

# Clinton J Whipple

## List of Publications by Year in descending order

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Version: 2024-02-01

30  
papers

2,056  
citations

394421

19  
h-index

477307

29  
g-index

34  
all docs

34  
docs citations

34  
times ranked

2175  
citing authors

#	ARTICLE	IF	CITATIONS
1	The maize SBP-box transcription factor encoded by <i>tasselsheath4</i> regulates bract development and the establishment of meristem boundaries. <i>Development (Cambridge)</i> , 2010, 137, 1243-1250.	2.5	217
2	<i>grassy tillers1</i> promotes apical dominance in maize and responds to shade signals in the grasses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E506-12.	7.1	215
3	Conservation of B-class floral homeotic gene function between maize and Arabidopsis. <i>Development (Cambridge)</i> , 2004, 131, 6083-6091.	2.5	205
4	<i>bearded-ear</i> Encodes a MADS Box Transcription Factor Critical for Maize Floral Development. <i>Plant Cell</i> , 2009, 21, 2578-2590.	6.6	154
5	Conservation of B class gene expression in the second whorl of a basal grass and outgroups links the origin of lodicules and petals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1081-1086.	7.1	137
6	The regulatory landscape of a core maize domestication module controlling bud dormancy and growth repression. <i>Nature Communications</i> , 2019, 10, 3810.	12.8	116
7	Early inflorescence development in the grasses (Poaceae). <i>Frontiers in Plant Science</i> , 2013, 4, 250.	3.6	113
8	From Many, One: Genetic Control of Prolificacy during Maize Domestication. <i>PLoS Genetics</i> , 2013, 9, e1003604.	3.5	111
9	A Conserved Mechanism of Bract Suppression in the Grass Family. <i>Plant Cell</i> , 2010, 22, 565-578.	6.6	97
10	Grass inflorescence architecture and meristem determinacy. <i>Seminars in Cell and Developmental Biology</i> , 2018, 79, 37-47.	5.0	90
11	Altered expression of maize PLASTOCHRON1 enhances biomass and seed yield by extending cell division duration. <i>Nature Communications</i> , 2017, 8, 14752.	12.8	89
12	BARREN STALK FASTIGIATE1 Is an AT-Hook Protein Required for the Formation of Maize Ears. <i>Plant Cell</i> , 2011, 23, 1756-1771.	6.6	84
13	Grass inflorescence architecture and evolution: the origin of novel signaling centers. <i>New Phytologist</i> , 2017, 216, 367-372.	7.3	71
14	Bulked-Segregant Analysis Coupled to Whole Genome Sequencing (BSA-Seq) for Rapid Gene Cloning in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3583-3592.	1.8	57
15	Evolutionary Dynamics of Floral Homeotic Transcription Factor Protein-Protein Interactions. <i>Molecular Biology and Evolution</i> , 2016, 33, 1486-1501.	8.9	47
16	The Maize <i>PI</i> / <i>GLO</i> Ortholog <i>Zmm16</i> / <i>sterile tassel silky ear1</i> Interacts with the Zygomorphy and Sex Determination Pathways in Flower Development. <i>Plant Cell</i> , 2015, 27, 3081-3098.	6.6	45
17	Genetics of Grass Flower Development. <i>Advances in Botanical Research</i> , 2006, 44, 385-424.	1.1	29
18	Evolutionary Variation in MADS Box Dimerization Affects Floral Development and Protein Abundance in Maize. <i>Plant Cell</i> , 2020, 32, 3408-3424.	6.6	27

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19	Prevalence and Persistence of Misconceptions in Tree Thinking. <i>Journal of Microbiology and Biology Education</i> , 2016, 17, 389-398.	1.0	24
20	Positional cloning in maize ( <i>Zea mays</i> subsp. <i>mays</i> , Poaceae). <i>Applications in Plant Sciences</i> , 2015, 3, 1400092.	2.1	21
21	Recruitment of an ancient branching program to suppress carpel development in maize flowers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	18
22	Defining the Plant Germ Line—Nature or Nurture?. <i>Science</i> , 2012, 337, 301-302.	12.6	16
23	Protein change in plant evolution: tracing one thread connecting molecular and phenotypic diversity. <i>Frontiers in Plant Science</i> , 2013, 4, 382.	3.6	15
24	A Gene for Genetic Background in <i>Zea mays</i> : Fine-Mapping <i>enhancer of teosinte branched1.2</i> to a YABBY Class Transcription Factor. <i>Genetics</i> , 2016, 204, 1573-1585.	2.9	15
25	Boundary domain genes were recruited to suppress bract growth and promote branching in maize. <i>Science Advances</i> , 2022, 8, .	10.3	15
26	The maize SBP-box transcription factor encoded by <i>tasselsheath4</i> regulates bract development and the establishment of meristem boundaries. <i>Development (Cambridge)</i> , 2010, 137, 1585-1585.	2.5	10
27	Development of an Evolutionary Tree Concept Inventory. <i>Journal of Microbiology and Biology Education</i> , 2019, 20, .	1.0	5
28	Integration of high-density genetic mapping with transcriptome analysis uncovers numerous agronomic QTL and reveals candidate genes for the control of tillering in sorghum. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	4
29	Chromosome-Scale Genome Assembly of <i>Gilia yorkii</i> Enables Genetic Mapping of Floral Traits in an Interspecies Cross. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	4
30	Wildflowers of the Mountain West Wildflowers of the Mountain West Richard M. Anderson, JayDee Gunnell, Jerry L. Goodspeed, 2012 Utah State University Press, an imprint of University Press of Colorado Boulder, CO. 300 pp. ISBN: 978-0-87421-895-4 (spiral bound) \$24.95; ISBN: 978-0-87421-896-1 (e-book), \$20.00.. <i>Madroño</i> , 2013, 60, 257-257.	0.4	0