

# Timothy J Close

## List of Publications by Year in descending order

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101  
papers

15,068  
citations

25034

57  
h-index

42399

92  
g-index

111  
all docs

111  
docs citations

111  
times ranked

11611  
citing authors

#	ARTICLE	IF	CITATIONS
1	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012, 491, 711-716.	27.8	1,416
2	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	27.8	1,365
3	Dehydrins: Emergence of a biochemical role of a family of plant dehydration proteins. <i>Physiologia Plantarum</i> , 1996, 97, 795-803.	5.2	855
4	Dehydrins: A commonality in the response of plants to dehydration and low temperature. <i>Physiologia Plantarum</i> , 1997, 100, 291-296.	5.2	774
5	Efficient and Accurate Construction of Genetic Linkage Maps from the Minimum Spanning Tree of a Graph. <i>PLoS Genetics</i> , 2008, 4, e1000212.	3.5	590
6	Development and implementation of high-throughput SNP genotyping in barley. <i>BMC Genomics</i> , 2009, 10, 582.	2.8	570
7	CLARK: fast and accurate classification of metagenomic and genomic sequences using discriminative k-mers. <i>BMC Genomics</i> , 2015, 16, 236.	2.8	514
8	Comparative DNA Sequence Analysis of Wheat and Rice Genomes. <i>Genome Research</i> , 2003, 13, 1818-1827.	5.5	369
9	The binding of Maize DHN1 to Lipid Vesicles. Gain of Structure and Lipid Specificity. <i>Plant Physiology</i> , 2003, 131, 309-316.	4.8	317
10	Recent history of artificial outcrossing facilitates whole-genome association mapping in elite inbred crop varieties. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18656-18661.	7.1	309
11	INTERMEDIUM-C, a modifier of lateral spikelet fertility in barley, is an ortholog of the maize domestication gene TEOSINTE BRANCHED 1. <i>Nature Genetics</i> , 2011, 43, 169-172.	21.4	302
12	A New Resource for Cereal Genomics: 22K Barley GeneChip Comes of Age. <i>Plant Physiology</i> , 2004, 134, 960-968.	4.8	287
13	Dehydrins: genes, proteins, and associations with phenotypic traits. <i>New Phytologist</i> , 1997, 137, 61-74.	7.3	265
14	Anchoring and ordering <sc>NGS</sc> contig assemblies by population sequencing (<sc>POPSEQ</sc>). <i>Plant Journal</i> , 2013, 76, 718-727.	5.7	264
15	The genome of cowpea (<i>Vigna unguiculata</i> [L.] Walp.). <i>Plant Journal</i> , 2019, 98, 767-782.	5.7	264
16	Purification, immunolocalization, cryoprotective, and antifreeze activity of PCA60: A dehydrin from peach ( <i>Prunus persica</i> ). <i>Physiologia Plantarum</i> , 1999, 105, 600-608.	5.2	257
17	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.	7.1	257
18	Genome-wide SNP discovery and linkage analysis in barley based on genes responsive to abiotic stress. <i>Molecular Genetics and Genomics</i> , 2005, 274, 515-527.	2.1	250

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19	Barley Cbf3 Gene Identification, Expression Pattern, and Map Location. <i>Plant Physiology</i> , 2002, 129, 1781-1787.	4.8	207
20	The K-Segment of Maize DHN1 Mediates Binding to Anionic Phospholipid Vesicles and Concomitant Structural Changes Å Å. <i>Plant Physiology</i> , 2009, 150, 1503-1514.	4.8	205
21	Genome resources for climateâ€resilient cowpea, an essential crop for food security. <i>Plant Journal</i> , 2017, 89, 1042-1054.	5.7	199
22	Large-scale expression profiling and physiological characterization of jasmonic acid-mediated adaptation of barley to salinity stress. <i>Plant, Cell and Environment</i> , 2007, 30, 410-421.	5.7	195
23	The International Barley Sequencing Consortiumâ€™ At the Threshold of Efficient Access to the Barley Genome Å. <i>Plant Physiology</i> , 2009, 149, 142-147.	4.8	195
24	Genome-wide transcriptional analysis of salinity stressed japonica and indica rice genotypes during panicle initiation stage. <i>Plant Molecular Biology</i> , 2007, 63, 609-623.	3.9	174
25	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.	3.5	173
26	Transcriptome Analysis of Cold Acclimation in Barley Albina and Xantha Mutants. <i>Plant Physiology</i> , 2006, 141, 257-270.	4.8	164
27	Purification and Partial Characterization of a Dehydrin Involved in Chilling Tolerance during Seedling Emergence of Cowpea1. <i>Plant Physiology</i> , 1999, 120, 237-244.	4.8	156
28	Association mapping of spot blotch resistance in wild barley. <i>Molecular Breeding</i> , 2010, 26, 243-256.	2.1	151
29	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.	2.8	150
30	Expression analysis of barley ( <i>Hordeum vulgare</i> L.) during salinity stress. <i>Functional and Integrative Genomics</i> , 2006, 6, 143-156.	3.5	138
31	A multiâ€parent advanced generation interâ€cross (<sc>MAGIC</sc>) population for genetic analysis and improvement of cowpea (<i>Vigna unguiculata</i> L. Walp.). <i>Plant Journal</i> , 2018, 93, 1129-1142.	5.7	132
32	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. <i>Scientific Data</i> , 2017, 4, 170044.	5.3	130
33	Coupling amplified DNA from flow-sorted chromosomes to high-density SNP mapping in barley. <i>BMC Genomics</i> , 2008, 9, 294.	2.8	120
34	An Integrated Resource for Barley Linkage Map and Malting Quality QTL Alignment. <i>Plant Genome</i> , 2009, 2, .	2.8	116
35	Genomic Tools in Cowpea Breeding Programs: Status and Perspectives. <i>Frontiers in Plant Science</i> , 2016, 7, 757.	3.6	112
36	Cryoprotective activity of a cold-induced dehydrin purified from barley. <i>Physiologia Plantarum</i> , 2003, 118, 262-269.	5.2	110

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37	Cowpea-Soybean Synteny Clarified through an Improved Genetic Map. <i>Plant Genome</i> , 2011, 4, 218-225.	2.8	108
38	Population Structure and Linkage Disequilibrium in U.S. Barley Germplasm: Implications for Association Mapping. <i>Crop Science</i> , 2010, 50, 556-566.	1.8	106
39	Accurate Construction of Consensus Genetic Maps via Integer Linear Programming. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 381-394.	3.0	105
40	Identification of QTL controlling domestication-related traits in cowpea ( <i>Vigna unguiculata</i> L. Walp). <i>Scientific Reports</i> , 2018, 8, 6261.	3.3	105
41	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.	2.8	97
42	Seasonal patterns of dehydrins and 70-kDa heat-shock proteins in bark tissues of eight species of woody plants. <i>Physiologia Plantarum</i> , 1996, 96, 496-505.	5.2	95
43	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.	3.6	95
44	Markers for breeding heat-tolerant cowpea. <i>Molecular Breeding</i> , 2013, 31, 529-536.	2.1	90
45	Genomic resources in plant breeding for sustainable agriculture. <i>Journal of Plant Physiology</i> , 2021, 257, 153351.	3.5	90
46	Gene Pools and the Genetic Architecture of Domesticated Cowpea. <i>Plant Genome</i> , 2013, 6, plantgenome2013.03.0005.	2.8	88
47	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.	7.1	86
48	The Barley <i>U4</i> Gene Encodes a BLADE-ON-PETIOLE-Like Protein That Controls Tillering and Leaf Patterning. <i>Plant Physiology</i> , 2015, 168, 164-174.	4.8	85
49	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.	2.1	85
50	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.	2.8	81
51	Detecting single-feature polymorphisms using oligonucleotide arrays and robustified projection pursuit. <i>Bioinformatics</i> , 2005, 21, 3852-3858.	4.1	74
52	Temporal accumulation and ultrastructural localization of dehydrins in <i>Zea mays</i> . <i>Physiologia Plantarum</i> , 1997, 101, 545-555.	5.2	73
53	Genetic Architecture of Delayed Senescence, Biomass, and Grain Yield under Drought Stress in Cowpea. <i>PLoS ONE</i> , 2013, 8, e70041.	2.5	73
54	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.	8.3	68

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55	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.	2.5	67
56	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.	2.8	65
57	Dehydrins. <i>Cell and Molecular Response To Stress</i> , 2002, 3, 155-171.	0.4	61
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.	2.1	59
59	ON THE ACCURATE CONSTRUCTION OF CONSENSUS GENETIC MAPS. , 2008, , .		57
60	Characterization of an 80-kDa dehydrin-like protein in barley responsive to cold acclimation. <i>Physiologia Plantarum</i> , 1999, 106, 177-183.	5.2	56
61	Identification of Candidate Genes Controlling Black Seed Coat and Pod Tip Color in Cowpea ( <i>Vigna</i> ) Tj ETQq1 1 0.784314 rgBT /Over	1.8	56
62	Identification, validation and high-throughput genotyping of transcribed gene SNPs in cassava. <i>Theoretical and Applied Genetics</i> , 2012, 124, 685-695.	3.6	55
63	A major QTL corresponding to the Rk locus for resistance to root-knot nematodes in cowpea ( <i>Vigna</i> ) Tj ETQq1 1 0.784314 rgBT /Over	3.6	54
64	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.	3.6	42
65	Patterns of polymorphism and linkage disequilibrium in cultivated barley. <i>Theoretical and Applied Genetics</i> , 2011, 122, 523-531.	3.6	41
66	PROTEINS IMMUNOLOGICALLY RELATED TO DEHYDRINS IN FUCOID ALGAE. <i>Journal of Phycology</i> , 1998, 34, 642-650.	2.3	40
67	Transcriptome analysis of barley anthers: effect of mannitol treatment on microspore embryogenesis. <i>Physiologia Plantarum</i> , 2006, 127, 551-560.	5.2	37
68	Array-based genotyping and expression analysis of barley cv. Maythorpe and Golden Promise. <i>BMC Genomics</i> , 2007, 8, 87.	2.8	37
69	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.	2.1	36
70	Sequencing of 15,622 gene-bearing BAC s clarifies the gene-dense regions of the barley genome. <i>Plant Journal</i> , 2015, 84, 216-227.	5.7	36
71	Seed Coat Pattern QTL and Development in Cowpea ( <i>Vigna unguiculata</i> [L.] Walp.). <i>Frontiers in Plant Science</i> , 2019, 10, 1346.	3.6	36
72	The <i>Hordeum</i> Toolbox: The Barley Coordinated Agricultural Project Genotype and Phenotype Resource. <i>Plant Genome</i> , 2012, 5, 81-91.	2.8	35

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73	Association Studies and Legume Synteny Reveal Haplotypes Determining Seed Size in <i>Vigna unguiculata</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 95.	3.6	35
74	On the accurate construction of consensus genetic maps. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2008, 7, 285-96.	0.4	35
75	Genetic, textual, and archeological evidence of the historical global spread of cowpea ( <i>Vigna</i> ) Tj ETQq1 1 0.784314 ggBT /Over	0.4	34
76	HarvEST. , 2005, 406, 161-177.		33
77	Single Nucleotide Polymorphism Mapping and Alignment of Recombinant Chromosome Substitution Lines in Barley. <i>Plant and Cell Physiology</i> , 2011, 52, 728-737.	3.1	32
78	The future of legume genetic data resources: Challenges, opportunities, and priorities. , 2019, 1, e16.		30
79	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
80	Markers for Quantitative Inheritance of Resistance to Foliar Thrips in Cowpea. <i>Crop Science</i> , 2012, 52, 2075-2081.	1.8	26
81	The UCR Minicore: a resource for cowpea research and breeding. , 2021, 3, e95.		26
82	When less is more: â€˜slicingâ€™™ sequencing data improves read decoding accuracy and <i>de novo</i> assembly quality. <i>Bioinformatics</i> , 2015, 31, 2972-2980.	4.1	25
83	<i>De novo</i> meta-assembly of ultra-deep sequencing data. <i>Bioinformatics</i> , 2015, 31, i9-i16.	4.1	25
84	Cowpea. <i>Handbook of Plant Breeding</i> , 2015, , 219-250.	0.1	22
85	Combinatorial Pooling Enables Selective Sequencing of the Barley Gene Space. <i>PLoS Computational Biology</i> , 2013, 9, e1003010.	3.2	20
86	A ca. 40 kDa maize ( <i>Zea mays</i> L.) embryo dehydrin is encoded by the <i>dhn2</i> locus on chromosome 9. <i>Plant Molecular Biology</i> , 1998, 38, 417-423.	3.9	15
87	Identification of QTL for perenniality and floral scent in cowpea ( <i>Vigna unguiculata</i> [L.] Walp.). <i>PLoS ONE</i> , 2020, 15, e0229167.	2.5	13
88	Introgression of a rare haplotype from Southeastern Africa to breed California blackeyes with larger seeds. <i>Frontiers in Plant Science</i> , 2015, 6, 126.	3.6	12
89	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.	4.8	12
90	Molecular mapping of greenbug ( <i>Schizaphis graminum</i> ) resistance gene <i>Rsg1</i> in barley. <i>Plant Breeding</i> , 2014, 133, 227-233.	1.9	11

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91	Breaks of macrosynteny and collinearity among moth bean ( <i>Vigna aconitifolia</i> ), cowpea ( <i>V. Tj ETQq1 1 0.784314 rgBT /Overlock 10 TFS</i> )	2.2	10
92	High-Resolution Single Nucleotide Polymorphism Genotyping Reveals a Significant Problem among Breeder Resources. <i>Plant Genome</i> , 2013, 6, plantgenome2012.08.0020.	2.8	8
93	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.	3.0	7
94	A novel aphid resistance locus in cowpea identified by combining <sc>SSR</sc> and <sc>SNP</sc> markers. <i>Plant Breeding</i> , 2018, 137, 203-209.	1.9	7
95	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.	0.5	7
96	A Compartmentalized Approach to the Assembly of Physical Maps. , 2007, , .		4
97	Legumes: Embracing the genome era. , 2021, 3, e113.		4
98	A compartmentalized approach to the assembly of physical maps. <i>BMC Bioinformatics</i> , 2009, 10, 217.	2.6	3
99	Registration of aphid-resistant "California Blackeye 77"™ cowpea. <i>Journal of Plant Registrations</i> , 2022, 16, 13-20.	0.5	3
100	Genetic Diversity in Latvian Spring Barley Association Mapping Population. , 2013, , 25-35.		2
101	DECONVOLUTIONING THE BAC-GENE RELATIONSHIPS USING A PHYSICAL MAP. , 2007, , .		1