Nese Sreenivasulu

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Is proline accumulation <i>per se</i> correlated with stress tolerance or is proline homeostasis a more critical issue?. Plant, Cell and Environment, 2014, 37, 300-311.	5.7	535
2	Integrated genomics, physiology and breeding approaches for improving drought tolerance in crops. Theoretical and Applied Genetics, 2012, 125, 625-645.	3.6	397
3	PageMan: An interactive ontology tool to generate, display, and annotate overview graphs for profiling experiments. BMC Bioinformatics, 2006, 7, 535.	2.6	309
4	Differential response of antioxidant compounds to salinity stress in salt-tolerant and salt-sensitive seedlings of foxtail millet (Setaria italica). Physiologia Plantarum, 2000, 109, 435-442.	5.2	292
5	Deciphering the regulatory mechanisms of abiotic stress tolerance in plants by genomic approaches. Gene, 2007, 388, 1-13.	2.2	281
6	A trehalose-6-phosphate phosphatase enhances anaerobic germination tolerance in rice. Nature Plants, 2015, 1, 15124.	9.3	263
7	ABA biosynthesis and degradation contributing to ABA homeostasis during barley seed development under control and terminal drought-stress conditions. Journal of Experimental Botany, 2011, 62, 2615-2632.	4.8	251
8	Barley Grain Maturation and Germination: Metabolic Pathway and Regulatory Network Commonalities and Differences Highlighted by New MapMan/PageMan Profiling Tools Â. Plant Physiology, 2008, 146, 1738-1758.	4.8	250
9	Contrapuntal role of ABA: Does it mediate stress tolerance or plant growth retardation under long-term drought stress?. Gene, 2012, 506, 265-273.	2.2	250
10	The phytohormone crosstalk paradigm takes center stage in understanding how plants respond to abiotic stresses. Plant Cell Reports, 2013, 32, 945-957.	5.6	218
11	Haplotyping, linkage mapping and expression analysis of barley genes regulated by terminal drought stress influencing seed quality. BMC Plant Biology, 2011, 11, 1.	3.6	214
12	Role of proline in cell wall synthesis and plant development and its implications in plant ontogeny. Frontiers in Plant Science, 2015, 6, 544.	3.6	202
13	Seed-Development Programs: A Systems Biology–Based Comparison Between Dicots and Monocots. Annual Review of Plant Biology, 2013, 64, 189-217.	18.7	196
14	A genetic playground for enhancing grain number in cereals. Trends in Plant Science, 2012, 17, 91-101.	8.8	194
15	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
16	Designing climate-resilient rice with ideal grain quality suited for high-temperature stress. Journal of Experimental Botany, 2015, 66, 1737-1748.	4.8	164
17	Spatiotemporal Profiling of Starch Biosynthesis and Degradation in the Developing Barley Grain Â. Plant Physiology, 2009, 150, 190-204.	4.8	148
18	<i>Six-rowed spike4</i> (<i>Vrs4</i>) controls spikelet determinacy and row-type in barley. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13198-13203.	7.1	140

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19	Largeâ€scale analysis of the barley transcriptome based on expressed sequence tags. Plant Journal, 2004, 40, 276-290.	5.7	137
20	VRS2 regulates hormone-mediated inflorescence patterning in barley. Nature Genetics, 2017, 49, 157-161.	21.4	127
21	Increasing Sucrose Uptake Capacity of Wheat Grains Stimulates Storage Protein Synthesis Â. Plant Physiology, 2010, 152, 698-710.	4.8	121
22	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
23	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
24	The Genetic Basis of Composite Spike Form in Barley and â€~Miracle-Wheat'. Genetics, 2015, 201, 155-165.	2.9	109
25	The Genetic Basis and Nutritional Benefits of Pigmented Rice Grain. Frontiers in Genetics, 2020, 11, 229.	2.3	108
26	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
27	Map-based Cloning and Characterization of the BPH18 Gene from Wild Rice Conferring Resistance to Brown Planthopper (BPH) Insect Pest. Scientific Reports, 2016, 6, 34376.	3.3	107
28	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
29	Robin: An Intuitive Wizard Application for R-Based Expression Microarray Quality Assessment and Analysis Â. Plant Physiology, 2010, 153, 642-651.	4.8	96
30	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
31	Abscisic Acid Flux Alterations Result in Differential Abscisic Acid Signaling Responses and Impact Assimilation Efficiency in Barley under Terminal Drought Stress. Plant Physiology, 2014, 164, 1677-1696.	4.8	85
32	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. PLoS ONE, 2014, 9, e89125.	2.5	84
33	Differential gene expression during seed germination in barley (Hordeum vulgare L.). Functional and Integrative Genomics, 2002, 2, 28-39.	3.5	81
34	Rice yield formation under high day and night temperatures—A prerequisite to ensure future food security. Plant, Cell and Environment, 2020, 43, 1595-1608.	5.7	81
35	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
36	Barley Grain Development. International Review of Cell and Molecular Biology, 2010, 281, 49-89.	3.2	75

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37	AtRD22 and AtUSPL1, Members of the Plant-Specific BURP Domain Family Involved in Arabidopsis thaliana Drought Tolerance. PLoS ONE, 2014, 9, e110065.	2.5	74
38	Identification of quantitative trait loci contributing to yield and seed quality parameters under terminal drought in barley advanced backcross lines. Molecular Breeding, 2013, 32, 71-90.	2.1	73
39	Staying Alive or Going to Die During Terminal Senescence—An Enigma Surrounding Yield Stability. Frontiers in Plant Science, 2015, 6, 1070.	3.6	73
40	Impact of ultrasonic treatment on rice starch and grain functional properties: A review. Ultrasonics Sonochemistry, 2021, 71, 105383.	8.2	73
41	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
42	Systems Genetics Identifies a Novel Regulatory Domain of Amylose Synthesis. Plant Physiology, 2017, 173, 887-906.	4.8	71
43	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
44	Dynamic ¹³ C/ ¹ H NMR imaging uncovers sugar allocation in the living seed. Plant Biotechnology Journal, 2011, 9, 1022-1037.	8.3	69
45	Whole genome sequencing-based association study to unravel genetic architecture of cooked grain width and length traits in rice. Scientific Reports, 2017, 7, 12478.	3.3	69
46	The Metabolic Signature of Biomass Formation in Barley. Plant and Cell Physiology, 2016, 57, 1943-1960.	3.1	66
47	Barley Genomics: An Overview. International Journal of Plant Genomics, 2008, 2008, 1-13.	2.2	64
48	Quantitative imaging of oil storage in developing crop seeds. Plant Biotechnology Journal, 2008, 6, 31-45.	8.3	60
49	De-regulation of abscisic acid contents causes abnormal endosperm development in the barley mutant seg8. Plant Journal, 2010, 64, 589-603.	5.7	59
50	Action of multiple intra-QTL genes concerted around a co-localized transcription factor underpins a large effect QTL. Scientific Reports, 2015, 5, 15183.	3.3	58
51	Investigating glycemic potential of rice by unraveling compositional variations in mature grain and starch mobilization patterns during seed germination. Scientific Reports, 2017, 7, 5854.	3.3	58
52	Low glycemic index rice—a desired trait in starchy staples. Trends in Food Science and Technology, 2020, 106, 132-149.	15.1	57
53	Tailoring Grain Storage Reserves for a Healthier Rice Diet and its Comparative Status with Other Cereals. International Review of Cell and Molecular Biology, 2016, 323, 31-70.	3.2	56
54	Integrating a genomeâ€wide association study with a largeâ€scale transcriptome analysis to predict genetic regions influencing the glycaemic index and texture in rice. Plant Biotechnology Journal, 2019, 17, 1261-1275.	8.3	56

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55	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
56	Prospects of breeding high-quality rice using post-genomic tools. Theoretical and Applied Genetics, 2015, 128, 1449-1466.	3.6	53
57	Abscisic acid influences tillering by modulation of strigolactones in barley. Journal of Experimental Botany, 2018, 69, 3883-3898.	4.8	51
58	Antioxidative response in different sorghum species under short-term salinity stress. Acta Physiologiae Plantarum, 2006, 28, 465-475.	2.1	49
59	The Methylation Cycle and its Possible Functions in Barley Endosperm Development. Plant Molecular Biology, 2005, 59, 289-307.	3.9	42
60	Laser Microdissection-Based Tissue-Specific Transcriptome Analysis Reveals a Novel Regulatory Network of Genes Involved in Heat-Induced Grain Chalk in Rice Endosperm. Plant and Cell Physiology, 2019, 60, 626-642.	3.1	40
61	A Potential Role of Flag Leaf Potassium in Conferring Tolerance to Drought-Induced Leaf Senescence in Barley. Frontiers in Plant Science, 2016, 7, 206.	3.6	38
62	Increase of DNA Methylation at the HvCKX2.1 Promoter by Terminal Drought Stress in Barley. Epigenomes, 2017, 1, 9.	1.8	37
63	Waxy Editing: Old Meets New. Trends in Plant Science, 2020, 25, 963-966.	8.8	37
64	Balancing the doubleâ€edged sword effect of increased resistant starch content and its impact on rice texture: its genetics and molecular physiological mechanisms. Plant Biotechnology Journal, 2020, 18, 1763-1777.	8.3	36
65	Photosynthetic Characteristics in Mulberry during Water Stress and Rewatering. Photosynthetica, 1998, 35, 259-263.	1.7	35
66	Effect of Water Stress on Photosynthesis in Two Mulberry Genotypes with Different drought Tolerance. Photosynthetica, 1998, 35, 279-283.	1.7	35
67	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. Molecular Breeding, 2015, 35, 138.	2.1	35
68	Improving Rice Grain Quality: State-of-the-Art and Future Prospects. Methods in Molecular Biology, 2019, 1892, 19-55.	0.9	35
69	Deciphering the Genetic Architecture of Cooked Rice Texture. Frontiers in Plant Science, 2018, 9, 1405.	3.6	34
70	Reverse Engineering: A Key Component of Systems Biology to Unravel Global Abiotic Stress Cross-Talk. Frontiers in Plant Science, 2012, 3, 294.	3.6	33
71	Meeting human dietary vitamin requirements in the staple rice via strategies of biofortification and post-harvest fortification. Trends in Food Science and Technology, 2021, 109, 65-82.	15.1	32
72	Dissecting the genome-wide genetic variants of milling and appearance quality traits in rice. Journal of Experimental Botany, 2019, 70, 5115-5130.	4.8	30

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73	Intriguing Role of Proline in Redox Potential Conferring High Temperature Stress Tolerance. Frontiers in Plant Science, 0, 13, .	3.6	30
74	Down-regulation of the sucrose transporters HvSUT1 and HvSUT2 affects sucrose homeostasis along its delivery path in barley grains. Journal of Experimental Botany, 2017, 68, 4595-4612.	4.8	28
75	Enhancing the functional properties of rice starch through biopolymer blending for industrial applications: A review. International Journal of Biological Macromolecules, 2021, 192, 100-117.	7.5	28
76	Multivariate-based classification of predicting cooking quality ideotypes in rice (Oryza sativa L.) indica germplasm. Rice, 2018, 11, 56.	4.0	27
77	Diversity: current and prospective secondary metabolites for nutrition and medicine. Current Opinion in Biotechnology, 2022, 74, 164-170.	6.6	27
78	Genomeâ€wide association coupled gene to gene interaction studies unveil novel epistatic targets among major effect loci impacting rice grain chalkiness. Plant Biotechnology Journal, 2021, 19, 910-925.	8.3	26
79	Metabolomics based inferences to unravel phenolic compound diversity in cereals and its implications for human gut health. Trends in Food Science and Technology, 2022, 127, 14-25.	15.1	26
80	Array Platforms and Bioinformatics Tools for the Analysis of Plant Transcriptome in Response to Abiotic Stress. Methods in Molecular Biology, 2010, 639, 71-93.	0.9	25
81	Leaf primordium size specifies leaf width and vein number among rowâ€ŧype classes in barley. Plant Journal, 2017, 91, 601-612.	5.7	25
82	Brown Rice, a Diet Rich in Health Promoting Properties. Journal of Nutritional Science and Vitaminology, 2019, 65, S26-S28.	0.6	25
83	Generalized relevance LVQ (GRLVQ) with correlation measures for gene expression analysis. Neurocomputing, 2006, 69, 651-659.	5.9	23
84	Food Processing Technologies to Develop Functional Foods With Enriched Bioactive Phenolic Compounds in Cereals. Frontiers in Plant Science, 2021, 12, 771276.	3.6	23
85	Long glucan chains reduce in vitro starch digestibility of freshly cooked and retrograded milled rice. Journal of Cereal Science, 2019, 86, 108-116.	3.7	22
86	The genetics underlying metabolic signatures in a brown rice diversity panel and their vital role in human nutrition. Plant Journal, 2021, 106, 507-525.	5.7	22
87	What happens at night? Physiological mechanisms related to maintaining grain yield under high night temperature in rice. Plant, Cell and Environment, 2021, 44, 2245-2261.	5.7	22
88	Role and Regulation of Osmolytes and ABA Interaction in Salt and Drought Stress Tolerance. , 2019, , 417-436.		19
89	Efficient fortification of folic acid in rice through ultrasonic treatment and absorption. Food Chemistry, 2021, 335, 127629.	8.2	19
90	Post-genomics revolution in the design of premium quality rice in a high-yielding background to meet consumer demands in the 21st century. Plant Communications, 2022, 3, 100271.	7.7	19

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91	Distinct tubulin genes are differentially expressed during barley grain development. Physiologia Plantarum, 2007, 131, 571-580.	5.2	17
92	Lysine biofortification of crops to promote sustained human health in the 21st century. Journal of Experimental Botany, 2022, 73, 1258-1267.	4.8	17
93	High-Throughput Multi-dimensional Scaling (HiT-MDS) for cDNA-Array Expression Data. Lecture Notes in Computer Science, 2005, , 625-633.	1.3	16
94	Importance of ABA homeostasis under terminal drought stress in regulating grain filling events. Plant Signaling and Behavior, 2011, 6, 1228-1231.	2.4	15
95	Deploying viscosity and starch polymer properties to predict cooking and eating quality models: A novel breeding tool to predict texture. Carbohydrate Polymers, 2021, 260, 117766.	10.2	15
96	Delineating the structural, functional and evolutionary relationships of sucrose phosphate synthase gene family II in wheat and related grasses. BMC Plant Biology, 2010, 10, 134.	3.6	14
97	Profiling of 2-Acetyl-1-Pyrroline and Other Volatile Compounds in Raw and Cooked Rice of Traditional and Improved Varieties of India. Foods, 2021, 10, 1917.	4.3	14
98	Improving Head Rice Yield and Milling Quality: State-of-the-Art and Future Prospects. Methods in Molecular Biology, 2019, 1892, 1-18.	0.9	13
99	Diversity of content and composition of cell wall-derived dietary fibre in polished rice. Journal of Cereal Science, 2020, 96, 103122.	3.7	12
100	Sonication increases the porosity of uncooked rice kernels affording softer textural properties, loss of intrinsic nutrients and increased uptake capacity during fortification. Ultrasonics Sonochemistry, 2020, 68, 105234.	8.2	12
101	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
102	Systems biology of seeds: deciphering the molecular mechanisms of seed storage, dormancy and onset of germination. Plant Cell Reports, 2017, 36, 633-635.	5.6	11
103	Measurement of Rice Grain Dimensions and Chalkiness, and Rice Grain Elongation Using Image Analysis. Methods in Molecular Biology, 2019, 1892, 99-108.	0.9	11
104	Linkage mapping of putative regulator genes of barley grain development characterized by expression profiling. BMC Plant Biology, 2009, 9, 4.	3.6	10
105	Osmolyte Diversity, Distribution, and Their Biosynthetic Pathways. , 2019, , 449-458.		10
106	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. Critical Reviews in Food Science and Nutrition, 2023, 63, 3867-3894.	10.3	10
107	Molecular Physiology of Seed Maturation and Seed Storage Protein Biosynthesis. , 2010, , 83-104.		9
108	Fertility in barley flowers depends on <i>Jekyll</i> functions in male and female sporophytes. New Phytologist, 2012, 194, 142-157.	7.3	9

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109	Improving Rice Dietary Fibre Content and Composition for Human Health. Journal of Nutritional Science and Vitaminology, 2019, 65, S48-S50.	0.6	9
110	OsTPR boosts the superior grains through increase in upper secondary rachis branches without incurring a grain quality penalty. Plant Biotechnology Journal, 2021, 19, 1396-1411.	8.3	9
111	Enhancing health benefits of milled rice: current status and future perspectives. Critical Reviews in Food Science and Nutrition, 2022, 62, 8099-8119.	10.3	9
112	Cross-Protection by Oxidative Stress: Improving Tolerance to Abiotic Stresses Including Salinity. , 2018, , 283-305.		8
113	High uptake and inward diffusion of iron fortificant in ultrasonicated milled rice. LWT - Food Science and Technology, 2020, 128, 109459.	5.2	8
114	Vitamin K in human health and metabolism: A nutri-genomics review. Trends in Food Science and Technology, 2022, 119, 412-427.	15.1	8
115	Drought Stress Tolerance Mechanisms in Barley and Its Relevance to Cereals. Biotechnology in Agriculture and Forestry, 2014, , 161-179.	0.2	7
116	Characterization of Mechanical Texture Attributes of Cooked Milled Rice by Texture Profile Analyses and Unraveling Viscoelasticity Properties Through Rheometry. Methods in Molecular Biology, 2019, 1892, 151-167.	0.9	7
117	Functional Genomics for Tolerance to Abiotic Stress in Cereals. , 2004, , 483-514.		6
118	Idealizing inflorescence architecture to enhance rice yield potential for feeding nine billion people in 2050. Molecular Plant, 2021, 14, 861-863.	8.3	6
119	Cloning and expression of the tubulin genes in barley. Cell Biology International, 2008, 32, 557-559.	3.0	5
120	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). Rice Science, 2021, 28, 427-430.	3.9	5
121	Mutagenesis and Highâ€Throughput Functional Genomics in Cereal Crops: Current Status. Advances in Agronomy, 2008, 98, 357-414.	5.2	4
122	Rice Grain Quality Benchmarking Through Profiling of Volatiles and Metabolites in Grains Using Gas Chromatography Mass Spectrometry. Methods in Molecular Biology, 2019, 1892, 187-199.	0.9	4
123	Determination of Macronutrient and Micronutrient Content in Rice Grains Using Inductively Coupled Plasma-Optical Emission Spectrometry (ICP-OES). Methods in Molecular Biology, 2019, 1892, 253-264.	0.9	4
124	Analysis of Developing Rice Grain Transcriptome Using the Agilent Microarray Platform. Methods in Molecular Biology, 2019, 1892, 277-300.	0.9	4
125	Method Development of Near-Infrared Spectroscopy Approaches for Nondestructive and Rapid Estimation of Total Protein in Brown Rice Flour. Methods in Molecular Biology, 2019, 1892, 109-135.	0.9	4
126	Application of classification models in screening superior rice grain quality in male sterile and pollen parents. Journal of Food Composition and Analysis, 2021, 104, 104137.	3.9	4

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127	Quantifying Grain Digestibility of Starch Fractions in Milled Rice. Methods in Molecular Biology, 2019, 1892, 241-252.	0.9	3
128	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. Data in Brief, 2020, 32, 106198.	1.0	3
129	Unsupervised Feature Selection for Biomarker Identification in Chromatography and Gene Expression Data. Lecture Notes in Computer Science, 2006, , 274-285.	1.3	2
130	Novel Imaging Techniques to Analyze Panicle Architecture. Methods in Molecular Biology, 2019, 1892, 75-88.	0.9	2
131	Measuring Head Rice Recovery in Rice. Methods in Molecular Biology, 2019, 1892, 89-98.	0.9	2
132	Multi-Dimensional Cooking Quality Classification Using Routine Quality Evaluation Methods. Methods in Molecular Biology, 2019, 1892, 137-150.	0.9	2
133	Dataset on viscosity and starch polymer properties to predict texture through modeling. Data in Brief, 2021, 36, 107038.	1.0	2
134	Laser microdissection transcriptome data derived gene regulatory networks of developing rice endosperm revealed tissue- and stage-specific regulators modulating starch metabolism. Plant Molecular Biology, 2022, 108, 443-467.	3.9	2
135	Determination of Cadmium Concentration in Milled and Brown Rice Grains Using Graphite Furnace Atomic Absorption Spectrometry. Methods in Molecular Biology, 2019, 1892, 265-275.	0.9	1
136	Breeding Temperate Japonica Rice Varieties Adaptable to Tropical Regions: Progress and Prospects. Agronomy, 2021, 11, 2253.	3.0	1
137	Systems seed biology to understand and manipulate rice grain quality and nutrition. Critical Reviews in Biotechnology, 2023, 43, 716-733.	9.0	1
138	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
139	Molecular Breeding for Malting Quality. , 2014, , 293-309.		0
140	Obtaining High-Quality Transcriptome Data from Cereal Seeds by a Modified Method for Gene Expression Profiling. Journal of Visualized Experiments, 2020, , .	0.3	0
141	<i>INTERMEDIUM-C</i> mediates the shade-induced bud growth arrest in barley. Journal of Experimental Botany, 2022, 73, 1963-1977.	4.8	Ο