

John C Cushman

List of Publications by Year in descending order

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138
papers

10,936
citations

23567

58
h-index

33894

99
g-index

142
all docs

142
docs citations

142
times ranked

10059
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic approaches to plant stress tolerance. <i>Current Opinion in Plant Biology</i> , 2000, 3, 117-124.	7.1	582
2	Water and salinity stress in grapevines: early and late changes in transcript and metabolite profiles. <i>Functional and Integrative Genomics</i> , 2007, 7, 111-134.	3.5	474
3	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	21.4	472
4	Water deficit alters differentially metabolic pathways affecting important flavor and quality traits in grape berries of Cabernet Sauvignon and Chardonnay. <i>BMC Genomics</i> , 2009, 10, 212.	2.8	418
5	Transcriptomic and metabolite analyses of Cabernet Sauvignon grape berry development. <i>BMC Genomics</i> , 2007, 8, 429.	2.8	391
6	Crassulacean Acid Metabolism. A Plastic Photosynthetic Adaptation to Arid Environments. <i>Plant Physiology</i> , 2001, 127, 1439-1448.	4.8	217
7	A Sister Group Contrast Using Untargeted Global Metabolomic Analysis Delineates the Biochemical Regulation Underlying Desiccation Tolerance in <i>Sporobolus stapfianus</i> . <i>Plant Cell</i> , 2011, 23, 1231-1248.	6.6	212
8	A roadmap for research on crassulacean acid metabolism (CAM) to enhance sustainable food and bioenergy production in a hotter, drier world. <i>New Phytologist</i> , 2015, 207, 491-504.	7.3	211
9	Engineering crassulacean acid metabolism to improve water-use efficiency. <i>Trends in Plant Science</i> , 2014, 19, 327-338.	8.8	206
10	Crassulacean Acid Metabolism and Epiphytism Linked to Adaptive Radiations in the Orchidaceae. <i>Plant Physiology</i> , 2009, 149, 1838-1847.	4.8	194
11	Tissue-specific mRNA expression profiling in grape berry tissues. <i>BMC Genomics</i> , 2007, 8, 187.	2.8	193
12	Proteomic profiling of tandem affinity purified 14-3-3 protein complexes in <i>Arabidopsis thaliana</i> . <i>Proteomics</i> , 2009, 9, 2967-2985.	2.2	193
13	Proteomic analysis reveals differences between <i>Vitis vinifera</i> L. cv. Chardonnay and cv. Cabernet Sauvignon and their responses to water deficit and salinity. <i>Journal of Experimental Botany</i> , 2007, 58, 1873-1892.	4.8	181
14	Evolution along the crassulacean acid metabolism continuum. <i>Functional Plant Biology</i> , 2010, 37, 995.	2.1	177
15	A genomics approach towards salt stress tolerance. <i>Plant Physiology and Biochemistry</i> , 2001, 39, 295-311.	5.8	176
16	Salt tolerance, salt accumulation, and ionic homeostasis in an epidermal bladder-cell-less mutant of the common ice plant <i>Mesembryanthemum crystallinum</i> . <i>Journal of Experimental Botany</i> , 2007, 58, 1957-1967.	4.8	166
17	Annotating Genes of Known and Unknown Function by Large-Scale Coexpression Analysis. <i>Plant Physiology</i> , 2008, 147, 41-57.	4.8	162
18	Characterizing the Grape Transcriptome. Analysis of Expressed Sequence Tags from Multiple <i>Vitis</i> Species and Development of a Compendium of Gene Expression during Berry Development. <i>Plant Physiology</i> , 2005, 139, 574-597.	4.8	159

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19	The <i>Kalanchoë</i> genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. <i>Nature Communications</i> , 2017, 8, 1899.	12.8	159
20	Transcript, protein and metabolite temporal dynamics in the CAM plant <i>Agave</i> . <i>Nature Plants</i> , 2016, 2, 16178.	9.3	158
21	CRASSULACEAN ACID METABOLISM:Molecular Genetics. <i>Annual Review of Plant Biology</i> , 1999, 50, 305-332.	14.3	144
22	An improved RNA isolation method for succulent plant species rich in polyphenols and polysaccharides. <i>Plant Molecular Biology Reporter</i> , 2000, 18, 369-376.	1.8	141
23	Proteomic and selected metabolite analysis of grape berry tissues under well-watered and water-deficit stress conditions. <i>Proteomics</i> , 2009, 9, 2503-2528.	2.2	136
24	Conservation and Divergence of Circadian Clock Operation in a Stress-Inducible Crassulacean Acid Metabolism Species Reveals Clock Compensation against Stress. <i>Plant Physiology</i> , 2005, 137, 969-982.	4.8	132
25	A Minimal Serine/Threonine Protein Kinase Circadianly Regulates Phosphoenolpyruvate Carboxylase Activity in Crassulacean Acid Metabolism-Induced Leaves of the Common Ice Plant. <i>Plant Physiology</i> , 2000, 123, 1471-1482.	4.8	131
26	The Ice Plant <i>Cometh</i> : Lessons in Abiotic Stress Tolerance. <i>Journal of Plant Growth Regulation</i> , 2000, 19, 334-346.	5.1	129
27	Large-scale mRNA expression profiling in the common ice plant, <i>Mesembryanthemum crystallinum</i> , performing C3 photosynthesis and Crassulacean acid metabolism (CAM). <i>Journal of Experimental Botany</i> , 2008, 59, 1875-1894.	4.8	128
28	A stress-induced calcium-dependent protein kinase from <i>Mesembryanthemum crystallinum</i> phosphorylates a two-component pseudo-response regulator. <i>Plant Journal</i> , 2000, 24, 679-691.	5.7	124
29	Linking genes of unknown function with abiotic stress responses by high-throughput phenotype screening. <i>Physiologia Plantarum</i> , 2013, 148, 322-333.	5.2	123
30	Transcript abundance profiles reveal larger and more complex responses of grapevine to chilling compared to osmotic and salinity stress. <i>Functional and Integrative Genomics</i> , 2007, 7, 317-333.	3.5	120
31	Metabolomic Profiling in <i>Selaginella lepidophylla</i> at Various Hydration States Provides New Insights into the Mechanistic Basis of Desiccation Tolerance. <i>Molecular Plant</i> , 2013, 6, 369-385.	8.3	117
32	Conformation of a Group 2 Late Embryogenesis Abundant Protein from Soybean. Evidence of Poly (l-Proline)-type II Structure. <i>Plant Physiology</i> , 2003, 131, 963-975.	4.8	112
33	Disentangling Sources of Gene Tree Discordance in Phylogenomic Data Sets: Testing Ancient Hybridizations in <i>Amaranthaceae</i> s.l. <i>Systematic Biology</i> , 2021, 70, 219-235.	5.6	112
34	Effect of hypermethylation of CCWGG sequences in DNA of <i>Mesembryanthemum crystallinum</i> plants on their adaptation to salt stress. <i>Biochemistry (Moscow)</i> , 2006, 71, 461-465.	1.5	106
35	Transcript profiling of salinity stress responses by large-scale expressed sequence tag analysis in <i>Mesembryanthemum crystallinum</i> . <i>Gene</i> , 2004, 341, 83-92.	2.2	105
36	Enhanced Tolerance to Oxidative Stress in Transgenic <i>Arabidopsis</i> Plants Expressing Proteins of Unknown Function Å Å. <i>Plant Physiology</i> , 2008, 148, 280-292.	4.8	105

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37	The <i>Dunaliella salina</i> organelle genomes: large sequences, inflated with intronic and intergenic DNA. <i>BMC Plant Biology</i> , 2010, 10, 83.	3.6	98
38	Autophosphorylation and Subcellular Localization Dynamics of a Salt- and Water Deficit-Induced Calcium-Dependent Protein Kinase from Ice Plant. <i>Plant Physiology</i> , 2004, 135, 1430-1446.	4.8	97
39	Biomass characterization of <i>Agave</i> and <i>Opuntia</i> as potential biofuel feedstocks. <i>Biomass and Bioenergy</i> , 2015, 76, 43-53.	5.7	97
40	Charting plant interactomes: possibilities and challenges. <i>Trends in Plant Science</i> , 2008, 13, 183-191.	8.8	93
41	The unicellular green alga <i>Dunaliella salina</i> Teod. as a model for abiotic stress tolerance: genetic advances and future perspectives. <i>Algae</i> , 2011, 26, 3-20.	2.3	92
42	Signaling Events Leading to Crassulacean Acid Metabolism Induction in the Common Ice Plant. <i>Plant Physiology</i> , 1999, 121, 545-556.	4.8	88
43	Development and use of bioenergy feedstocks for semi-arid and arid lands. <i>Journal of Experimental Botany</i> , 2015, 66, 4177-4193.	4.8	88
44	Comparative metabolic profiling between desiccation-sensitive and desiccation-tolerant species of <i>Selaginella</i> reveals insights into the resurrection trait. <i>Plant Journal</i> , 2012, 72, 983-999.	5.7	87
45	The Arabidopsis AtDi19 Gene Family Encodes a Novel Type of Cys2/His2 Zinc-finger Protein Implicated in ABA-independent Dehydration, High-salinity Stress and Light Signaling Pathways. <i>Plant Molecular Biology</i> , 2006, 61, 13-30.	3.9	85
46	Generic recircumscriptions of Oncidiinae (Orchidaceae: Cymbidieae) based on maximum likelihood analysis of combined DNA datasets. <i>Botanical Journal of the Linnean Society</i> , 2012, 168, 117-146.	1.6	85
47	The <i>Vitis vinifera</i> Repeat binding protein 4 (<i>VvCBF4</i>) transcriptional factor enhances freezing tolerance in wine grape. <i>Plant Biotechnology Journal</i> , 2012, 10, 105-124.	8.3	83
48	Draft Nuclear Genome Sequence of the Halophilic and Beta-Carotene-Accumulating Green Alga <i>Dunaliella salina</i> Strain CCAP19/18. <i>Genome Announcements</i> , 2017, 5, .	0.8	83
49	Calcium-Dependent Protein Kinases from Arabidopsis Show Substrate Specificity Differences in an Analysis of 103 Substrates. <i>Frontiers in Plant Science</i> , 2011, 2, 36.	3.6	80
50	Temporal and spatial transcriptomic and microRNA dynamics of CAM photosynthesis in pineapple. <i>Plant Journal</i> , 2017, 92, 19-30.	5.7	78
51	Integrating diel starch metabolism with the circadian and environmental regulation of Crassulacean acid metabolism in <i>Mesembryanthemum crystallinum</i> . <i>Planta</i> , 2003, 216, 789-797.	3.2	76
52	A phyloproteomic characterization of in vitro autophosphorylation in calcium-dependent protein kinases. <i>Proteomics</i> , 2006, 6, 3649-3664.	2.2	75
53	Water Deficit Increases Stilbene Metabolism in Cabernet Sauvignon Berries. <i>Journal of Agricultural and Food Chemistry</i> , 2011, 59, 289-297.	5.2	73
54	Characterization and expression of a NADP-malic enzyme cDNA induced by salt stress from the facultative crassulacean acid metabolism plant, <i>Mesembryanthemum crystallinum</i> . <i>FEBS Journal</i> , 1992, 208, 259-266.	0.2	72

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55	A novel yeast two-hybrid approach to identify CDPK substrates: Characterization of the interaction between AtCPK11 and AtDi19, a nuclear zinc finger protein1. FEBS Letters, 2006, 580, 904-911.	2.8	69
56	An EST catalogue from the resurrection plant <i>Selaginella lepidophylla</i> reveals abiotic stress-adaptive genes. Plant Science, 2006, 170, 1173-1184.	3.6	69
57	Isolation and Characterization of Mutants of Common Ice Plant Deficient in Crassulacean Acid Metabolism. Plant Physiology, 2008, 147, 228-238.	4.8	65
58	The incidence of crassulacean acid metabolism in Orchidaceae derived from carbon isotope ratios: a checklist of the flora of Panama and Costa Rica. Botanical Journal of the Linnean Society, 0, 163, 194-222.	1.6	65
59	What makes species unique? The contribution of proteins with obscure features. Genome Biology, 2006, 7, R57.	9.6	64
60	Crassulacean acid metabolism. A plastic photosynthetic adaptation to arid environments. Plant Physiology, 2001, 127, 1439-48.	4.8	63
61	Multiple isoforms of phosphoenolpyruvate carboxylase in the Orchidaceae (subtribe Oncidiinae): implications for the evolution of crassulacean acid metabolism. Journal of Experimental Botany, 2014, 65, 3623-3636.	4.8	62
62	<i>Sporobolus stapfianus</i> : Insights into desiccation tolerance in the resurrection grasses from linking transcriptomics to metabolomics. BMC Plant Biology, 2017, 17, 67.	3.6	61
63	Thiamin pyrophosphokinase is required for thiamin cofactor activation in Arabidopsis. Plant Molecular Biology, 2007, 65, 151-162.	3.9	60
64	The bracteatus pineapple genome and domestication of clonally propagated crops. Nature Genetics, 2019, 51, 1549-1558.	21.4	60
65	Climate-resilient agroforestry: physiological responses to climate change and engineering of crassulacean acid metabolism (CAM) as a mitigation strategy. Plant, Cell and Environment, 2015, 38, 1833-1849.	5.7	59
66	Are the metabolic components of crassulacean acid metabolism up-regulated in response to an increase in oxidative burden?. Journal of Experimental Botany, 2006, 57, 319-328.	4.8	55
67	Expressed sequence tag (EST) profiling in hyper saline shocked <i>Dunaliella salina</i> reveals high expression of protein synthetic apparatus components. Plant Science, 2010, 179, 437-449.	3.6	53
68	Salt Stress Leads to Differential Expression of Two Isogenes of Phosphoenolpyruvate Carboxylase during Crassulacean Acid Metabolism Induction in the Common Ice Plant. Plant Cell, 1989, 1, 715.	6.6	51
69	Synthetic biology as it relates to CAM photosynthesis: challenges and opportunities. Journal of Experimental Botany, 2014, 65, 3381-3393.	4.8	49
70	Orchestration of carbohydrate processing for crassulacean acid metabolism. Current Opinion in Plant Biology, 2016, 31, 118-124.	7.1	49
71	Molecular cloning and expression of chloroplast NADP-malate dehydrogenase during Crassulacean acid metabolism induction by salt stress. Photosynthesis Research, 1993, 35, 15-27.	2.9	48
72	A salinity-induced gene from the halophyte <i>M. crystallinum</i> encodes a glycolytic enzyme, cofactor-independent phosphoglyceromutase. Plant Molecular Biology, 1995, 29, 213-226.	3.9	48

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73	Evolution of <i>DOPA</i> 4,5-dioxygenase activity allows for recurrent specialisation to betalain pigmentation in Caryophyllales. <i>New Phytologist</i> , 2020, 227, 914-929.	7.3	48
74	Identification of Ice Plant (<i>Mesembryanthemum crystallinum</i> L.) MicroRNAs Using RNA-Seq and Their Putative Roles in High Salinity Responses in Seedlings. <i>Frontiers in Plant Science</i> , 2016, 7, 1143.	3.6	47
75	ESTAP—an automated system for the analysis of EST data. <i>Bioinformatics</i> , 2003, 19, 1720-1722.	4.1	46
76	Laying the Foundation for Crassulacean Acid Metabolism (CAM) Biodesign: Expression of the C4 Metabolism Cycle Genes of CAM in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 101.	3.6	45
77	Identification of proteins that interact with catalytically active calcium-dependent protein kinases from <i>Arabidopsis</i> . <i>Molecular Genetics and Genomics</i> , 2009, 281, 375-390.	2.1	44
78	Environmental, hormonal and circadian regulation of crassulacean acid metabolism expression. <i>Functional Plant Biology</i> , 2002, 29, 669.	2.1	43
79	Cladogram of Panamanian <i>Clusia</i> Based on Nuclear DNA: Implications for the Origins of Crassulacean Acid Metabolism. <i>Plant Biology</i> , 2003, 5, 59-70.	3.8	40
80	Nutritional and mineral content of prickly pear cactus: A highly water-use efficient forage, fodder and food species. <i>Journal of Agronomy and Crop Science</i> , 2019, 205, 625-634.	3.5	40
81	Induction of a cysteine protease cDNA from <i>Mesembryanthemum crystallinum</i> leaves by environmental stress and plant growth regulators. <i>Plant Science</i> , 1998, 136, 195-206.	3.6	39
82	A <i>Vitis vinifera</i> basic helix-loop-helix transcription factor enhances plant cell size, vegetative biomass and reproductive yield. <i>Plant Biotechnology Journal</i> , 2018, 16, 1595-1615.	8.3	39
83	Understanding trait diversity associated with crassulacean acid metabolism (CAM). <i>Current Opinion in Plant Biology</i> , 2019, 49, 74-85.	7.1	38
84	Analysis of Triacylglycerols and Free Fatty Acids in Algae Using Ultra-Performance Liquid Chromatography Mass Spectrometry. <i>JAOCS, Journal of the American Oil Chemists' Society</i> , 2013, 90, 53-64.	1.9	37
85	Plant tissue succulence engineering improves water-use efficiency, water-deficit stress attenuation and salinity tolerance in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2020, 103, 1049-1072.	5.7	36
86	POFs: what we don't know can hurt us. <i>Trends in Plant Science</i> , 2007, 12, 492-496.	8.8	35
87	Identification of tissue-specific, abiotic stress-responsive gene expression patterns in wine grape (<i>Vitis</i>) Tj ETQq1 1 0.784314 ggBT /Over	3.6	35
88	Nucleotide sequence of the gene encoding a CAM specific isoform of phosphoenolpyruvate carboxylase from <i>Mesembryanthemum crystallinum</i> . <i>Nucleic Acids Research</i> , 1989, 17, 6745-6746.	14.5	32
89	Abscisic acid signaling and protein synthesis requirements for phosphoenolpyruvate carboxylase transcript induction in the common ice plant. <i>Journal of Plant Physiology</i> , 2002, 159, 1235-1243.	3.5	32
90	Transcriptional profiles of organellar metabolite transporters during induction of crassulacean acid metabolism in <i>Mesembryanthemum crystallinum</i> . <i>Functional Plant Biology</i> , 2005, 32, 451.	2.1	29

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91	Crassulacean Acid Metabolism Abiotic Stress-Responsive Transcription Factors: a Potential Genetic Engineering Approach for Improving Crop Tolerance to Abiotic Stress. <i>Frontiers in Plant Science</i> , 2019, 10, 129.	3.6	28
92	Ion accumulation and expression of ion homeostasis-related genes associated with halophilism, NaCl-promoted growth in a halophyte <i>Mesembryanthemum crystallinum</i> L.. <i>Plant Production Science</i> , 2020, 23, 91-102.	2.0	28
93	Research note: Large gene family of phosphoenolpyruvate carboxylase in the crassulacean acid metabolism plant <i>Kalanchoe pinnata</i> (Crassulaceae) characterised by partial cDNA sequence analysis. <i>Functional Plant Biology</i> , 2005, 32, 467.	2.1	26
94	Identification of Genes Encoding Enzymes Catalyzing the Early Steps of Carrot Polyacetylene Biosynthesis. <i>Plant Physiology</i> , 2018, 178, 1507-1521.	4.8	26
95	A CAM- and starch-deficient mutant of the facultative CAM species <i>Mesembryanthemum crystallinum</i> reconciles sink demands by repartitioning carbon during acclimation to salinity. <i>Journal of Experimental Botany</i> , 2012, 63, 1985-1996.	4.8	25
96	Crassulacean Acid Metabolism May Alleviate Production of Reactive Oxygen Species in a Facultative CAM Plant, the Common Ice Plant <i>Mesembryanthemum crystallinum</i> L.. <i>Plant Production Science</i> , 2010, 13, 256-260.	2.0	24
97	Quantitative ROS bioreporters: A robust toolkit for studying biological roles of ROS in response to abiotic and biotic stresses. <i>Physiologia Plantarum</i> , 2019, 165, 356-368.	5.2	24
98	Realizing the Potential of <i>Camelina sativa</i> as a Bioenergy Crop for a Changing Global Climate. <i>Plants</i> , 2022, 11, 772.	3.5	24
99	Expression, purification, and initial characterization of a recombinant form of plant PEP-carboxylase kinase from CAM-induced <i>Mesembryanthemum crystallinum</i> with enhanced solubility in <i>Escherichia coli</i> . <i>Protein Expression and Purification</i> , 2003, 29, 123-131.	1.3	22
100	Five-year field trial of the biomass productivity and water input response of cactus pear (<i>Opuntia</i> spp.) as a bioenergy feedstock for arid lands. <i>GCB Bioenergy</i> , 2021, 13, 719-741.	5.6	20
101	A novel coiled-coil protein co-localizes and interacts with a calcium-dependent protein kinase in the common ice plant during low-humidity stress. <i>Planta</i> , 2006, 225, 57-73.	3.2	19
102	Perspectives on the basic and applied aspects of crassulacean acid metabolism (CAM) research. <i>Plant Science</i> , 2018, 274, 394-401.	3.6	18
103	Genomic adaptations of the green alga <i>Dunaliella salina</i> to life under high salinity. <i>Algal Research</i> , 2020, 50, 101990.	4.6	18
104	C ₃ Photosynthesis to Crassulacean Acid Metabolism Shift in <i>Mesembryanthemum crystallinum</i> : A Stress Tolerance Mechanism. , 2004, , 241-244.		18
105	Understanding Vegetative Desiccation Tolerance Using Integrated Functional Genomics Approaches Within a Comparative Evolutionary Framework. <i>Ecological Studies</i> , 2011, , 307-338.	1.2	17
106	Metabolic rates associated with membrane fatty acids in mice selected for increased maximal metabolic rate. <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2013, 165, 70-78.	1.8	17
107	Exploring the Relationship between Crassulacean Acid Metabolism (CAM) and Mineral Nutrition with a Special Focus on Nitrogen. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4363.	4.1	16
108	Biosystems Design to Accelerate C ₃ -to-CAM Progression. <i>Biodesign Research</i> , 2020, 2020, .	1.9	16

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109	Five-Year Field Trial of Eight <i>Camelina sativa</i> Cultivars for Biomass to be Used in Biofuel under Irrigated Conditions in a Semi-Arid Climate. <i>Agronomy</i> , 2020, 10, 562.	3.0	14
110	Editorial: Systems Biology and Synthetic Biology in Relation to Drought Tolerance or Avoidance in Plants. <i>Frontiers in Plant Science</i> , 2020, 11, 394.	3.6	13
111	Light-responsive expression atlas reveals the effects of light quality and intensity in <i>Kalanchoë fedtschenkoi</i> , a plant with crassulacean acid metabolism. <i>GigaScience</i> , 2020, 9, .	6.4	11
112	Induction of Crassulacean Acid Metabolism—Molecular Aspects. <i>Advances in Photosynthesis and Respiration</i> , 2000, , 551-582.	1.0	11
113	Isolation and characterization of a novel v-SNARE family protein that interacts with a calcium-dependent protein kinase from the common ice plant, <i>Mesembryanthemum crystallinum</i> . <i>Planta</i> , 2007, 225, 783-799.	3.2	10
114	Transgressive, reiterative selection by continuous buoyant density gradient centrifugation of <i>Dunaliella salina</i> results in enhanced lipid and starch content. <i>Algal Research</i> , 2015, 9, 194-203.	4.6	10
115	New perspectives on crassulacean acid metabolism biology. <i>Journal of Experimental Botany</i> , 2019, 70, 6489-6493.	4.8	10
116	Induction of Crassulacean Acid Metabolism by Salinity - Molecular Aspects. , 2002, , 361-393.		10
117	Divide and Conquer (DC) BLAST: fast and easy BLAST execution within HPC environments. <i>PeerJ</i> , 2017, 5, e3486.	2.0	10
118	Evaluation of Diverse Microalgal Species as Potential Biofuel Feedstocks Grown Using Municipal Wastewater. <i>Frontiers in Energy Research</i> , 2015, 3, .	2.3	9
119	Plant responses and adaptations to a changing climate. <i>Plant Journal</i> , 2022, 109, 319-322.	5.7	9
120	Suppression subtractive hybridization library construction and identification of epidermal bladder cell related genes in the common ice plant, <i>Mesembryanthemum crystallinum</i> L.. <i>Plant Production Science</i> , 2016, 19, 552-561.	2.0	8
121	MYB and HD-ZIP IV homologs related to trichome formation are involved in epidermal bladder cell development in the halophyte <i>Mesembryanthemum crystallinum</i> L.. <i>Plant Production Science</i> , 2017, 20, 72-82.	2.0	8
122	Fast Pyrolysis of <i>Opuntia ficus-indica</i> (Prickly Pear) and <i>Grindelia squarrosa</i> (Gumweed). <i>Energy & Fuels</i> , 2018, 32, 3510-3518.	5.1	8
123	Crassulacean acid metabolism: recent advances and future opportunities. <i>Functional Plant Biology</i> , 2005, 32, 375.	2.1	7
124	Leaf carbohydrates influence transcriptional and post-transcriptional regulation of nocturnal carboxylation and starch degradation in the facultative CAM plant, <i>Mesembryanthemum crystallinum</i> . <i>Journal of Plant Physiology</i> , 2017, 218, 144-154.	3.5	7
125	An <i>rbcl</i> mRNA-binding protein is associated with C3 to C4 evolution and light-induced production of Rubisco in <i>Flaveria</i> . <i>Journal of Experimental Botany</i> , 2017, 68, 4635-4649.	4.8	7
126	An <i>Agrobacterium</i> -mediated transformation via organogenesis regeneration of a facultative CAM plant, the common ice plant <i>Mesembryanthemum crystallinum</i> L. <i>Plant Production Science</i> , 2020, 23, 343-349.	2.0	5

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127	Chapter 10 Climate Change Responses and Adaptations in Crassulacean Acid Metabolism (CAM) Plants. <i>Advances in Photosynthesis and Respiration</i> , 2021, , 283-329.	1.0	5
128	Membrane Profiling by Free Flow Electrophoresis and SWATH-MS to Characterize Subcellular Compartment Proteomes in <i>Mesembryanthemum crystallinum</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 5020.	4.1	5
129	Biomass Production, Nutritional and Mineral Content of Desiccation-Sensitive and Desiccation-Tolerant Species of <i>Sporobolus</i> under Multiple Irrigation Regimes. <i>Journal of Agronomy and Crop Science</i> , 2013, 199, 309-320.	3.5	4
130	Characterization of a microbial consortium with potential for biological degradation of cactus pear biomass for biofuel production. <i>Heliyon</i> , 2021, 7, e07854.	3.2	4
131	Simultaneous chloroplast, mitochondria isolation and mitochondrial protein preparation for two-dimensional electrophoresis analysis of Ice plant leaves under well watered and water-deficit stressed treatments. <i>Protein Expression and Purification</i> , 2019, 155, 86-94.	1.3	3
132	Metabolic profiling of epidermal and mesophyll tissues under water-deficit stress in <i>Opuntia ficus-indica</i> reveals stress-adaptive metabolic responses. <i>Functional Plant Biology</i> , 2021, 48, 717.	2.1	3
133	Characterization of Seed, Oil, and Fatty Acid Methyl Esters of an Ethyl Methanesulfonate Mutant of <i>Camelina sativa</i> with Reduced Seed Coat Mucilage. <i>JAOCS, Journal of the American Oil Chemists' Society</i> , 2020, 97, 157-174.	1.9	2
134	Genes of malate and pyruvate metabolism. <i>Plant Molecular Biology Reporter</i> , 1994, 12, S43-S44.	1.8	1
135	Functional Genomics of Plant Abiotic Stress Tolerance. , 2003, , .		1
136	Sexual Recombination and Selection During Domestication of Clonally Propagated Pineapple. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
137	Interview with John C. Cushman. <i>Trends in Plant Science</i> , 2014, 19, 274-275.	8.8	0
138	Multiscale Catalytic Fast Pyrolysis of <i>Grindelia</i> Reveals Opportunities for Generating Low Oxygen Content Bio-Oils from Drought Tolerant Biomass. <i>Energy & Fuels</i> , 0, , .	5.1	0