John C Cushman

List of Publications by Year
in descending order

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138 papers	10,936 citations	27035 58 h-index	38517 99 g-index
142 all docs	142 docs citations	142 times ranked	11160 citing authors

#	Article	IF	Citations
1	Plant responses and adaptations to a changing climate. Plant Journal, 2022, 109, 319-322.	2.8	9
2	Realizing the Potential of Camelina sativa as a Bioenergy Crop for a Changing Global Climate. Plants, 2022, 11, 772.	1.6	24
3	Disentangling Sources of Gene Tree Discordance in Phylogenomic Data Sets: Testing Ancient Hybridizations in Amaranthaceae s.l. Systematic Biology, 2021, 70, 219-235.	2.7	112
4	Metabolic profiling of epidermal and mesophyll tissues under water-deficit stress in Opuntia ficus-indica reveals stress-adaptive metabolic responses. Functional Plant Biology, 2021, 48, 717.	1.1	3
5	Chapter 10 Climate Change Responses and Adaptations in Crassulacean Acid Metabolism (CAM) Plants. Advances in Photosynthesis and Respiration, 2021, , 283-329.	1.0	5
6	Fiveâ€year field trial of the biomass productivity and water input response of cactus pear (Opuntia spp.) as a bioenergy feedstock for arid lands. GCB Bioenergy, 2021, 13, 719-741.	2.5	20
7	Membrane Profiling by Free Flow Electrophoresis and SWATH-MS to Characterize Subcellular Compartment Proteomes in Mesembryanthemum crystallinum. International Journal of Molecular Sciences, 2021, 22, 5020.	1.8	5
8	Characterization of a microbial consortium with potential for biological degradation of cactus pear biomass for biofuel production. Heliyon, 2021, 7, e07854.	1.4	4
9	Ion accumulation and expression of ion homeostasis-related genes associated with halophilism, NaCl-promoted growth in a halophyte Mesembryanthemum crystallinum L.. Plant Production Science, 2020, 23, 91-102.	0.9	28
10	Evolution of <scp>l</scp>â€<scp>DOPA</scp> 4,5â€dioxygenase activity allows for recurrent specialisation to betalain pigmentation in Caryophyllales. New Phytologist, 2020, 227, 914-929.	3.5	48
11	Characterization of Seed, Oil, and Fatty Acid Methyl Esters of an Ethyl Methanesulfonate Mutant of Camelina sativa with Reduced Seedâ€Coat Mucilage. JAOCS, Journal of the American Oil Chemists' Society, 2020, 97, 157-174.	0.8	2
12	Genomic adaptations of the green alga Dunaliella salina to life under high salinity. Algal Research, 2020, 50, 101990.	2.4	18
13	Light-responsive expression atlas reveals the effects of light quality and intensity in KalanchoÃ« fedtschenkoi, a plant with crassulacean acid metabolism. GigaScience, 2020, 9, .	3.3	11
14	Editorial: Systems Biology and Synthetic Biology in Relation to Drought Tolerance or Avoidance in Plants. Frontiers in Plant Science, 2020, 11, 394.	1.7	13
15	AnAgrobacterium-mediated transformation via organogenesis regeneration of a facultative CAM plant, the common ice plantMesembryanthemum crystallinumL. Plant Production Science, 2020, 23, 343-349.	0.9	5
16	Plant tissue succulence engineering improves waterâ€use efficiency, waterâ€deficit stress attenuation and salinity tolerance in Arabidopsis. Plant Journal, 2020, 103, 1049-1072.	2.8	36
17	Five-Year Field Trial of Eight Camelina sativa Cultivars for Biomass to be Used in Biofuel under Irrigated Conditions in a Semi-Arid Climate. Agronomy, 2020, 10, 562.	1.3	14
18	Biosystems Design to Accelerate C ₃ -to-CAM Progression. Biodesign Research, 2020, 2020, .	0.8	16

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19	Nutritional and mineral content of prickly pear cactus: A highly waterâ€use efficient forage, fodder and food species. Journal of Agronomy and Crop Science, 2019, 205, 625-634.	1.7	40
20	Understanding trait diversity associated with crassulacean acid metabolism (CAM). Current Opinion in Plant Biology, 2019, 49, 74-85.	3.5	38
21	Exploring the Relationship between Crassulacean Acid Metabolism (CAM) and Mineral Nutrition with a Special Focus on Nitrogen. International Journal of Molecular Sciences, 2019, 20, 4363.	1.8	16
22	The bracteatus pineapple genome and domestication of clonally propagated crops. Nature Genetics, 2019, 51, 1549-1558.	9.4	60
23	Laying the Foundation for Crassulacean Acid Metabolism (CAM) Biodesign: Expression of the C4 Metabolism Cycle Genes of CAM in Arabidopsis. Frontiers in Plant Science, 2019, 10, 101.	1.7	45
24	Crassulacean Acid Metabolism Abiotic Stress-Responsive Transcription Factors: a Potential Genetic Engineering Approach for Improving Crop Tolerance to Abiotic Stress. Frontiers in Plant Science, 2019, 10, 129.	1.7	28
25	New perspectives on crassulacean acid metabolism biology. Journal of Experimental Botany, 2019, 70, 6489-6493.	2.4	10
26	Quantitative ROS bioreporters: A robust toolkit for studying biological roles of ROS in response to abiotic and biotic stresses. Physiologia Plantarum, 2019, 165, 356-368.	2.6	24
27	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. Protein Expression and Purification, 2019, 155, 86-94.	0.6	3
28	Fast Pyrolysis of Opuntia ficus-indica (Prickly Pear) and Grindelia squarrosa (Gumweed). Energy & Fuels, 2018, 32, 3510-3518.	2.5	8
29	A Vitis vinifera basic helixâ€“loopâ€“helix transcription factor enhances plant cell size, vegetative biomass and reproductive yield. Plant Biotechnology Journal, 2018, 16, 1595-1615.	4.1	39
30	Identification of Genes Encoding Enzymes Catalyzing the Early Steps of Carrot Polyacetylene Biosynthesis. Plant Physiology, 2018, 178, 1507-1521.	2.3	26
31	Perspectives on the basic and applied aspects of crassulacean acid metabolism (CAM) research. Plant Science, 2018, 274, 394-401.	1.7	18
32	Sporobolus stapfianus: Insights into desiccation tolerance in the resurrection grasses from linking transcriptomics to metabolomics. BMC Plant Biology, 2017, 17, 67.	1.6	61
33	Draft Nuclear Genome Sequence of the Halophilic and Beta-Carotene-Accumulating Green Alga Dunaliella salina Strain CCAP19/18. Genome Announcements, 2017, 5, .	0.8	83
34	Leaf carbohydrates influence transcriptional and post-transcriptional regulation of nocturnal carboxylation and starch degradation in the facultative CAM plant, Mesembryanthemum crystallinum. Journal of Plant Physiology, 2017, 218, 144-154.	1.6	7
35	Temporal and spatial transcriptomic and micro<scp>RNA</scp> dynamics of <scp>CAM</scp> photosynthesis in pineapple. Plant Journal, 2017, 92, 19-30.	2.8	78
36	MYB and HD-ZIP IV homologs related to trichome formation are involved in epidermal bladder cell development in the halophyteMesembryanthemum crystallinumL.. Plant Production Science, 2017, 20, 72-82.	0.9	8

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37	The KalanchoÃ« genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. Nature Communications, 2017, 8, 1899.	5.8	159
38	An rbcL mRNA-binding protein is associated with C3 to C4 evolution and light-induced production of Rubisco in Flaveria. Journal of Experimental Botany, 2017, 68, 4635-4649.	2.4	7
39	Divide and Conquer (DC) BLAST: fast and easy BLAST execution within HPC environments. PeerJ, 2017, 5, e3486.	0.9	10
40	Identification of Ice Plant (Mesembryanthemum crystallinum L.) MicroRNAs Using RNA-Seq and Their Putative Roles in High Salinity Responses in Seedlings. Frontiers in Plant Science, 2016, 7, 1143.	1.7	47
41	Orchestration of carbohydrate processing for crassulacean acid metabolism. Current Opinion in Plant Biology, 2016, 31, 118-124.	3.5	49
42	Transcript, protein and metabolite temporal dynamics in the CAM plant Agave. Nature Plants, 2016, 2, 16178.	4.7	158
43	Suppression subtractive hybridization library construction and identification of epidermal bladder cell related genes in the common ice plant, Mesembryanthemum crystallinum L.. Plant Production Science, 2016, 19, 552-561.	0.9	8
44	A roadmap for research on crassulacean acid metabolism (<scp>CAM</scp>) to enhance sustainable food and bioenergy production in a hotter, drier world. New Phytologist, 2015, 207, 491-504.	3.5	211
45	Evaluation of Diverse Microalgal Species as Potential Biofuel Feedstocks Grown Using Municipal Wastewater. Frontiers in Energy Research, 2015, 3, .	1.2	9
46	Development and use of bioenergy feedstocks for semi-arid and arid lands. Journal of Experimental Botany, 2015, 66, 4177-4193.	2.4	88
47	Transgressive, reiterative selection by continuous buoyant density gradient centrifugation of Dunaliella salina results in enhanced lipid and starch content. Algal Research, 2015, 9, 194-203.	2.4	10
48	Biomass characterization of Agave and Opuntia as potential biofuel feedstocks. Biomass and Bioenergy, 2015, 76, 43-53.	2.9	97
49	The pineapple genome and the evolution of CAM photosynthesis. Nature Genetics, 2015, 47, 1435-1442.	9.4	472
50	Climateâ€resilient agroforestry: physiological responses to climate change and engineering of crassulacean acid metabolism (<scp>CAM</scp>) as a mitigation strategy. Plant, Cell and Environment, 2015, 38, 1833-1849.	2.8	59
51	Engineering crassulacean acid metabolism to improve water-use efficiency. Trends in Plant Science, 2014, 19, 327-338.	4.3	206
52	Synthetic biology as it relates to CAM photosynthesis: challenges and opportunities. Journal of Experimental Botany, 2014, 65, 3381-3393.	2.4	49
53	Interview with John C. Cushman. Trends in Plant Science, 2014, 19, 274-275.	4.3	0
54	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.	2.4	62

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55	Metabolomic Profiling in Selaginella lepidophylla at Various Hydration States Provides New Insights into the Mechanistic Basis of Desiccation Tolerance. Molecular Plant, 2013, 6, 369-385.	3.9	117
56	Analysis of Triacylglycerols and Free Fatty Acids in Algae Using Ultraâ€Performance Liquid Chromatography Mass Spectrometry. JAOCS, Journal of the American Oil Chemists' Society, 2013, 90, 53-64.	0.8	37
57	Metabolic rates associated with membrane fatty acids in mice selected for increased maximal metabolic rate. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2013, 165, 70-78.	0.8	17
58	Linking genes of unknown function with abiotic stress responses by highâ€throughput phenotype screening. Physiologia Plantarum, 2013, 148, 322-333.	2.6	123
59	Biomass Production, Nutritional and Mineral Content of Desiccation-Sensitive and Desiccation-Tolerant Species of Sporobolus under Multiple Irrigation Regimes. Journal of Agronomy and Crop Science, 2013, 199, 309-320.	1.7	4
60	A CAM- and starch-deficient mutant of the facultative CAM species Mesembryanthemum crystallinum reconciles sink demands by repartitioning carbon during acclimation to salinity. Journal of Experimental Botany, 2012, 63, 1985-1996.	2.4	25
61	Comparative metabolic profiling between desiccationâ€sensitive and desiccationâ€tolerant species of Selaginella reveals insights into the resurrection trait. Plant Journal, 2012, 72, 983-999.	2.8	87
62	The Vitis vinifera Câ€repeat binding protein 4 (VvCBF4) transcriptional factor enhances freezing tolerance in wine grape. Plant Biotechnology Journal, 2012, 10, 105-124.	4.1	83
63	Generic recircumscriptions of Oncidiinae (Orchidaceae: Cymbidieae) based on maximum likelihood analysis of combined DNA datasets. Botanical Journal of the Linnean Society, 2012, 168, 117-146.	0.8	85
64	Water Deficit Increases Stilbene Metabolism in Cabernet Sauvignon Berries. Journal of Agricultural and Food Chemistry, 2011, 59, 289-297.	2.4	73
65	Identification of tissue-specific, abiotic stress-responsive gene expression patterns in wine grape (Vitis) Tj ETQq1 1 0.784314 rgBT /Over	1.6	35
66	Calcium-Dependent Protein Kinases from Arabidopsis Show Substrate Specificity Differences in an Analysis of 103 Substrates. Frontiers in Plant Science, 2011, 2, 36.	1.7	80
67	Understanding Vegetative Desiccation Tolerance Using Integrated Functional Genomics Approaches Within a Comparative Evolutionary Framework. Ecological Studies, 2011, , 307-338.	0.4	17
68	A Sister Group Contrast Using Untargeted Global Metabolomic Analysis Delineates the Biochemical Regulation Underlying Desiccation Tolerance in Sporobolus stapfianus Â Â Â. Plant Cell, 2011, 23, 1231-1248.	3.1	212
69	The unicellular green alga Dunaliella salina Teod. as a model for abiotic stress tolerance: genetic advances and future perspectives. Algae, 2011, 26, 3-20.	0.9	92
70	The Dunaliella salina organelle genomes: large sequences, inflated with intronic and intergenic DNA. BMC Plant Biology, 2010, 10, 83.	1.6	98
71	Crassulacean Acid Metabolism May Alleviate Production of Reactive Oxygen Species in a Facultative CAM Plant, the Common Ice PlantMesembryanthemum crystallinumL.. Plant Production Science, 2010, 13, 256-260.	0.9	24
72	Evolution along the crassulacean acid metabolism continuum. Functional Plant Biology, 2010, 37, 995.	1.1	177

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73	Expressed sequence tag (EST) profiling in hyper saline shocked Dunaliella salina reveals high expression of protein synthetic apparatus components. Plant Science, 2010, 179, 437-449.	1.7	53
74	Crassulacean Acid Metabolism and Epiphytism Linked to Adaptive Radiations in the Orchidaceae. Plant Physiology, 2009, 149, 1838-1847.	2.3	194
75	Water deficit alters differentially metabolic pathways affecting important flavor and quality traits in grape berries of Cabernet Sauvignon and Chardonnay. BMC Genomics, 2009, 10, 212.	1.2	418
76	Identification of proteins that interact with catalytically active calcium-dependent protein kinases from Arabidopsis. Molecular Genetics and Genomics, 2009, 281, 375-390.	1.0	44
77	Proteomic and selected metabolite analysis of grape berry tissues under wellâ€watered and waterâ€deficit stress conditions. Proteomics, 2009, 9, 2503-2528.	1.3	136
78	Proteomic profiling of tandem affinity purified 14â€3â€3 protein complexes inArabidopsis thaliana. Proteomics, 2009, 9, 2967-2985.	1.3	193
79	Charting plant interactomes: possibilities and challenges. Trends in Plant Science, 2008, 13, 183-191.	4.3	93
80	Isolation and Characterization of Mutants of Common Ice Plant Deficient in Crassulacean Acid Metabolism Â Â. Plant Physiology, 2008, 147, 228-238.	2.3	65
81	Enhanced Tolerance to Oxidative Stress in Transgenic Arabidopsis Plants Expressing Proteins of Unknown Function Â Â. Plant Physiology, 2008, 148, 280-292.	2.3	105
82	Large-scale mRNA expression profiling in the common ice plant, Mesembryanthemum crystallinum, performing C3 photosynthesis and Crassulacean acid metabolism (CAM). Journal of Experimental Botany, 2008, 59, 1875-1894.	2.4	128
83	Annotating Genes of Known and Unknown Function by Large-Scale Coexpression Analysis Â Â. Plant Physiology, 2008, 147, 41-57.	2.3	162
84	Salt tolerance, salt accumulation, and ionic homeostasis in an epidermal bladder-cell-less mutant of the common ice plant Mesembryanthemum crystallinum. Journal of Experimental Botany, 2007, 58, 1957-1967.	2.4	166
85	POFs: what we donâ€™t know can hurt us. Trends in Plant Science, 2007, 12, 492-496.	4.3	35
86	Proteomic analysis reveals differences between Vitis vinifera L. cv. Chardonnay and cv. Cabernet Sauvignon and their responses to water deficit and salinity. Journal of Experimental Botany, 2007, 58, 1873-1892.	2.4	181
87	Tissue-specific mRNA expression profiling in grape berry tissues. BMC Genomics, 2007, 8, 187.	1.2	193
88	Transcriptomic and metabolite analyses of Cabernet Sauvignon grape berry development. BMC Genomics, 2007, 8, 429.	1.2	391
89	Thiamin pyrophosphokinase is required for thiamin cofactor activation in Arabidopsis. Plant Molecular Biology, 2007, 65, 151-162.	2.0	60
90	Water and salinity stress in grapevines: early and late changes in transcript and metabolite profiles. Functional and Integrative Genomics, 2007, 7, 111-134.	1.4	474

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91	Transcript abundance profiles reveal larger and more complex responses of grapevine to chilling compared to osmotic and salinity stress. Functional and Integrative Genomics, 2007, 7, 317-333.	1.4	120
92	Isolation and characterization of a novel v-SNARE family protein that interacts with a calcium-dependent protein kinase from the common ice plant, Mesembryanthemum crystallinum. Planta, 2007, 225, 783-799.	1.6	10
93	What makes species unique? The contribution of proteins with obscure features. Genome Biology, 2006, 7, R57.	13.9	64
94	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.	1.3	69
95	An EST catalogue from the resurrection plant Selaginella lepidophylla reveals abiotic stress-adaptive genes. Plant Science, 2006, 170, 1173-1184.	1.7	69
96	A phyloproteomic characterization ofin vitro autophosphorylation in calcium-dependent protein kinases. Proteomics, 2006, 6, 3649-3664.	1.3	75
97	Effect of hypermethylation of CCWGG sequences in DNA of Mesembryanthemum crystallinum plants on their adaptation to salt stress. Biochemistry (Moscow), 2006, 71, 461-465.	0.7	106
98	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. Plant Molecular Biology, 2006, 61, 13-30.	2.0	85
99	A novel coiled-coil protein co-localizes and interacts with a calcium-dependent protein kinase in the common ice plant during low-humidity stress. Planta, 2006, 225, 57-73.	1.6	19
100	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.	2.4	55
101	Transcriptional profiles of organellar metabolite transporters during induction of crassulacean acid metabolism in Mesembryanthemum crystallinum. Functional Plant Biology, 2005, 32, 451.	1.1	29
102	Research note: Large gene family of phosphoenolpyruvate carboxylase in the crassulacean acid metabolism plant Kalanchoe pinnata (Crassulaceae) characterised by partial cDNA sequence analysis. Functional Plant Biology, 2005, 32, 467.	1.1	26
103	Conservation and Divergence of Circadian Clock Operation in a Stress-Inducible Crassulacean Acid Metabolism Species Reveals Clock Compensation against Stress. Plant Physiology, 2005, 137, 969-982.	2.3	132
104	Characterizing the Grape Transcriptome. Analysis of Expressed Sequence Tags from Multiple Vitis Species and Development of a Compendium of Gene Expression during Berry Development. Plant Physiology, 2005, 139, 574-597.	2.3	159
105	Crassulacean acid metabolism: recent advances and future opportunities. Functional Plant Biology, 2005, 32, 375.	1.1	7
106	Autophosphorylation and Subcellular Localization Dynamics of a Salt- and Water Deficit-Induced Calcium-Dependent Protein Kinase from Ice Plant. Plant Physiology, 2004, 135, 1430-1446.	2.3	97
107	Transcript profiling of salinity stress responses by large-scale expressed sequence tag analysis in Mesembryanthemum crystallinum. Gene, 2004, 341, 83-92.	1.0	105
108	C₃Photosynthesis to Crassulacean Acid Metabolism Shift inMesembryanthenum crystallinum: A Stress Tolerance Mechanism. , 2004, , 241-244.		18

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109	Cladogram of Panamanian Clusia Based on Nuclear DNA: Implications for the Origins of Crassulacean Acid Metabolism. Plant Biology, 2003, 5, 59-70.	1.8	40
110	Integrating diel starch metabolism with the circadian and environmental regulation of Crassulacean acid metabolism in Mesembryanthemum crystallinum. Planta, 2003, 216, 789-797.	1.6	76
111	Conformation of a Group 2 Late Embryogenesis Abundant Protein from Soybean. Evidence of Poly (l-Proline)-type II Structure. Plant Physiology, 2003, 131, 963-975.	2.3	112
112	Expression, purification, and initial characterization of a recombinant form of plant PEP-carboxylase kinase from CAM-induced Mesembryanthemum crystallinum with enhanced solubility in Escherichia coli. Protein Expression and Purification, 2003, 29, 123-131.	0.6	22
113	ESTAP--an automated system for the analysis of EST data. Bioinformatics, 2003, 19, 1720-1722.	1.8	46
114	Functional Genomics of Plant Abiotic Stress Tolerance. , 2003, , .		1
115	Abscisic acid signaling and protein synthesis requirements for phosphoenolpyruvate carboxylase transcript induction in the common ice plant. Journal of Plant Physiology, 2002, 159, 1235-1243.	1.6	32
116	Induction of Crassulacean Acid Metabolism by Salinity - Molecular Aspects. , 2002, , 361-393.		10
117	Environmental, hormonal and circadian regulation of crassulacean acid metabolism expression. Functional Plant Biology, 2002, 29, 669.	1.1	43
118	Crassulacean Acid Metabolism. A Plastic Photosynthetic Adaptation to Arid Environments. Plant Physiology, 2001, 127, 1439-1448.	2.3	217
119	A genomics approach towards salt stress tolerance. Plant Physiology and Biochemistry, 2001, 39, 295-311.	2.8	176
120	Crassulacean acid metabolism. A plastic photosynthetic adaptation to arid environments. Plant Physiology, 2001, 127, 1439-48.	2.3	63
121	A stress-induced calcium-dependent protein kinase from Mesembryanthemum crystallinum phosphorylates a two-component pseudo-response regulator. Plant Journal, 2000, 24, 679-691.	2.8	124
122	Genomic approaches to plant stress tolerance. Current Opinion in Plant Biology, 2000, 3, 117-124.	3.5	582
123	The Ice Plant Cometh: Lessons in Abiotic Stress Tolerance. Journal of Plant Growth Regulation, 2000, 19, 334-346.	2.8	129
124	An improved RNA isolation method for succulent plant species rich in polyphenols and polysaccharides. Plant Molecular Biology Reporter, 2000, 18, 369-376.	1.0	141
125	A Minimal Serine/Threonine Protein Kinase Circadianly Regulates Phosphoenolpyruvate Carboxylase Activity in Crassulacean Acid Metabolism-Induced Leaves of the Common Ice Plant. Plant Physiology, 2000, 123, 1471-1482.	2.3	131
126	Induction of Crassulacean Acid Metabolismâ€"Molecular Aspects. Advances in Photosynthesis and Respiration, 2000, , 551-582.	1.0	11

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127	Signaling Events Leading to Crassulacean Acid Metabolism Induction in the Common Ice Plant. Plant Physiology, 1999, 121, 545-556.	2.3	88
128	CRASSULACEAN ACID METABOLISM:Molecular Genetics. Annual Review of Plant Biology, 1999, 50, 305-332.	14.2	144
129	Induction of a cysteine protease cDNA from Mesembryanthemum crystallinum leaves by environmental stress and plant growth regulators. Plant Science, 1998, 136, 195-206.	1.7	39
130	A salinity-induced gene from the halophyte M. crystallinum encodes a glycolytic enzyme, cofactor-independent phosphoglyceromutase. Plant Molecular Biology, 1995, 29, 213-226.	2.0	48
131	Genes of malate and pyruvate metabolism. Plant Molecular Biology Reporter, 1994, 12, S43-S44.	1.0	1
132	Molecular cloning and expression of chloroplast NADP-malate dehydrogenase during Crassulacean acid metabolism induction by salt stress. Photosynthesis Research, 1993, 35, 15-27.	1.6	48
133	Characterization and expression of a NADP-malic enzyme cDNA induced by salt stress from the facultative crassulacean acid metabolism plant, Mesembryanthemum crystallinum. FEBS Journal, 1992, 208, 259-266.	0.2	72
134	Nucleotide sequence of the gene encoding a CAM specific isoform of phosphoenolpyruvate carboxylase fromMesembryanthemum crystallinum. Nucleic Acids Research, 1989, 17, 6745-6746.	6.5	32
135	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.	3.1	51
136	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.	0.8	65
137	Sexual Recombination and Selection During Domestication of Clonally Propagated Pineapple. SSRN Electronic Journal, 0, , .	0.4	1
138	Multiscale Catalytic Fast Pyrolysis of Grindelia Reveals Opportunities for Generating Low Oxygen Content Bio-Oils from Drought Tolerant Biomass. Energy & Fuels, 0, , .	2.5	0