

# Timothy J Close

## List of Publications by Year in descending order

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101  
papers

15,068  
citations

28736

57  
h-index

48101

92  
g-index

111  
all docs

111  
docs citations

111  
times ranked

12928  
citing authors

#	ARTICLE	IF	CITATIONS
1	Registration of aphid-resistant "California Blackeye 77"™ cowpea. <i>Journal of Plant Registrations</i> , 2022, 16, 13-20.	0.4	3
2	Genomic resources in plant breeding for sustainable agriculture. <i>Journal of Plant Physiology</i> , 2021, 257, 153351.	1.6	90
3	The UCR Minicore: a resource for cowpea research and breeding. , 2021, 3, e95.		26
4	Legumes: Embracing the genome era. , 2021, 3, e113.		4
5	Genetic, anatomical, and environmental patterns related to pod shattering resistance in domesticated cowpea [ <i>Vigna unguiculata</i> (L.) Walp]. <i>Journal of Experimental Botany</i> , 2021, 72, 6219-6229.	2.4	12
6	Breaks of macrosynteny and collinearity among moth bean ( <i>Vigna aconitifolia</i> ), cowpea ( <i>V. unguiculata</i> ) and pigeon pea ( <i>V. radiata</i> ). <i>Genome Biology and Evolution</i> , 2021, 13, 1-10.	1.0	10
7	A receptor-like protein mediates plant immune responses to herbivore-associated molecular patterns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31510-31518.	3.3	86
8	Genetic, textual, and archeological evidence of the historical global spread of cowpea ( <i>Vigna unguiculata</i> (L.) Walp.). <i>PLoS ONE</i> , 2020, 15, e0229167.	1.1	13
9	Identification of QTL for perenniality and floral scent in cowpea ( <i>Vigna unguiculata</i> (L.) Walp.). <i>PLoS ONE</i> , 2020, 15, e0229167.	1.1	13
10	A genome-wide association and meta-analysis reveal regions associated with seed size in cowpea [ <i>Vigna unguiculata</i> (L.) Walp]. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3079-3087.	1.8	42
11	Seed Coat Pattern QTL and Development in Cowpea ( <i>Vigna unguiculata</i> [L.] Walp.). <i>Frontiers in Plant Science</i> , 2019, 10, 1346.	1.7	36
12	Registration of a Cowpea [ <i>Vigna unguiculata</i> (L.) Walp.] Multiparent Advanced Generation Intercross (MAGIC) Population. <i>Journal of Plant Registrations</i> , 2019, 13, 281-286.	0.4	7
13	The genome of cowpea ( <i>Vigna unguiculata</i> [L.] Walp.). <i>Plant Journal</i> , 2019, 98, 767-782.	2.8	264
14	The future of legume genetic data resources: Challenges, opportunities, and priorities. , 2019, 1, e16.		30
15	A novel aphid resistance locus in cowpea identified by combining SSR and SNP markers. <i>Plant Breeding</i> , 2018, 137, 203-209.	1.0	7
16	Identification of QTL controlling domestication-related traits in cowpea ( <i>Vigna unguiculata</i> L. Walp). <i>Scientific Reports</i> , 2018, 8, 6261.	1.6	105
17	A multiparent advanced generation intercross (MAGIC) population for genetic analysis and improvement of cowpea ( <i>Vigna unguiculata</i> L. Walp.). <i>Plant Journal</i> , 2018, 93, 1129-1142.	2.8	132
18	Identification of Candidate Genes Controlling Black Seed Coat and Pod Tip Color in Cowpea ( <i>Vigna unguiculata</i> (L.) Walp.). <i>Journal of Plant Registrations</i> , 2018, 12, 1-10.	0.8	56

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19	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	13.7	1,365
20	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. <i>Scientific Data</i> , 2017, 4, 170044.	2.4	130
21	Genome resources for climate-resilient cowpea, an essential crop for food security. <i>Plant Journal</i> , 2017, 89, 1042-1054.	2.8	199
22	Genomic regions, cellular components and gene regulatory basis underlying pod length variations in cowpea ( <i>V. unguiculata</i> L. Walp). <i>Plant Biotechnology Journal</i> , 2017, 15, 547-557.	4.1	68
23	Genomic Tools in Cowpea Breeding Programs: Status and Perspectives. <i>Frontiers in Plant Science</i> , 2016, 7, 757.	1.7	112
24	A major QTL corresponding to the Rk locus for resistance to root-knot nematodes in cowpea ( <i>Vigna</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 54	1.8	54
25	When less is more: $\tilde{\text{slicing}}^{\text{TM}}$ sequencing data improves read decoding accuracy and <i>de novo</i> assembly quality. <i>Bioinformatics</i> , 2015, 31, 2972-2980.	1.8	25
26	The Barley <i>Uniculme4</i> Gene Encodes a BLADE-ON-PETIOLE-Like Protein That Controls Tillering and Leaf Patterning. <i>Plant Physiology</i> , 2015, 168, 164-174.	2.3	85
27	<i>De novo</i> meta-assembly of ultra-deep sequencing data. <i>Bioinformatics</i> , 2015, 31, i9-i16.	1.8	25
28	Genetic mapping and legume synteny of aphid resistance in African cowpea ( <i>Vigna unguiculata</i> L. Walp.) grown in California. <i>Molecular Breeding</i> , 2015, 35, 36.	1.0	85
29	Introgression of a rare haplotype from Southeastern Africa to breed California blackeyes with larger seeds. <i>Frontiers in Plant Science</i> , 2015, 6, 126.	1.7	12
30	CLARK: fast and accurate classification of metagenomic and genomic sequences using discriminative k-mers. <i>BMC Genomics</i> , 2015, 16, 236.	1.2	514
31	Sequencing of 15,622 gene-bearing BACs clarifies the gene-dense regions of the barley genome. <i>Plant Journal</i> , 2015, 84, 216-227.	2.8	36
32	Cowpea. <i>Handbook of Plant Breeding</i> , 2015, , 219-250.	0.1	22
33	Genetic mapping, synteny, and physical location of two loci for <i>Fusarium oxysporum</i> f. sp. <i>tracheiphilum</i> race 4 resistance in cowpea [ <i>Vigna unguiculata</i> (L.) Walp]. <i>Molecular Breeding</i> , 2014, 33, 779-791.	1.0	36
34	Molecular mapping of greenbug ( <i>Schizaphis graminum</i> ) resistance gene <i>Rsg1</i> in barley. <i>Plant Breeding</i> , 2014, 133, 227-233.	1.0	11
35	Identification of candidate genes and molecular markers for heat-induced brown discoloration of seed coats in cowpea [ <i>Vigna unguiculata</i> (L.) Walp]. <i>BMC Genomics</i> , 2014, 15, 328.	1.2	65
36	Markers for breeding heat-tolerant cowpea. <i>Molecular Breeding</i> , 2013, 31, 529-536.	1.0	90

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37	Anchoring and ordering <scp>NGS</scp> contig assemblies by population sequencing (<scp>POPSEQ</scp>). <i>Plant Journal</i> , 2013, 76, 718-727.	2.8	264
38	A Graph-Theoretical Approach to the Selection of the Minimum Tiling Path from a Physical Map. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 352-360.	1.9	7
39	Association Studies and Legume Synteny Reveal Haplotypes Determining Seed Size in <i>Vigna unguiculata</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 95.	1.7	35
40	Combinatorial Pooling Enables Selective Sequencing of the Barley Gene Space. <i>PLoS Computational Biology</i> , 2013, 9, e1003010.	1.5	20
41	Gene Pools and the Genetic Architecture of Domesticated Cowpea. <i>Plant Genome</i> , 2013, 6, plantgenome2013.03.0005.	1.6	88
42	Genetic Architecture of Delayed Senescence, Biomass, and Grain Yield under Drought Stress in Cowpea. <i>PLoS ONE</i> , 2013, 8, e70041.	1.1	73
43	Genetic Diversity in Latvian Spring Barley Association Mapping Population. , 2013, , 25-35.		2
44	High-Resolution Single Nucleotide Polymorphism Genotyping Reveals a Significant Problem among Breeder Resources. <i>Plant Genome</i> , 2013, 6, plantgenome2012.08.0020.	1.6	8
45	Markers for Quantitative Inheritance of Resistance to Foliar Thrips in Cowpea. <i>Crop Science</i> , 2012, 52, 2075-2081.	0.8	26
46	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012, 491, 711-716.	13.7	1,416
47	Genetic and Physical Mapping of Candidate Genes for Resistance to <i>Fusarium oxysporum</i> f.sp. <i>tracheiphilum</i> Race 3 in Cowpea [ <i>Vigna unguiculata</i> (L.) Walp]. <i>PLoS ONE</i> , 2012, 7, e41600.	1.1	67
48	The <i>Hordeum</i> Toolbox: The Barley Coordinated Agricultural Project Genotype and Phenotype Resource. <i>Plant Genome</i> , 2012, 5, 81-91.	1.6	35
49	Identification, validation and high-throughput genotyping of transcribed gene SNPs in cassava. <i>Theoretical and Applied Genetics</i> , 2012, 124, 685-695.	1.8	55
50	Cowpea-Soybean Synteny Clarified through an Improved Genetic Map. <i>Plant Genome</i> , 2011, 4, 218-225.	1.6	108
51	An Improved Consensus Linkage Map of Barley Based on Flow-Sorted Chromosomes and Single Nucleotide Polymorphism Markers. <i>Plant Genome</i> , 2011, 4, 238-249.	1.6	150
52	INTERMEDIUM-C, a modifier of lateral spikelet fertility in barley, is an ortholog of the maize domestication gene <i>TEOSINTE BRANCHED 1</i> . <i>Nature Genetics</i> , 2011, 43, 169-172.	9.4	302
53	Patterns of polymorphism and linkage disequilibrium in cultivated barley. <i>Theoretical and Applied Genetics</i> , 2011, 122, 523-531.	1.8	41
54	Genic SNP markers and legume synteny reveal candidate genes underlying QTL for <i>Macrophomina phaseolina</i> resistance and maturity in cowpea [ <i>Vigna unguiculata</i> (L) Walp.]. <i>BMC Genomics</i> , 2011, 12, 8.	1.2	97

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55	Accurate Construction of Consensus Genetic Maps via Integer Linear Programming. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 381-394.	1.9	105
56	Single Nucleotide Polymorphism Mapping and Alignment of Recombinant Chromosome Substitution Lines in Barley. <i>Plant and Cell Physiology</i> , 2011, 52, 728-737.	1.5	32
57	Population Structure and Linkage Disequilibrium in U.S. Barley Germplasm: Implications for Association Mapping. <i>Crop Science</i> , 2010, 50, 556-566.	0.8	106
58	Development and polymorphism of <i>Vigna unguiculata</i> ssp. <i>unguiculata</i> microsatellite markers used for phylogenetic analysis in asparagus bean ( <i>Vigna unguiculata</i> ssp. <i>sesquipedialis</i> (L.) Verdc.). <i>Molecular Breeding</i> , 2010, 25, 675-684.	1.0	59
59	Association mapping of spot blotch resistance in wild barley. <i>Molecular Breeding</i> , 2010, 26, 243-256.	1.0	151
60	Genome-wide SNPs and re-sequencing of growth habit and inflorescence genes in barley: implications for association mapping in germplasm arrays varying in size and structure. <i>BMC Genomics</i> , 2010, 11, 707.	1.2	81
61	An Integrated Resource for Barley Linkage Map and Malting Quality QTL Alignment. <i>Plant Genome</i> , 2009, 2, .	1.6	116
62	A consensus genetic map of cowpea [ <i>Vigna unguiculata</i> (L) Walp.] and synteny based on EST-derived SNPs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18159-18164.	3.3	257
63	The International Barley Sequencing Consortium At the Threshold of Efficient Access to the Barley Genome. <i>Plant Physiology</i> , 2009, 149, 142-147.	2.3	195
64	A compartmentalized approach to the assembly of physical maps. <i>BMC Bioinformatics</i> , 2009, 10, 217.	1.2	3
65	Development and implementation of high-throughput SNP genotyping in barley. <i>BMC Genomics</i> , 2009, 10, 582.	1.2	570
66	Mapping QTL for drought stress-induced premature senescence and maturity in cowpea [ <i>Vigna unguiculata</i> (L.) Walp.]. <i>Theoretical and Applied Genetics</i> , 2009, 118, 849-863.	1.8	95
67	The K-Segment of Maize DHN1 Mediates Binding to Anionic Phospholipid Vesicles and Concomitant Structural Changes. <i>Plant Physiology</i> , 2009, 150, 1503-1514.	2.3	205
68	Dehydrin gene expression provides an indicator of low temperature and drought stress: transcriptome-based analysis of Barley ( <i>Hordeum vulgare</i> L.). <i>Functional and Integrative Genomics</i> , 2008, 8, 387-405.	1.4	173
69	Towards systems genetic analyses in barley: Integration of phenotypic, expression and genotype data into GeneNetwork. <i>BMC Genetics</i> , 2008, 9, 73.	2.7	26
70	Coupling amplified DNA from flow-sorted chromosomes to high-density SNP mapping in barley. <i>BMC Genomics</i> , 2008, 9, 294.	1.2	120
71	Efficient and Accurate Construction of Genetic Linkage Maps from the Minimum Spanning Tree of a Graph. <i>PLoS Genetics</i> , 2008, 4, e1000212.	1.5	590
72	ON THE ACCURATE CONSTRUCTION OF CONSENSUS GENETIC MAPS. , 2008, , .		57

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73	On the accurate construction of consensus genetic maps. Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2008, 7, 285-96.	0.4	35
74	A Compartmentalized Approach to the Assembly of Physical Maps. , 2007, , .		4
75	Large-scale expression profiling and physiological characterization of jasmonic acid-mediated adaptation of barley to salinity stress. Plant, Cell and Environment, 2007, 30, 410-421.	2.8	195
76	Array-based genotyping and expression analysis of barley cv. Maythorpe and Golden Promise. BMC Genomics, 2007, 8, 87.	1.2	37
77	Genome-wide transcriptional analysis of salinity stressed japonica and indica rice genotypes during panicle initiation stage. Plant Molecular Biology, 2007, 63, 609-623.	2.0	174
78	DECONVOLUTING THE BAC-GENE RELATIONSHIPS USING A PHYSICAL MAP. , 2007, , .		1
79	Transcriptome analysis of barley anthers: effect of mannitol treatment on microspore embryogenesis. Physiologia Plantarum, 2006, 127, 551-560.	2.6	37
80	Expression analysis of barley ( <i>Hordeum vulgare</i> L.) during salinity stress. Functional and Integrative Genomics, 2006, 6, 143-156.	1.4	138
81	Recent history of artificial outcrossing facilitates whole-genome association mapping in elite inbred crop varieties. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 18656-18661.	3.3	309
82	Transcriptome Analysis of Cold Acclimation in Barley Albina and Xantha Mutants. Plant Physiology, 2006, 141, 257-270.	2.3	164
83	HarvEST. , 2005, 406, 161-177.		33
84	Genome-wide SNP discovery and linkage analysis in barley based on genes responsive to abiotic stress. Molecular Genetics and Genomics, 2005, 274, 515-527.	1.0	250
85	Detecting single-feature polymorphisms using oligonucleotide arrays and robustified projection pursuit. Bioinformatics, 2005, 21, 3852-3858.	1.8	74
86	A New Resource for Cereal Genomics: 22K Barley GeneChip Comes of Age. Plant Physiology, 2004, 134, 960-968.	2.3	287
87	Cryoprotective activity of a cold-induced dehydrin purified from barley. Physiologia Plantarum, 2003, 118, 262-269.	2.6	110
88	The binding of Maize DHN1 to Lipid Vesicles. Gain of Structure and Lipid Specificity. Plant Physiology, 2003, 131, 309-316.	2.3	317
89	Comparative DNA Sequence Analysis of Wheat and Rice Genomes. Genome Research, 2003, 13, 1818-1827.	2.4	369
90	Barley Cbf3 Gene Identification, Expression Pattern, and Map Location. Plant Physiology, 2002, 129, 1781-1787.	2.3	207

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91	Dehydrins. Cell and Molecular Response To Stress, 2002, 3, 155-171.	0.4	61
92	Purification and Partial Characterization of a Dehydrin Involved in Chilling Tolerance during Seedling Emergence of Cowpea1. Plant Physiology, 1999, 120, 237-244.	2.3	156
93	Purification, immunolocalization, cryoprotective, and antifreeze activity of PCA60: A dehydrin from peach ( <i>Prunus persica</i> ). Physiologia Plantarum, 1999, 105, 600-608.	2.6	257
94	Characterization of an 80-kDa dehydrin-like protein in barley responsive to cold acclimation. Physiologia Plantarum, 1999, 106, 177-183.	2.6	56
95	A ca. 40 kDa maize ( <i>Zea mays</i> L.) embryo dehydrin is encoded by the <i>dhn2</i> locus on chromosome 9. Plant Molecular Biology, 1998, 38, 417-423.	2.0	15
96	PROTEINS IMMUNOLOGICALLY RELATED TO DEHYDRINS IN FUCOID ALGAE. Journal of Phycology, 1998, 34, 642-650.	1.0	40
97	Temporal accumulation and ultrastructural localization of dehydrins in <i>Zea mays</i> . Physiologia Plantarum, 1997, 101, 545-555.	2.6	73
98	Dehydrins: A commonalty in the response of plants to dehydration and low temperature. Physiologia Plantarum, 1997, 100, 291-296.	2.6	774
99	Dehydrins: genes, proteins, and associations with phenotypic traits. New Phytologist, 1997, 137, 61-74.	3.5	265
100	Seasonal patterns of dehydrins and 70-kDa heat-shock proteins in bark tissues of eight species of woody plants. Physiologia Plantarum, 1996, 96, 496-505.	2.6	95
101	Dehydrins: Emergence of a biochemical role of a family of plant dehydration proteins. Physiologia Plantarum, 1996, 97, 795-803.	2.6	855