Thomas P Brutnell

List of Publications by Year
in descending order

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108
papers

13,826
citations

34016

52
h-index

27345

106
g-index

119
all docs

119
docs citations

119
times ranked

14440
citing authors

#	ARTICLE	IF	CITATIONS
1	The CLV3 Homolog in Setaria viridis Selectively Controls Inflorescence Meristem Size. Frontiers in Plant Science, 2021, 12, 636749.	1.7	8
2	<i>DCT4</i>â€”A New Member of the Dicarboxylate Transporter Family in C4 Grasses. Genome Biology and Evolution, 2021, 13, .	1.1	1
3	Engineering chloroplast development in rice through cellâ€‘specific control of endogenous genetic circuits. Plant Biotechnology Journal, 2021, 19, 2291-2303.	4.1	15
4	A genome resource for green millet Setaria viridis enables discovery of agronomically valuable loci. Nature Biotechnology, 2020, 38, 1203-1210.	9.4	103
5	CRISPR-Cas12a (Cpf1): A Versatile Tool in the Plant Genome Editing Tool Box for Agricultural Advancement. Frontiers in Plant Science, 2020, 11, 584151.	1.7	66
6	Evidence for independent peripheral and central ageâ€‘related hearing impairment. Journal of Neuroscience Research, 2020, 98, 1800-1814.	1.3	11
7	The rhizosphere and cropping system, but not arbuscular mycorrhizae, affect ammonia oxidizing archaea and bacteria abundances in two agricultural soils. Applied Soil Ecology, 2020, 151, 103540.	2.1	21
8	Biochemical and physiological flexibility accompanies reduced cellulose biosynthesis in Brachypodium cesa1S830N. AoB PLANTS, 2019, 11, plz041.	1.2	2
9	Editorial: Setaria as a Model Genetic System to Accelerate Yield Increases in Cereals, Forage Crops, and Bioenergy Grasses. Frontiers in Plant Science, 2019, 10, 1211.	1.7	5
10	Transcriptomic Analysis of Leaf Sheath Maturation in Maize. International Journal of Molecular Sciences, 2019, 20, 2472.	1.8	15
11	Metabolomics of sorghum roots during nitrogen stress reveals compromised metabolic capacity for salicylic acid biosynthesis. Plant Direct, 2019, 3, e00122.	0.8	32
12	Characterization of maize leaf pyruvate orthophosphate dikinase using high throughput sequencing. Journal of Integrative Plant Biology, 2018, 60, 670-690.	4.1	12
13	Making Roots, Shoots, and Seeds: IDD Gene Family Diversification in Plants. Trends in Plant Science, 2018, 23, 66-78.	4.3	29
14	Carbonic Anhydrase Mutants in <i>Zea mays</i> Have Altered Stomatal Responses to Environmental Signals. Plant Physiology, 2018, 177, 980-989.	2.3	37
15	Climate-smart crops with enhanced photosynthesis. Journal of Experimental Botany, 2018, 69, 3801-3809.	2.4	50
16	The maize W22 genome provides a foundation for functional genomics and transposon biology. Nature Genetics, 2018, 50, 1282-1288.	9.4	183
17	Sparse panicle1 is required for inflorescence development in Setaria viridis and maize. Nature Plants, 2017, 3, 17054.	4.7	63
18	An N-acetylglucosamine transporter required for arbuscular mycorrhizal symbioses in rice and maize. Nature Plants, 2017, 3, 17073.	4.7	72

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19	Setaria viridis as a Model for C4 Photosynthesis. Plant Genetics and Genomics: Crops and Models, 2017, , 291-300.	0.3	3
20	Genome-Guided Phylo-Transcriptomic Methods and the Nuclear Phylogenetic Tree of the Paniceae Grasses. Scientific Reports, 2017, 7, 13528.	1.6	27
21	Precise insertion and guided editing of higher plant genomes using Cpf1 CRISPR nucleases. Scientific Reports, 2017, 7, 11606.	1.6	164
22	Cross species selection scans identify components of C ₄ photosynthesis in the grasses. Journal of Experimental Botany, 2017, 68, 127-135.	2.4	61
23	Time dependent genetic analysis links field and controlled environment phenotypes in the model C4 grass Setaria. PLoS Genetics, 2017, 13, e1006841.	1.5	53
24	Forward Genetics in Setaria viridis. Plant Genetics and Genomics: Crops and Models, 2017, , 303-322.	0.3	1
25	Transposon Tagging in Setaria viridis. Plant Genetics and Genomics: Crops and Models, 2017, , 323-342.	0.3	4
26	Characterization and Transposon Mutagenesis of the Maize (Zea mays) Pho1 Gene Family. PLoS ONE, 2016, 11, e0161882.	1.1	13
27	Setaria viridis as a Model System to Advance Millet Genetics and Genomics. Frontiers in Plant Science, 2016, 7, 1781.	1.7	58
28	Interactions of C₄ Subtype Metabolic Activities and Transport in Maize Are Revealed through the Characterization of <i>DCT2</i> Mutants. Plant Cell, 2016, 28, 466-484.	3.1	39
29	A synthesis of transcriptomic surveys to dissect the genetic basis of C4 photosynthesis. Current Opinion in Plant Biology, 2016, 31, 91-99.	3.5	30
30	Grasses suppress shoot-borne roots to conserve water during drought. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 8861-8866.	3.3	111
31	The draft genome of the C3 panicoid grass species Dichanthelium oligosanthes. Genome Biology, 2016, 17, 223.	3.8	48
32	Advancing Crop Transformation in the Era of Genome Editing. Plant Cell, 2016, 28, tpc.00196.2016.	3.1	429
33	Standards for plant synthetic biology: a common syntax for exchange of <scp>DNA</scp> parts. New Phytologist, 2015, 208, 13-19.	3.5	263
34	Identification of Photosynthesis-Associated C4 Candidate Genes through Comparative Leaf Gradient Transcriptome in Multiple Lineages of C3 and C4 Species. PLoS ONE, 2015, 10, e0140629.	1.1	63
35	Transcriptional response to petiole heat girdling in cassava. Scientific Reports, 2015, 5, 8414.	1.6	19
36	<i>Brachypodium distachyon</i> and <i>Setaria viridis</i>: Model Genetic Systems for the Grasses. Annual Review of Plant Biology, 2015, 66, 465-485.	8.6	126

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37	Growthâ€"defence balance in grass biomass production: the role of jasmonates. Journal of Experimental Botany, 2015, 66, 4165-4176.	2.4	41
38	A Versatile Phenotyping System and Analytics Platform Reveals Diverse Temporal Responses to Water Availability in Setaria. Molecular Plant, 2015, 8, 1520-1535.	3.9	202
39	Genome-Wide Association of Carbon and Nitrogen Metabolism in the Maize Nested Association Mapping Population. Plant Physiology, 2015, 168, 575-583.	2.3	80
40	Model grasses hold key to crop improvement. Nature Plants, 2015, 1, .	4.7	13
41	Tillering in the<i>sugary1</i>sweet corn is maintained by overriding the teosinte branched1 repressive signal. Plant Signaling and Behavior, 2015, 10, e1078954.	1.2	14
42	A Limited Role for Carbonic Anhydrase in C4 Photosynthesis as Revealed by a <i>ca1ca2</i> Double Mutant in Maize Â Â. Plant Physiology, 2014, 165, 608-617.	2.3	78
43	Developmental dynamics of Kranz cell transcriptional specificity in maize leaf reveals early onset of C4-related processes. Journal of Experimental Botany, 2014, 65, 3543-3555.	2.4	78
44	Model-based clustering for RNA-seq data. Bioinformatics, 2014, 30, 197-205.	1.8	112
45	Comparative analyses of C4 and C3 photosynthesis in developing leaves of maize and rice. Nature Biotechnology, 2014, 32, 1158-1165.	9.4	228
46	Enhancing the productivity of grasses under high-density planting by engineering light responses: from model systems to feedstocks. Journal of Experimental Botany, 2014, 65, 2825-2834.	2.4	35
47	Bundle sheath suberization in grass leaves: multiple barriers to characterization. Journal of Experimental Botany, 2014, 65, 3371-3380.	2.4	59
48	Editorial overview: Growing the future: synthetic biology in plants. Current Opinion in Plant Biology, 2014, 19, iv-v.	3.5	3
49	Genetic Control and Comparative Genomic Analysis of Flowering Time in Setaria (Poaceae). G3: Genes, Genomes, Genetics, 2013, 3, 283-295.	0.8	97
50	Methods for Performing Crosses in Setaria viridis, a New Model System for the Grasses. Journal of Visualized Experiments, 2013, , .	0.2	26
51	Comparative feedstock analysis in Setaria viridis L. as a model for C4 bioenergy grasses and Panicoid crop species. Frontiers in Plant Science, 2013, 4, 181.	1.7	21
52	Engineering C4 photosynthetic regulatory networks. Current Opinion in Biotechnology, 2012, 23, 298-304.	3.3	19
53	Reference genome sequence of the model plant Setaria. Nature Biotechnology, 2012, 30, 555-561.	9.4	864
54	The iPlant Collaborative: Cyberinfrastructure for Plant Biology. Frontiers in Plant Science, 2011, 2, 34.	1.7	396

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55	Regulatory mechanisms underlying C₄ photosynthesis. New Phytologist, 2011, 190, 9-20.	3.5	42
56	The Activator/Dissociation Transposable Elements Comprise a Two-Component Gene Regulatory Switch That Controls Endogenous Gene Expression in Maize. Genetics, 2011, 187, 749-759.	1.2	5
57	Setaria viridis and Setaria italica, model genetic systems for the Panicoid grasses. Journal of Experimental Botany, 2011, 62, 3031-3037.	2.4	312
58	<i>grassy tillers1</i> promotes apical dominance in maize and responds to shade signals in the grasses. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E506-12.	3.3	215
59	Topology of a maize field. Plant Signaling and Behavior, 2011, 6, 467-470.	1.2	12
60	Identification of the <i>Pr1</i> Gene Product Completes the Anthocyanin Biosynthesis Pathway of Maize. Genetics, 2011, 188, 69-79.	1.2	78
61	Brachypodium as a Model for the Grasses: Today and the Future Â. Plant Physiology, 2011, 157, 3-13.	2.3	243
62	A Low-Cost Library Construction Protocol and Data Analysis Pipeline for Illumina-Based Strand-Specific Multiplex RNA-Seq. PLoS ONE, 2011, 6, e26426.	1.1	135
63	Rare genetic variation at Zea mays crtRB1 increases Î²-carotene in maize grain. Nature Genetics, 2010, 42, 322-327.	9.4	421
64	The developmental dynamics of the maize leaf transcriptome. Nature Genetics, 2010, 42, 1060-1067.	9.4	660
65	<i>Setaria viridis</i>: A Model for C4 Photosynthesis Â. Plant Cell, 2010, 22, 2537-2544.	3.1	320
66	Physiological and Genetic Characterization of End-of-Day Far-Red Light Response in Maize Seedlings Â Â. Plant Physiology, 2010, 154, 173-186.	2.3	47
67	Genome-Wide Distribution of Transposed<i>Dissociation</i>Elements in Maize Â. Plant Cell, 2010, 22, 1667-1685.	3.1	123
68	Vegetative axillary bud dormancy induced by shade and defoliation signals in the grasses. Plant Signaling and Behavior, 2010, 5, 317-319.	1.2	21
69	Exploring plant transcriptomes using ultra high-throughput sequencing. Briefings in Functional Genomics, 2010, 9, 118-128.	1.3	108
70	Concepts and Strategies for Reverse Genetics in Field, Forest and Bioenergy Crop Species. , 2010, , 354-398.		1
71	A Recommendation for Naming Transcription Factor Proteins in the Grasses. Plant Physiology, 2009, 149, 4-6.	2.3	45
72	High Glycolate Oxidase Activity Is Required for Survival of Maize in Normal Air Â. Plant Physiology, 2009, 149, 195-204.	2.3	178

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73	Suppression of sorghum axillary bud outgrowth by shade, phyB and defoliation signalling pathways. Plant, Cell and Environment, 2009, 33, 48-58.	2.8	121
74	Novel lycopene epsilon cyclase activities in maize revealed through perturbation of carotenoid biosynthesis. Plant Journal, 2009, 59, 588-599.	2.8	120
75	Light Signal Transduction Networks in Maize. , 2009, , 205-227.		4
76	Regional mutagenesis using Dissociation in maize. Methods, 2009, 49, 248-254.	1.9	40
77	The B73 Maize Genome: Complexity, Diversity, and Dynamics. Science, 2009, 326, 1112-1115.	6.0	3,612
78	Natural Genetic Variation in <i>Lycopene Epsilon Cyclase</i> Tapped for Maize Biofortification. Science, 2008, 319, 330-333.	6.0	692
79	Deregulation of Maize C4 Photosynthetic Development in a Mesophyll Cell-Defective Mutant Â Â Â. Plant Physiology, 2008, 146, 1469-1481.	2.3	45
80	State II<i>Dissociation</i>Element Formation Following<i>Activator</i>Excision in Maize. Genetics, 2007, 177, 737-747.	1.2	11
81	Generating Novel Allelic Variation Through Activator Insertional Mutagenesis in Maize. Genetics, 2007, 175, 981-992.	1.2	35
82	The molecular analysis of the shade avoidance syndrome in the grasses has begun. Journal of Experimental Botany, 2007, 58, 3079-3089.	2.4	91
83	Light and Metabolic Signals Control the Selective Degradation of Sucrose Synthase in Maize Leaves during Deetiolation. Plant Physiology, 2007, 144, 468-478.	2.3	12
84	Subfunctionalization of PhyB1 and PhyB2 in the control of seedling and mature plant traits in maize. Plant Journal, 2007, 49, 338-353.	2.8	107
85	A multi-treatment experimental system to examine photosynthetic differentiation in the maize leaf. BMC Genomics, 2007, 8, 12.	1.2	57
86	In planta transient expression as a system for genetic and biochemical analyses of chlorophyll biosynthesis. Plant Methods, 2006, 2, 15.	1.9	12
87	The Maize Oil Yellow1 (Oy1) Gene Encodes the I Subunit of Magnesium Chelatase. Plant Molecular Biology, 2006, 60, 95-106.	2.0	79
88	Light-regulated overexpression of an Arabidopsis phytochrome A gene in rice alters plant architecture and increases grain yield. Planta, 2006, 223, 627-636.	1.6	84
89	Ac-Immobilized, a Stable Source of Activator Transposase That Mediates Sporophytic and Gametophytic Excision of Dissociation Elements in Maize. Genetics, 2005, 171, 1999-2012.	1.2	36
90	Distribution of Activator (Ac) Throughout the Maize Genome for Use in Regional MutagenesisSequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY559172, AY559173, AY559174, AY559175, AY559176, AY559177, AY559178, AY559179, AY559180, AY559181, AY559182, AY559183, AY559184, AY559185, AY559186, AY559187, AY559188, AY559189, AY559190, AY559191, AY559192, AY559193, AY559194, AY559195, AY559196, AY559197, AY559198, AY559199, AY559200, AY559201, AY559202, AY. Genetics, 2005, 169, 981-995.	1.2	60

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91	Cereal phytochromes: targets of selection, targets for manipulation?. Trends in Plant Science, 2005, 10, 138-143.	4.3	66
92	The Elm1 (ZmHy2) Gene of Maize Encodes a Phytochromobilin Synthase. Plant Physiology, 2004, 136, 2771-2781.	2.3	44
93	Structure and Expression of Maize Phytochrome Family HomeologsSequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY234825, AY234826, AY234827, AY234828, AY234829, AY234830.. Genetics, 2004, 167, 1395-1405.	1.2	73
94	The globby1-1 (glo1-1) mutation disrupts nuclear and cell division in the developing maize seed causing alterations in endosperm cell fate and tissue differentiation. Development (Cambridge), 2003, 130, 5009-5017.	1.2	64
95	Photomorphogenic Responses in Maize Seedling Development Â. Plant Physiology, 2003, 133, 1578-1591.	2.3	67
96	Activator Mutagenesis of the Pink scutellum1/viviparous7 Locus of Maize. Plant Cell, 2003, 15, 874-884.	3.1	108
97	Transposon Tagging Using Activator (Ac) in Maize. , 2003, 236, 157-176.		28
98	elongated mesocotyl1, a Phytochrome-Deficient Mutant of Maize. Plant Physiology, 2002, 130, 155-163.	2.3	68
99	Transposon tagging in maize. Functional and Integrative Genomics, 2002, 2, 4-12.	1.4	64
100	Maize high chlorophyll fluorescent 60 mutation is caused by an Ac disruption of the gene encoding the chloroplast ribosomal small subunit protein 17. Plant Journal, 2000, 21, 317-327.	2.8	67
101	BUNDLE SHEATH DEFECTIVE2, a Novel Protein Required for Post-Translational Regulation of the rbcL Gene of Maize. Plant Cell, 1999, 11, 849-864.	3.1	149
102	Viruses making plants greener. Trends in Genetics, 1999, 15, 96.	2.9	0
103	Signals in Leaf Development. Advances in Botanical Research, 1998, 28, 161-195.	0.5	14
104	Cellular differentiation in the maize leaf is disrupted by bundle sheath defective mutations. Symposia of the Society for Experimental Biology, 1998, 51, 27-31.	0.0	9
105	The Ac-st2 Element of Maize Exhibits a Positive Dosage Effect and Epigenetic Regulation. Genetics, 1997, 147, 823-834.	1.2	19
106	bundle sheath defective2, a Mutation That Disrupts the Coordinated Development of Bundle Sheath and Mesophyll Cells in the Maize Leaf.. Plant Cell, 1996, 8, 915-927.	3.1	61
107	Leaf permease1 gene of maize is required for chloroplast development.. Plant Cell, 1996, 8, 463-475.	3.1	65
108	bundle sheath defective2, a Mutation That Disrupts the Coordinated Development of Bundle Sheath and Mesophyll Cells in the Maize Leaf. Plant Cell, 1996, 8, 915.	3.1	25