 1290-1294.	3.6	77
171	Characterization of microsatellites and development of chromosome specific STMS markers in bread wheat. Plant Molecular Biology Reporter, 2000, 18, 5-16.	1.8	34
172	Identification of a microsatellite on chromosomes 6B and a STS on 7D of bread wheat showing an association with preharvest sprouting tolerance. Theoretical and Applied Genetics, 1999, 99, 336-340.	3.6	117
173	A microsatellite marker associated with a QTL for grain protein content on chromosome arm 2DL of bread wheat. Theoretical and Applied Genetics, 1999, 99, 341-345.	3.6	114