

John E Mullet

List of Publications by Year in descending order

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128
papers

11,912
citations

18887

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133
docs citations

133
times ranked

9423
citing authors

#	ARTICLE	IF	CITATIONS
1	Ruggedized, field-ready snapshot light-guide-based imaging spectrometer for environmental and remote sensing applications. <i>Optics Express</i> , 2022, 30, 10614.	1.7	9
2	Bioenergy sorghum's deep roots: A key to sustainable biomass production on annual cropland. <i>GCB Bioenergy</i> , 2022, 14, 132-156.	2.5	3
3	The AGCVIII kinase Dw2 modulates cell proliferation, endomembrane trafficking, and MLG/xylan cell wall localization in elongating stem internodes of <i>Sorghum bicolor</i> . <i>Plant Journal</i> , 2021, 105, 1053-1071.	2.8	11
4	High planting density induces the expression of GA3-oxidase in leaves and GA mediated stem elongation in bioenergy sorghum. <i>Scientific Reports</i> , 2021, 11, 46.	1.6	3
5	Regulation of dhurrin pathway gene expression during <i>Sorghum bicolor</i> development. <i>Planta</i> , 2021, 254, 119.	1.6	9
6	Shade signals alter the expression of circadian clock genes in newly formed bioenergy sorghum internodes. <i>Plant Direct</i> , 2020, 4, e00235.	0.8	8
7	The genetic architecture of biomechanical traits in sorghum. <i>Crop Science</i> , 2020, 60, 82-99.	0.8	10
8	Low-field magnetic resonance imaging of roots in intact clayey and silty soils. <i>Geoderma</i> , 2020, 370, 114356.	2.3	19
9	Maturity2, a novel regulator of flowering time in <i>Sorghum bicolor</i> , increases expression of SbPRR37 and SbCO in long days delaying flowering. <i>PLoS ONE</i> , 2019, 14, e0212154.	1.1	33
10	Complementarity of Raman and Infrared Spectroscopy for Structural Characterization of Plant Epicuticular Waxes. <i>ACS Omega</i> , 2019, 4, 3700-3707.	1.6	76
11	Integration of Pretreatment With Simultaneous Counter-Current Extraction of Energy Sorghum for High-Titer Mixed Sugar Production. <i>Frontiers in Energy Research</i> , 2019, 6, .	1.2	7
12	Nanoscale Structural Organization of Plant Epicuticular Wax Probed by Atomic Force Microscope Infrared Spectroscopy. <i>Analytical Chemistry</i> , 2019, 91, 2472-2479.	3.2	53
13	The <i>Sorghum bicolor</i> reference genome: improved assembly, gene annotations, a transcriptome atlas, and signatures of genome organization. <i>Plant Journal</i> , 2018, 93, 338-354.	2.8	431
14	Sorghum stem aerenchyma formation is regulated by <i>SbNAC_D</i> during internode development. <i>Plant Direct</i> , 2018, 2, e00085.	0.8	30
15	Developmental dynamics of stem starch accumulation in <i>Sorghum bicolor</i> . <i>Plant Direct</i> , 2018, 2, e00074.	0.8	19
16	Variation in energy sorghum hybrid TX08001 biomass composition and lignin chemistry during development under irrigated and non-irrigated field conditions. <i>PLoS ONE</i> , 2018, 13, e0195863.	1.1	24
17	Physical fractionation of sweet sorghum and forage/energy sorghum for optimal processing in a biorefinery. <i>Industrial Crops and Products</i> , 2018, 124, 607-616.	2.5	22
18	High-biomass C4 grasses "Filling the yield gap. <i>Plant Science</i> , 2017, 261, 10-17.	1.7	31

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19	Leaves Segmentation in 3D Point Cloud. Lecture Notes in Computer Science, 2017, , 664-674.	1.0	6
20	Sorghum Dw2 Encodes a Protein Kinase Regulator of Stem Internode Length. Scientific Reports, 2017, 7, 4616.	1.6	91
21	Dynamics of gene expression during development and expansion of vegetative stem internodes of bioenergy sorghum. Biotechnology for Biofuels, 2017, 10, 159.	6.2	50
22	Bioenergy Sorghum Crop Model Predicts VPD-Limited Transpiration Traits Enhance Biomass Yield in Water-Limited Environments. Frontiers in Plant Science, 2017, 8, 335.	1.7	17
23	Identification of Dw1, a Regulator of Sorghum Stem Internode Length. PLoS ONE, 2016, 11, e0151271.	1.1	109
24	Discovery of a Dhurrin QTL in Sorghum: Co-localization of Dhurrin Biosynthesis and a Novel Stay-green QTL. Crop Science, 2016, 56, 104-112.	0.8	34
25	3D sorghum reconstructions from depth images identify QTL regulating shoot architecture. Plant Physiology, 2016, 172, pp.00948.2016.	2.3	81
26	Dynamics of biomass partitioning, stem gene expression, cell wall biosynthesis, and sucrose accumulation during development of <i>Sorghum bicolor</i> . Plant Journal, 2016, 88, 662-680.	2.8	75
27	Transcriptome Profiling of Tiller Buds Provides New Insights into PhyB Regulation of Tillering and Indeterminate Growth in Sorghum. Plant Physiology, 2016, 170, 2232-2250.	2.3	65
28	Harnessing Genetic Variation in Leaf Angle to Increase Productivity of <i>Sorghum bicolor</i> . Genetics, 2015, 201, 1229-1238.	1.2	79
29	Photosynthetic leaf area modulates tiller bud outgrowth in sorghum. Plant, Cell and Environment, 2015, 38, 1471-1478.	2.8	82
30	RIG: Recalibration and Interrelation of Genomic Sequence Data with the GATK. G3: Genes, Genomes, Genetics, 2015, 5, 655-665.	0.8	75
31	<i>Ghd7</i> (<i>Ma6</i>) Represses Sorghum Flowering in Long Days: Alleles Enhance Biomass Accumulation and Grain Production. Plant Genome, 2014, 7, plantgenome2013.11.0040.	1.6	97
32	Resolution of Genetic Map Expansion Caused by Excess Heterozygosity in Plant Recombinant Inbred Populations. G3: Genes, Genomes, Genetics, 2014, 4, 1963-1969.	0.8	24
33	Energy Sorghum—a genetic model for the design of C4 grass bioenergy crops. Journal of Experimental Botany, 2014, 65, 3479-3489.	2.4	179
34	Stay-green alleles individually enhance grain yield in sorghum under drought by modifying canopy development and water uptake patterns. New Phytologist, 2014, 203, 817-830.	3.5	163
35	Drought adaptation of stay-green sorghum is associated with canopy development, leaf anatomy, root growth, and water uptake. Journal of Experimental Botany, 2014, 65, 6251-6263.	2.4	264
36	CONSTANS is a photoperiod regulated activator of flowering in sorghum. BMC Plant Biology, 2014, 14, 148.	1.6	83

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37	Quantitative trait locus mapping of the transpiration ratio related to preflowering drought tolerance in sorghum (<i>Sorghum bicolor</i>). <i>Functional Plant Biology</i> , 2014, 41, 1049.	1.1	29
38	Sorghum Phytochrome B Inhibits Flowering in Long Days by Activating Expression of SbPRR37 and SbGHD7, Repressors of SbEHD1, SbCN8 and SbCN12. <i>PLoS ONE</i> , 2014, 9, e105352.	1.1	97
39	Digital genotyping of sorghum – a diverse plant species with a large repeat-rich genome. <i>BMC Genomics</i> , 2013, 14, 448.	1.2	51
40	Energy sorghum hybrids: Functional dynamics of high nitrogen use efficiency. <i>Biomass and Bioenergy</i> , 2013, 56, 307-316.	2.9	33
41	Extensive Variation in the Density and Distribution of DNA Polymorphism in Sorghum Genomes. <i>PLoS ONE</i> , 2013, 8, e79192.	1.1	49
42	High biomass yield energy sorghum: developing a genetic model for <i>C4</i> grass bioenergy crops. <i>Biofuels, Bioproducts and Biorefining</i> , 2012, 6, 640-655.	1.9	109
43	Coincident light and clock regulation of <i>pseudoregulator protein 37</i> (<i>PRR37</i>) controls photoperiodic flowering in sorghum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 16469-16474.	3.3	299
44	Traits and Genes for Plant Drought Tolerance. <i>Biotechnology in Agriculture and Forestry</i> , 2009, , 55-64.	0.2	5
45	Genetic Improvement of Sorghum as a Biofuel Feedstock: II. QTL for Stem and Leaf Structural Carbohydrates. <i>Crop Science</i> , 2008, 48, 2180-2193.	0.8	162
46	Genetic Improvement of Sorghum as a Biofuel Feedstock: I. QTL for Stem Sugar and Grain Nonstructural Carbohydrates. <i>Crop Science</i> , 2008, 48, 2165-2179.	0.8	243
47	Sequence Analysis of Bacterial Artificial Chromosome Clones from the Apospory-Specific Genomic Region of <i>Pennisetum</i> and <i>Cenchrus</i> . <i>Plant Physiology</i> , 2008, 147, 1396-1411.	2.3	107
48	The Effect of Tropical Sorghum Conversion and Inbred Development on Genome Diversity as Revealed by High-Resolution Genotyping. <i>Crop Science</i> , 2008, 48, S-12.	0.8	90
49	Designing sorghum as a dedicated bioenergy feedstock. <i>Biofuels, Bioproducts and Biorefining</i> , 2007, 1, 147-157.	1.9	539
50	Phytochrome B and shade signals regulate phytochrome A expression. <i>Physiologia Plantarum</i> , 2006, 127, 326-338.	2.6	5
51	A Segment of the Apospory-Specific Genomic Region Is Highly Microsyntenic Not Only between the Apomicts <i>Pennisetum squamulatum</i> and Buffelgrass, But Also with a Rice Chromosome 11 Centromeric-Proximal Genomic Region. <i>Plant Physiology</i> , 2006, 140, 963-971.	2.3	32
52	Sorghum stay-green QTL individually reduce post-flowering drought-induced leaf senescence. <i>Journal of Experimental Botany</i> , 2006, 58, 327-338.	2.4	286
53	Sorghum <i>bicolor</i> 's Transcriptome Response to Dehydration, High Salinity and ABA. <i>Plant Molecular Biology</i> , 2005, 58, 699-720.	2.0	262
54	Sorghum Expressed Sequence Tags Identify Signature Genes for Drought, Pathogenesis, and Skotomorphogenesis from a Milestone Set of 16,801 Unique Transcripts. <i>Plant Physiology</i> , 2005, 139, 869-884.	2.3	66

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55	Transcriptional Profiling of Sorghum Induced by Methyl Jasmonate, Salicylic Acid, and Aminocyclopropane Carboxylic Acid Reveals Cooperative Regulation and Novel Gene Responses. <i>Plant Physiology</i> , 2005, 138, 352-368.	2.3	189
56	Molecular Cytogenetic Maps of Sorghum Linkage Groups 2 and 8. <i>Genetics</i> , 2005, 169, 955-965.	1.2	38
57	Chromosome Identification and Nomenclature of Sorghum bicolor. <i>Genetics</i> , 2005, 169, 1169-1173.	1.2	117
58	Genetic Diversity of Public Inbreds of Sorghum Determined by Mapped AFLP and SSR Markers. <i>Crop Science</i> , 2004, 44, 1236-1244.	0.8	139
59	Phylogenetic Analysis of 5' Noncoding Regions From the ABA-Responsive rab16/17 Gene Family of Sorghum, Maize and Rice Provides Insight Into the Composition, Organization and Function of cis-Regulatory Modules. Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession no. AY177889. <i>Genetics</i> , 2004, 168, 1639-1654.	1.2	17
60	High-Resolution Physical Mapping in Pennisetum squamulatum Reveals Extensive Chromosomal Heteromorphism of the Genomic Region Associated with Apomixis. <i>Plant Physiology</i> , 2004, 134, 1733-1741.	2.3	109
61	Sequence-based alignment of sorghum chromosome 3 and rice chromosome 1 reveals extensive conservation of gene order and one major chromosomal rearrangement. <i>Plant Journal</i> , 2003, 34, 605-621.	2.8	54
62	A Mechanism for Light-Induced Translation of the rbcL mRNA Encoding the Large Subunit of Ribulose-1,5-bisphosphate Carboxylase in Barley Chloroplasts. <i>Plant and Cell Physiology</i> , 2003, 44, 491-499.	1.5	23
63	Integrated karyotyping of sorghum by in situ hybridization of landed BACs. <i>Genome</i> , 2002, 45, 402-412.	0.9	84
64	Targeted Analysis of Orthologous Phytochrome A Regions of the Sorghum, Maize, and Rice Genomes using Comparative Gene-Island Sequencing. <i>Plant Physiology</i> , 2002, 130, 1614-1625.	2.3	21
65	Opportunities to Improve Adaptability and Yield in Grasses. <i>Crop Science</i> , 2002, 42, 1791-1799.	0.8	46
66	Sorghum bicolor "an important species for comparative grass genomics and a source of beneficial genes for agriculture. <i>Current Opinion in Plant Biology</i> , 2002, 5, 118-121.	3.5	50
67	Mapping genes on an integrated sorghum genetic and physical map using cDNA selection technology. <i>Plant Journal</i> , 2001, 27, 243-255.	2.8	21
68	Analysis of barley chloroplast psbD light-responsive promoter elements in transplastomic tobacco. <i>Plant Molecular Biology</i> , 2001, 47, 353-366.	2.0	65
69	Homeodomain Leucine Zipper Proteins Bind to the Phosphate Response Domain of the Soybean VspB Tripartite Promoter. <i>Plant Physiology</i> , 2001, 125, 797-809.	2.3	44
70	Cryptochrome 1, Cryptochrome 2, and Phytochrome A Co-Activate the Chloroplast psbD Blue Light-Responsive Promoter. <i>Plant Cell</i> , 2001, 13, 2747-2760.	3.1	60
71	Jasmonic Acid Signaling Modulates Ozone-Induced Hypersensitive Cell Death. <i>Plant Cell</i> , 2000, 12, 1633-1646.	3.1	437
72	A High-throughput AFLP-based Method for Constructing Integrated Genetic and Physical Maps: Progress Toward a Sorghum Genome Map. <i>Genome Research</i> , 2000, 10, 789-807.	2.4	187

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73	Ozone Sensitivity in Hybrid Poplar Correlates with Insensitivity to Both Salicylic Acid and Jasmonic Acid. The Role of Programmed Cell Death in Lesion Formation. <i>Plant Physiology</i> , 2000, 123, 487-496.	2.3	126
74	Molecular mapping of QTLs conferring stay-green in grain sorghum (<i>Sorghum bicolor</i> L.) Tj ETQq0 0 0 rgBT /Overlock 10 If 50 702	0.9	237
75	Molecular mapping of QTLs conferring stay-green in grain sorghum (<i>Sorghum bicolor</i> L.) Tj ETQq1 1 0.784314 rgBT /Overlock 1	0.9	93
76	ADP-Dependent Phosphorylation Regulates Association of a DNA-Binding Complex with the Barley Chloroplast psbD-Blue-Light-Responsive Promoter. <i>Plant Physiology</i> , 1999, 119, 663-670.	2.3	32
77	Detailed Architecture of the Barley Chloroplast psbD-psbC Blue Light-responsive Promoter. <i>Journal of Biological Chemistry</i> , 1999, 274, 4684-4692.	1.6	52
78	In vivo analysis of plastid psbA, rbcL and rpl32 UTR elements by chloroplast transformation: tobacco plastid gene expression is controlled by modulation of transcript levels and translation efficiency. <i>Plant Journal</i> , 1999, 19, 333-345.	2.8	156
79	The Mechanism of Rhythmic Ethylene Production in Sorghum. The Role of Phytochrome B and Simulated Shading. <i>Plant Physiology</i> , 1999, 119, 1083-1090.	2.3	92
80	High Throughput BAC DNA Isolation for Physical Map Construction of Sorghum (<i>Sorghum bicolor</i>). <i>Plant Molecular Biology Reporter</i> , 1998, 16, 351-364.	1.0	12
81	RNA-binding proteins of 37/38 kDa bind specifically to the barley chloroplast psbA 3'-end untranslated RNA. <i>Plant Molecular Biology</i> , 1996, 30, 1195-1205.	2.0	30
82	Plant cellular responses to water deficit. <i>Plant Growth Regulation</i> , 1996, 20, 119-124.	1.8	63
83	Developmental expression of a turgor-responsive gene that encodes an intrinsic membrane protein. <i>Plant Molecular Biology</i> , 1995, 28, 983-996.	2.0	29
84	A salt- and dehydration-inducible pea gene, Cyp15a, encodes a cell-wall protein with sequence similarity to cysteine proteases. <i>Plant Molecular Biology</i> , 1995, 28, 1055-1065.	2.0	62
85	<i>Arabidopsis thaliana</i> Atvsp is homologous to soybean VspA and VspB, genes encoding vegetative storage protein acid phosphatases, and is regulated similarly by methyl jasmonate, wounding, sugars, light and phosphate. <i>Plant Molecular Biology</i> , 1995, 27, 933-942.	2.0	198
86	Characterization and expression of rpoC2 in CMS and fertile lines of sorghum. <i>Plant Molecular Biology</i> , 1995, 28, 799-809.	2.0	22
87	Construction and characterization of a bacterial artificial chromosome library of <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology Reporter</i> , 1995, 13, 124-128.	1.0	97
88	Phosphate Modulates Transcription of Soybean VspB and Other Sugar-Inducible Genes. <i>Plant Cell</i> , 1994, 6, 737.	3.1	30
89	Ribosome-binding sites on chloroplast rbcL and psbA mRNAs and light-induced initiation of D1 translation. <i>Plant Molecular Biology</i> , 1994, 25, 437-448.	2.0	73
90	Vir-115 gene product is required to stabilize D1 translation intermediates in chloroplasts. <i>Plant Molecular Biology</i> , 1994, 25, 459-467.	2.0	31

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91	Direct evidence for selective modulation of psbA, rpoA, rbcL and 16S RNA stability during barley chloroplast development. <i>Plant Molecular Biology</i> , 1993, 22, 447-463.	2.0	123
92	Coregulation of Soybean Vegetative Storage Protein Gene Expression by Methyl Jasmonate and Soluble Sugars. <i>Plant Physiology</i> , 1992, 98, 859-867.	2.3	111
93	Involvement of a Lipoxygenase-Like Enzyme in Abscisic Acid Biosynthesis. <i>Plant Physiology</i> , 1992, 99, 1258-1260.	2.3	102
94	Plastid DNA synthesis and nucleic acid-binding proteins in developing barley chloroplasts. <i>Journal of Photochemistry and Photobiology B: Biology</i> , 1991, 11, 203-218.	1.7	12
95	Lipoxygenase gene expression is modulated in plants by water deficit, wounding, and methyl jasmonate. <i>Molecular Genetics and Genomics</i> , 1991, 230, 456-462.	2.4	141
96	Water deficit modulates gene expression in growing zones of soybean seedlings. Analysis of differentially expressed cDNAs, a new β -tubulin gene, and expression of genes encoding cell wall proteins. <i>Plant Molecular Biology</i> , 1991, 17, 591-608.	2.0	54
97	Chloroplast transcription is required to express the nuclear genes rbcS and cab. Plastid DNA copy number is regulated independently. <i>Plant Molecular Biology</i> , 1991, 17, 813-823.	2.0	99
98	Abscisic Acid Accumulates at Positive Turgor Potential in Excised Soybean Seedling Growing Zones. <i>Plant Physiology</i> , 1991, 95, 1209-1213.	2.3	31
99	Turgor-responsive gene transcription and RNA levels increase rapidly when pea shoots are wilted. Sequence and expression of three inducible genes. <i>Plant Molecular Biology</i> , 1990, 15, 11-26.	2.0	335
100	Sequence and transcriptional analysis of the barley ctDNA region upstream of psbD-psbC encoding trnK(UUU), rps16, trnQ(UUG), psbK, psbI, and trnS(GCU). <i>Current Genetics</i> , 1990, 17, 445-454.	0.8	68
101	Detection of Endogenous Gibberellins and Their Relationship to Hypocotyl Elongation in Soybean Seedlings. <i>Plant Physiology</i> , 1990, 94, 77-84.	2.3	37
102	Water Deficit and Abscisic Acid Cause Differential Inhibition of Shoot versus Root Growth in Soybean Seedlings. <i>Plant Physiology</i> , 1990, 92, 205-214.	2.3	232
103	Plastid Transcription Activity and DNA Copy Number Increase Early in Barley Chloroplast Development. <i>Plant Physiology</i> , 1989, 89, 1011-1018.	2.3	202
104	Proteins homologous to leaf glycoproteins are abundant in stems of dark-grown soybean seedlings. Analysis of proteins and cDNAs. <i>Plant Molecular Biology</i> , 1988, 11, 845-856.	2.0	70
105	Reduction of Turgor Induces Rapid Changes in Leaf Translatable RNA. <i>Plant Physiology</i> , 1988, 88, 401-408.	2.3	61
106	Polysomes, Messenger RNA, and Growth in Soybean Stems during Development and Water Deficit. <i>Plant Physiology</i> , 1988, 86, 725-733.	2.3	65
107	Light-Dependent Accumulation of Radiolabeled Plastid-Encoded Chlorophyll <i>a</i> -Apoproteins Requires Chlorophyll <i>a</i> . <i>Plant Physiology</i> , 1988, 88, 1246-1256.	2.3	67
108	The sequence of the maize plastid encoded rpl23 locus. <i>Nucleic Acids Research</i> , 1988, 16, 8184-8184.	6.5	40

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109	Water Deficit-Induced Changes in Abscisic Acid, Growth, Polysomes, and Translatable RNA in Soybean Hypocotyls. <i>Plant Physiology</i> , 1988, 88, 289-294.	2.3	100
110	Cell Wall Proteins at Low Water Potentials. <i>Plant Physiology</i> , 1987, 85, 261-267.	2.3	75
111	Characterization of the barley chloroplast transcription units containing psaA-psaB and psbD-psbC. <i>Nucleic Acids Research</i> , 1987, 15, 5217-5240.	6.5	64
112	Pea Chloroplast Glutathione Reductase: Purification and Characterization. <i>Plant Physiology</i> , 1986, 82, 351-356.	2.3	82
113	Characterization of <i>P. sativum</i> chloroplast psbA transcripts produced in vivo, in vitro and in <i>E. coli</i> . <i>Plant Molecular Biology</i> , 1986, 6, 229-243.	2.0	48
114	Localization of the genes coding for the 51 kDa PSII chlorophyll apoprotein, apocytochrome b6, the 65?70 kDa PSI chlorophyll apoproteins and the 44 kDa PSII chlorophyll apoprotein in pea chloroplast DNA. <i>Plant Molecular Biology</i> , 1986, 6, 125-134.	2.0	20
115	Optimization of protein synthesis in isolated higher plant chloroplasts. Identification of paused translation intermediates. <i>FEBS Journal</i> , 1986, 155, 331-338.	0.2	74
116	Inhibition of carotenoid accumulation and abscisic acid biosynthesis in fluridone-treated dark-grown barley. <i>FEBS Journal</i> , 1986, 160, 117-121.	0.2	104
117	In vitro transcription of chloroplast protein genes. <i>Methods in Enzymology</i> , 1986, 118, 232-253.	0.4	70
118	Increased Abscisic Acid Biosynthesis during Plant Dehydration Requires Transcription. <i>Plant Physiology</i> , 1986, 80, 588-591.	2.3	99
119	Multiple transcripts for higher plant rbcL and atpB genes and localization of the transcription initiation site of the rbcL gene. <i>Plant Molecular Biology</i> , 1985, 4, 39-54.	2.0	110
120	Accumulation of Heat Shock Proteins in Field-Grown Cotton. <i>Plant Physiology</i> , 1985, 78, 394-398.	2.3	121
121	An in vitro system for accurate transcription initiation of chloroplast protein genes. <i>Nucleic Acids Research</i> , 1985, 13, 1283-1302.	6.5	109
122	The life history and ecology of the snow alga <i>Chloromonas polyptera</i> comb. nov. (Chlorophyta), <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	1.2	75
123	[45] In Vitro reconstitution of synthesis, uptake, and assembly of cytoplasmically synthesized chloroplast proteins. <i>Methods in Enzymology</i> , 1983, 97, 502-509.	0.4	39
124	Chlorophyll Proteins of Photosystem I. <i>Plant Physiology</i> , 1980, 65, 814-822.	2.3	559
125	A Developmental Study of Photosystem I Peripheral Chlorophyll Proteins. <i>Plant Physiology</i> , 1980, 65, 823-827.	2.3	137
126	The life history and ecology of the snow alga <i>Chloromonas brevispina</i> comb. nov. (Chlorophyta), <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6</i>	0.6	91

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127	Chloromonas nivalis (Chod.) Hoh. & Mull. comb. nov., and additional comments on the snow alga, Scotiella. Phycologia, 1978, 17, 106-107.	0.6	38
128	The life history and ecology of the snow alga Chloromonas cryophila sp. nov. (Chlorophyta), Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702 T	0.6	60