

Nese Sreenivasulu

List of Publications by Year in descending order

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Version: 2024-02-01

141
papers

8,988
citations

34105

52
h-index

45317

90
g-index

147
all docs

147
docs citations

147
times ranked

9913
citing authors

#	ARTICLE	IF	CITATIONS
1	The nutritional profile and human health benefit of pigmented rice and the impact of post-harvest processes and product development on the nutritional components: A review. <i>Critical Reviews in Food Science and Nutrition</i> , 2023, 63, 3867-3894.	10.3	10
2	Systems seed biology to understand and manipulate rice grain quality and nutrition. <i>Critical Reviews in Biotechnology</i> , 2023, 43, 716-733.	9.0	1
3	Enhancing health benefits of milled rice: current status and future perspectives. <i>Critical Reviews in Food Science and Nutrition</i> , 2022, 62, 8099-8119.	10.3	9
4	Lysine biofortification of crops to promote sustained human health in the 21st century. <i>Journal of Experimental Botany</i> , 2022, 73, 1258-1267.	4.8	17
5	Vitamin K in human health and metabolism: A nutri-genomics review. <i>Trends in Food Science and Technology</i> , 2022, 119, 412-427.	15.1	8
6	Diversity: current and prospective secondary metabolites for nutrition and medicine. <i>Current Opinion in Biotechnology</i> , 2022, 74, 164-170.	6.6	27
7	Laser microdissection transcriptome data derived gene regulatory networks of developing rice endosperm revealed tissue- and stage-specific regulators modulating starch metabolism. <i>Plant Molecular Biology</i> , 2022, 108, 443-467.	3.9	2
8	<i>INTERMEDIUM-C</i> mediates the shade-induced bud growth arrest in barley. <i>Journal of Experimental Botany</i> , 2022, 73, 1963-1977.	4.8	0
9	Post-genomics revolution in the design of premium quality rice in a high-yielding background to meet consumer demands in the 21st century. <i>Plant Communications</i> , 2022, 3, 100271.	7.7	19
10	Metabolomics based inferences to unravel phenolic compound diversity in cereals and its implications for human gut health. <i>Trends in Food Science and Technology</i> , 2022, 127, 14-25.	15.1	26
11	Efficient fortification of folic acid in rice through ultrasonic treatment and absorption. <i>Food Chemistry</i> , 2021, 335, 127629.	8.2	19
12	Impact of ultrasonic treatment on rice starch and grain functional properties: A review. <i>Ultrasonics Sonochemistry</i> , 2021, 71, 105383.	8.2	73
13	Genome-wide association coupled gene to gene interaction studies unveil novel epistatic targets among major effect loci impacting rice grain chalkiness. <i>Plant Biotechnology Journal</i> , 2021, 19, 910-925.	8.3	26
14	OsTPR boosts the superior grains through increase in upper secondary rachis branches without incurring a grain quality penalty. <i>Plant Biotechnology Journal</i> , 2021, 19, 1396-1411.	8.3	9
15	The genetics underlying metabolic signatures in a brown rice diversity panel and their vital role in human nutrition. <i>Plant Journal</i> , 2021, 106, 507-525.	5.7	22
16	Meeting human dietary vitamin requirements in the staple rice via strategies of biofortification and post-harvest fortification. <i>Trends in Food Science and Technology</i> , 2021, 109, 65-82.	15.1	32
17	What happens at night? Physiological mechanisms related to maintaining grain yield under high night temperature in rice. <i>Plant, Cell and Environment</i> , 2021, 44, 2245-2261.	5.7	22
18	Deploying viscosity and starch polymer properties to predict cooking and eating quality models: A novel breeding tool to predict texture. <i>Carbohydrate Polymers</i> , 2021, 260, 117766.	10.2	15

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19	Idealizing inflorescence architecture to enhance rice yield potential for feeding nine billion people in 2050. <i>Molecular Plant</i> , 2021, 14, 861-863.	8.3	6
20	Dataset on viscosity and starch polymer properties to predict texture through modeling. <i>Data in Brief</i> , 2021, 36, 107038.	1.0	2
21	Profiling of 2-Acetyl-1-Pyrroline and Other Volatile Compounds in Raw and Cooked Rice of Traditional and Improved Varieties of India. <i>Foods</i> , 2021, 10, 1917.	4.3	14
22	Improved Eating and Cooking Quality of indica Rice Cultivar YK17 via Adenine Base Editing of Wx Allele of Granule-Bound Starch Synthase I (GBSS I). <i>Rice Science</i> , 2021, 28, 427-430.	3.9	5
23	Application of classification models in screening superior rice grain quality in male sterile and pollen parents. <i>Journal of Food Composition and Analysis</i> , 2021, 104, 104137.	3.9	4
24	Enhancing the functional properties of rice starch through biopolymer blending for industrial applications: A review. <i>International Journal of Biological Macromolecules</i> , 2021, 192, 100-117.	7.5	28
25	Breeding Temperate Japonica Rice Varieties Adaptable to Tropical Regions: Progress and Prospects. <i>Agronomy</i> , 2021, 11, 2253.	3.0	1
26	Food Processing Technologies to Develop Functional Foods With Enriched Bioactive Phenolic Compounds in Cereals. <i>Frontiers in Plant Science</i> , 2021, 12, 771276.	3.6	23
27	Low glycemic index rice—a desired trait in starchy staples. <i>Trends in Food Science and Technology</i> , 2020, 106, 132-149.	15.1	57
28	Diversity of content and composition of cell wall-derived dietary fibre in polished rice. <i>Journal of Cereal Science</i> , 2020, 96, 103122.	3.7	12
29	Waxy Editing: Old Meets New. <i>Trends in Plant Science</i> , 2020, 25, 963-966.	8.8	37
30	Dataset on the folic acid uptake and the effect of sonication-based fortification on the color, pasting and textural properties of brown and milled rice. <i>Data in Brief</i> , 2020, 32, 106198.	1.0	3
31	Obtaining High-Quality Transcriptome Data from Cereal Seeds by a Modified Method for Gene Expression Profiling. <i>Journal of Visualized Experiments</i> , 2020, , .	0.3	0
32	Sonication increases the porosity of uncooked rice kernels affording softer textural properties, loss of intrinsic nutrients and increased uptake capacity during fortification. <i>Ultrasonics Sonochemistry</i> , 2020, 68, 105234.	8.2	12
33	The Genetic Basis and Nutritional Benefits of Pigmented Rice Grain. <i>Frontiers in Genetics</i> , 2020, 11, 229.	2.3	108
34	Rice yield formation under high day and night temperatures—a prerequisite to ensure future food security. <i>Plant, Cell and Environment</i> , 2020, 43, 1595-1608.	5.7	81
35	Balancing the double-edged sword effect of increased resistant starch content and its impact on rice texture: its genetics and molecular physiological mechanisms. <i>Plant Biotechnology Journal</i> , 2020, 18, 1763-1777.	8.3	36
36	High uptake and inward diffusion of iron fortificant in ultrasonicated milled rice. <i>LWT - Food Science and Technology</i> , 2020, 128, 109459.	5.2	8

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37	Brown Rice, a Diet Rich in Health Promoting Properties. <i>Journal of Nutritional Science and Vitaminology</i> , 2019, 65, S26-S28.	0.6	25
38	Improving Rice Dietary Fibre Content and Composition for Human Health. <i>Journal of Nutritional Science and Vitaminology</i> , 2019, 65, S48-S50.	0.6	9
39	Dissecting the genome-wide genetic variants of milling and appearance quality traits in rice. <i>Journal of Experimental Botany</i> , 2019, 70, 5115-5130.	4.8	30
40	Role and Regulation of Osmolytes and ABA Interaction in Salt and Drought Stress Tolerance. , 2019, , 417-436.		19
41	Osmolyte Diversity, Distribution, and Their Biosynthetic Pathways. , 2019, , 449-458.		10
42	Long glucan chains reduce in vitro starch digestibility of freshly cooked and retrograded milled rice. <i>Journal of Cereal Science</i> , 2019, 86, 108-116.	3.7	22
43	Integrating a genome-wide association study with a large-scale transcriptome analysis to predict genetic regions influencing the glycaemic index and texture in rice. <i>Plant Biotechnology Journal</i> , 2019, 17, 1261-1275.	8.3	56
44	Improving Head Rice Yield and Milling Quality: State-of-the-Art and Future Prospects. <i>Methods in Molecular Biology</i> , 2019, 1892, 1-18.	0.9	13
45	Rice Grain Quality Benchmarking Through Profiling of Volatiles and Metabolites in Grains Using Gas Chromatography Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2019, 1892, 187-199.	0.9	4
46	Quantifying Grain Digestibility of Starch Fractions in Milled Rice. <i>Methods in Molecular Biology</i> , 2019, 1892, 241-252.	0.9	3
47	Determination of Macronutrient and Micronutrient Content in Rice Grains Using Inductively Coupled Plasma-Optical Emission Spectrometry (ICP-OES). <i>Methods in Molecular Biology</i> , 2019, 1892, 253-264.	0.9	4
48	Determination of Cadmium Concentration in Milled and Brown Rice Grains Using Graphite Furnace Atomic Absorption Spectrometry. <i>Methods in Molecular Biology</i> , 2019, 1892, 265-275.	0.9	1
49	Analysis of Developing Rice Grain Transcriptome Using the Agilent Microarray Platform. <i>Methods in Molecular Biology</i> , 2019, 1892, 277-300.	0.9	4
50	Improving Rice Grain Quality: State-of-the-Art and Future Prospects. <i>Methods in Molecular Biology</i> , 2019, 1892, 19-55.	0.9	35
51	Novel Imaging Techniques to Analyze Panicle Architecture. <i>Methods in Molecular Biology</i> , 2019, 1892, 75-88.	0.9	2
52	Measuring Head Rice Recovery in Rice. <i>Methods in Molecular Biology</i> , 2019, 1892, 89-98.	0.9	2
53	Measurement of Rice Grain Dimensions and Chalkiness, and Rice Grain Elongation Using Image Analysis. <i>Methods in Molecular Biology</i> , 2019, 1892, 99-108.	0.9	11
54	Method Development of Near-Infrared Spectroscopy Approaches for Nondestructive and Rapid Estimation of Total Protein in Brown Rice Flour. <i>Methods in Molecular Biology</i> , 2019, 1892, 109-135.	0.9	4

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55	Multi-Dimensional Cooking Quality Classification Using Routine Quality Evaluation Methods. <i>Methods in Molecular Biology</i> , 2019, 1892, 137-150.	0.9	2
56	Characterization of Mechanical Texture Attributes of Cooked Milled Rice by Texture Profile Analyses and Unraveling Viscoelasticity Properties Through Rheometry. <i>Methods in Molecular Biology</i> , 2019, 1892, 151-167.	0.9	7
57	Laser Microdissection-Based Tissue-Specific Transcriptome Analysis Reveals a Novel Regulatory Network of Genes Involved in Heat-Induced Grain Chalk in Rice Endosperm. <i>Plant and Cell Physiology</i> , 2019, 60, 626-642.	3.1	40
58	Cross-Protection by Oxidative Stress: Improving Tolerance to Abiotic Stresses Including Salinity. , 2018, , 283-305.		8
59	Deciphering the Genetic Architecture of Cooked Rice Texture. <i>Frontiers in Plant Science</i> , 2018, 9, 1405.	3.6	34
60	Multivariate-based classification of predicting cooking quality ideotypes in rice (<i>Oryza sativa</i> L.) indica germplasm. <i>Rice</i> , 2018, 11, 56.	4.0	27
61	Abscisic acid influences tillering by modulation of strigolactones in barley. <i>Journal of Experimental Botany</i> , 2018, 69, 3883-3898.	4.8	51
62	Systems biology of seeds: deciphering the molecular mechanisms of seed storage, dormancy and onset of germination. <i>Plant Cell Reports</i> , 2017, 36, 633-635.	5.6	11
63	Leaf primordium size specifies leaf width and vein number among row-type classes in barley. <i>Plant Journal</i> , 2017, 91, 601-612.	5.7	25
64	Down-regulation of the sucrose transporters HvSUT1 and HvSUT2 affects sucrose homeostasis along its delivery path in barley grains. <i>Journal of Experimental Botany</i> , 2017, 68, 4595-4612.	4.8	28
65	Whole genome sequencing-based association study to unravel genetic architecture of cooked grain width and length traits in rice. <i>Scientific Reports</i> , 2017, 7, 12478.	3.3	69
66	Investigating glyceemic potential of rice by unraveling compositional variations in mature grain and starch mobilization patterns during seed germination. <i>Scientific Reports</i> , 2017, 7, 5854.	3.3	58
67	VRS2 regulates hormone-mediated inflorescence patterning in barley. <i>Nature Genetics</i> , 2017, 49, 157-161.	21.4	127
68	Systems Genetics Identifies a Novel Regulatory Domain of Amylose Synthesis. <i>Plant Physiology</i> , 2017, 173, 887-906.	4.8	71
69	Increase of DNA Methylation at the HvCKX2.1 Promoter by Terminal Drought Stress in Barley. <i>Epigenomes</i> , 2017, 1, 9.	1.8	37
70	A Potential Role of Flag Leaf Potassium in Conferring Tolerance to Drought-Induced Leaf Senescence in Barley. <i>Frontiers in Plant Science</i> , 2016, 7, 206.	3.6	38
71	The Metabolic Signature of Biomass Formation in Barley. <i>Plant and Cell Physiology</i> , 2016, 57, 1943-1960.	3.1	66
72	Tailoring Grain Storage Reserves for a Healthier Rice Diet and its Comparative Status with Other Cereals. <i>International Review of Cell and Molecular Biology</i> , 2016, 323, 31-70.	3.2	56

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73	Map-based Cloning and Characterization of the BPH18 Gene from Wild Rice Conferring Resistance to Brown Planthopper (BPH) Insect Pest. <i>Scientific Reports</i> , 2016, 6, 34376.	3.3	107
74	A trehalose-6-phosphate phosphatase enhances anaerobic germination tolerance in rice. <i>Nature Plants</i> , 2015, 1, 15124.	9.3	263
75	Action of multiple intra-QTL genes concerted around a co-localized transcription factor underpins a large effect QTL. <i>Scientific Reports</i> , 2015, 5, 15183.	3.3	58
76	The Genetic Basis of Composite Spike Form in Barley and "Miracle-Wheat"™. <i>Genetics</i> , 2015, 201, 155-165.	2.9	109
77	Role of proline in cell wall synthesis and plant development and its implications in plant ontogeny. <i>Frontiers in Plant Science</i> , 2015, 6, 544.	3.6	202
78	Staying Alive or Going to Die During Terminal Senescence"An Enigma Surrounding Yield Stability. <i>Frontiers in Plant Science</i> , 2015, 6, 1070.	3.6	73
79	Prospects of breeding high-quality rice using post-genomic tools. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1449-1466.	3.6	53
80	Designing climate-resilient rice with ideal grain quality suited for high-temperature stress. <i>Journal of Experimental Botany</i> , 2015, 66, 1737-1748.	4.8	164
81	Variation in primary metabolites in parental and near-isogenic lines of the QTL qDTY 12.1 : altered roots and flag leaves but similar spikelets of rice under drought. <i>Molecular Breeding</i> , 2015, 35, 138.	2.1	35
82	AtRD22 and AtUSPL1, Members of the Plant-Specific BURP Domain Family Involved in Arabidopsis thaliana Drought Tolerance. <i>PLoS ONE</i> , 2014, 9, e110065.	2.5	74
83	Molecular Breeding for Malting Quality. , 2014, , 293-309.		0
84	Drought Stress Tolerance Mechanisms in Barley and Its Relevance to Cereals. <i>Biotechnology in Agriculture and Forestry</i> , 2014, , 161-179.	0.2	7
85	Is proline accumulation <i>per se</i> correlated with stress tolerance or is proline homeostasis a more critical issue?. <i>Plant, Cell and Environment</i> , 2014, 37, 300-311.	5.7	535
86	Abscisic Acid Flux Alterations Result in Differential Abscisic Acid Signaling Responses and Impact Assimilation Efficiency in Barley under Terminal Drought Stress. <i>Plant Physiology</i> , 2014, 164, 1677-1696.	4.8	85
87	Unraveling Regulation of the Small Heat Shock Proteins by the Heat Shock Factor HvHsfB2c in Barley: Its Implications in Drought Stress Response and Seed Development. <i>PLoS ONE</i> , 2014, 9, e89125.	2.5	84
88	Seed-Development Programs: A Systems Biology-Based Comparison Between Dicots and Monocots. <i>Annual Review of Plant Biology</i> , 2013, 64, 189-217.	18.7	196
89	The phytohormone crosstalk paradigm takes center stage in understanding how plants respond to abiotic stresses. <i>Plant Cell Reports</i> , 2013, 32, 945-957.	5.6	218
90	Different Omics Approaches in Cereals and Their Possible Implications for Developing a System Biology Approach to Study the Mechanism of Abiotic Stress Tolerance. , 2013, , 177-214.		0

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91	Identification of quantitative trait loci contributing to yield and seed quality parameters under terminal drought in barley advanced backcross lines. <i>Molecular Breeding</i> , 2013, 32, 71-90.	2.1	73
92	<i>Six-rowed spike4</i> (<i>Vrs4</i>) controls spikelet determinacy and row-type in barley. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13198-13203.	7.1	140
93	Reverse Engineering: A Key Component of Systems Biology to Unravel Global Abiotic Stress Cross-Talk. <i>Frontiers in Plant Science</i> , 2012, 3, 294.	3.6	33
94	Integrated genomics, physiology and breeding approaches for improving drought tolerance in crops. <i>Theoretical and Applied Genetics</i> , 2012, 125, 625-645.	3.6	397
95	A genetic playground for enhancing grain number in cereals. <i>Trends in Plant Science</i> , 2012, 17, 91-101.	8.8	194
96	Contrapuntal role of ABA: Does it mediate stress tolerance or plant growth retardation under long-term drought stress?. <i>Gene</i> , 2012, 506, 265-273.	2.2	250
97	Fertility in barley flowers depends on <i>Jekyll</i> functions in male and female sporophytes. <i>New Phytologist</i> , 2012, 194, 142-157.	7.3	9
98	Comparative transcriptome analysis of contrasting foxtail millet cultivars in response to short-term salinity stress. <i>Journal of Plant Physiology</i> , 2011, 168, 280-287.	3.5	79
99	Dynamic ¹³ C/ ¹ H NMR imaging uncovers sugar allocation in the living seed. <i>Plant Biotechnology Journal</i> , 2011, 9, 1022-1037.	8.3	69
100	Differential antioxidative responses to dehydration-induced oxidative stress in core set of foxtail millet cultivars [<i>Setaria italica</i> (L.)]. <i>Protoplasma</i> , 2011, 248, 817-828.	2.1	95
101	Haplotyping, linkage mapping and expression analysis of barley genes regulated by terminal drought stress influencing seed quality. <i>BMC Plant Biology</i> , 2011, 11, 1.	3.6	214
102	Importance of ABA homeostasis under terminal drought stress in regulating grain filling events. <i>Plant Signaling and Behavior</i> , 2011, 6, 1228-1231.	2.4	15
103	ABA biosynthesis and degradation contributing to ABA homeostasis during barley seed development under control and terminal drought-stress conditions. <i>Journal of Experimental Botany</i> , 2011, 62, 2615-2632.	4.8	251
104	Array Platforms and Bioinformatics Tools for the Analysis of Plant Transcriptome in Response to Abiotic Stress. <i>Methods in Molecular Biology</i> , 2010, 639, 71-93.	0.9	25
105	Delineating the structural, functional and evolutionary relationships of sucrose phosphate synthase gene family II in wheat and related grasses. <i>BMC Plant Biology</i> , 2010, 10, 134.	3.6	14
106	De-regulation of abscisic acid contents causes abnormal endosperm development in the barley mutant <i>seg8</i> . <i>Plant Journal</i> , 2010, 64, 589-603.	5.7	59
107	Increasing Sucrose Uptake Capacity of Wheat Grains Stimulates Storage Protein Synthesis. <i>Plant Physiology</i> , 2010, 152, 698-710.	4.8	121
108	Robin: An Intuitive Wizard Application for R-Based Expression Microarray Quality Assessment and Analysis. <i>Plant Physiology</i> , 2010, 153, 642-651.	4.8	96

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109	Molecular Physiology of Seed Maturation and Seed Storage Protein Biosynthesis. , 2010, , 83-104.		9
110	Barley Grain Development. International Review of Cell and Molecular Biology, 2010, 281, 49-89.	3.2	75
111	Linkage mapping of putative regulator genes of barley grain development characterized by expression profiling. BMC Plant Biology, 2009, 9, 4.	3.6	10
112	Identification and functional validation of a unique set of drought induced genes preferentially expressed in response to gradual water stress in peanut. Molecular Genetics and Genomics, 2009, 281, 591-605.	2.1	110
113	Spatiotemporal Profiling of Starch Biosynthesis and Degradation in the Developing Barley Grain. Plant Physiology, 2009, 150, 190-204.	4.8	148
114	Quantitative imaging of oil storage in developing crop seeds. Plant Biotechnology Journal, 2008, 6, 31-45.	8.3	60
115	Cloning and expression of the tubulin genes in barley. Cell Biology International, 2008, 32, 557-559.	3.0	5
116	Mutagenesis and High-Throughput Functional Genomics in Cereal Crops: Current Status. Advances in Agronomy, 2008, 98, 357-414.	5.2	4
117	Barley Grain Maturation and Germination: Metabolic Pathway and Regulatory Network Commonalities and Differences Highlighted by New MapMan/PageMan Profiling Tools. Plant Physiology, 2008, 146, 1738-1758.	4.8	250
118	Different Hormonal Regulation of Cellular Differentiation and Function in Nucellar Projection and Endosperm Transfer Cells: A Microdissection-Based Transcriptome Study of Young Barley Grains. Plant Physiology, 2008, 148, 1436-1452.	4.8	104
119	Barley Genomics: An Overview. International Journal of Plant Genomics, 2008, 2008, 1-13.	2.2	64
120	Deciphering the regulatory mechanisms of abiotic stress tolerance in plants by genomic approaches. Gene, 2007, 388, 1-13.	2.2	281
121	Distinct tubulin genes are differentially expressed during barley grain development. Physiologia Plantarum, 2007, 131, 571-580.	5.2	17
122	Correlation-maximizing surrogate gene space for visual mining of gene expression patterns in developing barley endosperm tissue. BMC Bioinformatics, 2007, 8, 165.	2.6	11
123	Gene expression patterns reveal tissue-specific signaling networks controlling programmed cell death and ABA-regulated maturation in developing barley seeds. Plant Journal, 2006, 47, 310-327.	5.7	172
124	Antioxidative response in different sorghum species under short-term salinity stress. Acta Physiologiae Plantarum, 2006, 28, 465-475.	2.1	49
125	Generalized relevance LVQ (GRLVQ) with correlation measures for gene expression analysis. Neurocomputing, 2006, 69, 651-659.	5.9	23
126	PageMan: An interactive ontology tool to generate, display, and annotate overview graphs for profiling experiments. BMC Bioinformatics, 2006, 7, 535.	2.6	309

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127	Unsupervised Feature Selection for Biomarker Identification in Chromatography and Gene Expression Data. Lecture Notes in Computer Science, 2006, , 274-285.	1.3	2
128	The Methylation Cycle and its Possible Functions in Barley Endosperm Development. Plant Molecular Biology, 2005, 59, 289-307.	3.9	42
129	High-Throughput Multi-dimensional Scaling (HiT-MDS) for cDNA-Array Expression Data. Lecture Notes in Computer Science, 2005, , 625-633.	1.3	16
130	Large-scale analysis of the barley transcriptome based on expressed sequence tags. Plant Journal, 2004, 40, 276-290.	5.7	137
131	Functional association between malting quality trait components and cDNA array based expression patterns in barley (<i>Hordeum vulgare</i> L.). Molecular Breeding, 2004, 14, 153-170.	2.1	72
132	Transcript profiles and deduced changes of metabolic pathways in maternal and filial tissues of developing barley grains. Plant Journal, 2004, 37, 539-553.	5.7	115
133	Transcriptome changes in foxtail millet genotypes at high salinity: Identification and characterization of a PHGPX gene specifically up-regulated by NaCl in a salt-tolerant line. Journal of Plant Physiology, 2004, 161, 467-477.	3.5	70
134	Functional Genomics for Tolerance to Abiotic Stress in Cereals. , 2004, , 483-514.		6
135	Identification of genes specifically expressed in maternal and filial tissues of barley caryopses: a cDNA array analysis. Molecular Genetics and Genomics, 2002, 266, 758-767.	2.1	53
136	Differential gene expression during seed germination in barley (<i>Hordeum vulgare</i> L.). Functional and Integrative Genomics, 2002, 2, 28-39.	3.5	81
137	Differential response of antioxidant compounds to salinity stress in salt-tolerant and salt-sensitive seedlings of foxtail millet (<i>Setaria italica</i>). Physiologia Plantarum, 2000, 109, 435-442.	5.2	292
138	Total peroxidase activity and peroxidase isoforms as modified by salt stress in two cultivars of fox-tail millet with differential salt tolerance. Plant Science, 1999, 141, 1-9.	3.6	107
139	Photosynthetic Characteristics in Mulberry during Water Stress and Rewatering. Photosynthetica, 1998, 35, 259-263.	1.7	35
140	Effect of Water Stress on Photosynthesis in Two Mulberry Genotypes with Different drought Tolerance. Photosynthetica, 1998, 35, 279-283.	1.7	35
141	Intriguing Role of Proline in Redox Potential Conferring High Temperature Stress Tolerance. Frontiers in Plant Science, 0, 13, .	3.6	30