

# Thomas Altmann

## List of Publications by Year in descending order

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128  
papers

17,266  
citations

22099

59  
h-index

16127

124  
g-index

134  
all docs

134  
docs citations

134  
times ranked

18488  
citing authors

#	ARTICLE	IF	CITATIONS
1	Temporal dynamics of QTL effects on vegetative growth in <i>Arabidopsis thaliana</i> . Journal of Experimental Botany, 2021, 72, 476-490.	2.4	7
2	Multi-omics-based prediction of hybrid performance in canola. Theoretical and Applied Genetics, 2021, 134, 1147-1165.	1.8	23
3	Dynamics of Maize Vegetative Growth and Drought Adaptability Using Image-Based Phenotyping Under Controlled Conditions. Frontiers in Plant Science, 2021, 12, 652116.	1.7	13
4	Fully-automated root image analysis (faRIA). Scientific Reports, 2021, 11, 16047.	1.6	15
5	Semi-Automated Ground Truth Segmentation and Phenotyping of Plant Structures Using k-Means Clustering of Eigen-Colors (kmSeg). Agriculture (Switzerland), 2021, 11, 1098.	1.4	4
6	Biomarkers for grain yield stability in rice under drought stress. Journal of Experimental Botany, 2020, 71, 669-683.	2.4	71
7	Strong temporal dynamics of QTL action on plant growth progression revealed through high-throughput phenotyping in canola. Plant Biotechnology Journal, 2020, 18, 68-82.	4.1	45
8	Age-dependent loss of seed viability is associated with increased lipid oxidation and hydrolysis. Plant, Cell and Environment, 2020, 43, 303-314.	2.8	49
9	A two-step registration-classification approach to automated segmentation of multimodal images for high-throughput greenhouse plant phenotyping. Plant Methods, 2020, 16, 95.	1.9	6
10	Image Phenotyping of Spring Barley ( <i>Hordeum vulgare</i> L.) RIL Population Under Drought: Selection of Traits and Biological Interpretation. Frontiers in Plant Science, 2020, 11, 743.	1.7	8
11	Epigenetic Variation at a Genomic Locus Affecting Biomass Accumulation under Low Nitrogen in <i>Arabidopsis thaliana</i> . Agronomy, 2020, 10, 636.	1.3	8
12	Image-Derived Traits Related to Mid-Season Growth Performance of Maize Under Nitrogen and Water Stress. Frontiers in Plant Science, 2019, 10, 814.	1.7	18
13	Comparison of feature point detectors for multimodal image registration in plant phenotyping. PLoS ONE, 2019, 14, e0221203.	1.1	3
14	Combining next-generation sequencing and progeny testing for rapid identification of induced recessive and dominant mutations in maize M2 individuals. Plant Journal, 2019, 100, 851-862.	2.8	7
15	Natural variation of BSK3 tunes brassinosteroid signaling to regulate root foraging under low nitrogen. Nature Communications, 2019, 10, 2378.	5.8	116
16	Comparison and extension of three methods for automated registration of multimodal plant images. Plant Methods, 2019, 15, 44.	1.9	8
17	Genetic diversity for nitrogen use efficiency in <i>Arabidopsis thaliana</i> . Planta, 2019, 250, 41-57.	1.6	24
18	Semi-automated Root Image Analysis (saRIA). Scientific Reports, 2019, 9, 19674.	1.6	33

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19	Phenotyping roots in darkness: disturbance-free root imaging with near infrared illumination. <i>Functional Plant Biology</i> , 2018, 45, 400.	1.1	17
20	Automated Alignment of Multi-Modal Plant Images Using Integrative Phase Correlation Approach. <i>Frontiers in Plant Science</i> , 2018, 9, 1519.	1.7	7
21	Identification of Rapeseed ( <i>Brassica napus</i> ) Cultivars With a High Tolerance to Boron-Deficient Conditions. <i>Frontiers in Plant Science</i> , 2018, 9, 1142.	1.7	31
22	Exploring traditional aus-type rice for metabolites conferring drought tolerance. <i>Rice</i> , 2018, 11, 9.	1.7	42
23	Structure Annotation and Quantification of Wheat Seed Oxidized Lipids by High-Resolution LC-MS/MS. <i>Plant Physiology</i> , 2017, 175, 600-618.	2.3	25
24	Genetic variation of growth dynamics in maize ( <i>Zea mays</i> L.) revealed through automated non-invasive phenotyping. <i>Plant Journal</i> , 2017, 89, 366-380.	2.8	85
25	Establishment of integrated protocols for automated high throughput kinetic chlorophyll fluorescence analyses. <i>Plant Methods</i> , 2017, 13, 54.	1.9	66
26	Genetic dissection of metabolite variation in <i>Arabidopsis</i> seeds: evidence for mQTL hotspots and a master regulatory locus of seed metabolism. <i>Journal of Experimental Botany</i> , 2017, 68, 1655-1667.	2.4	36
27	QTL analysis of the developmental response to L-glutamate in <i>Arabidopsis</i> roots and its genotype-by-environment interactions. <i>Journal of Experimental Botany</i> , 2017, 68, 2919-2931.	2.4	4
28	Measures for interoperability of phenotypic data: minimum information requirements and formatting. <i>Plant Methods</i> , 2016, 12, 44.	1.9	109
29	Phenomic prediction of maize hybrids. <i>BioSystems</i> , 2016, 146, 102-109.	0.9	11
30	Association mapping for cold tolerance in two large maize inbred panels. <i>BMC Plant Biology</i> , 2016, 16, 127.	1.6	73
31	A naturally occurring promoter polymorphism of the <i>Arabidopsis</i> <i>FUM2</i> gene causes expression variation, and is associated with metabolic and growth traits. <i>Plant Journal</i> , 2016, 88, 826-838.	2.8	35
32	Quantitative monitoring of <i>Arabidopsis thaliana</i> growth and development using high-throughput plant phenotyping. <i>Scientific Data</i> , 2016, 3, 160055.	2.4	30
33	Non-canonical structure, function and phylogeny of the B sister MADS box gene OsMADS30 of rice ( <i>Oryza sativa</i> ). <i>Plant Journal</i> , 2016, 88, 1023-1034.	2.8	16
34	Targeted Sequencing Reveals Large-Scale Sequence Polymorphism in Maize Candidate Genes for Biomass Production and Composition. <i>PLoS ONE</i> , 2015, 10, e0132120.	1.1	28
35	Overexpression of <i>Arabidopsis thaliana</i> ERI, the homolog of <i>C. elegans</i> Enhancer of RNA interference, leads to enhanced growth. <i>Frontiers in Plant Science</i> , 2015, 6, 531.	1.7	5
36	Century-scale Methylome Stability in a Recently Diverged <i>Arabidopsis thaliana</i> Lineage. <i>PLoS Genetics</i> , 2015, 11, e1004920.	1.5	148

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37	Towards a Graph-Theoretic Approach to Hybrid Performance Prediction from Large-Scale Phenotypic Data. Lecture Notes in Computer Science, 2015, , 173-184.	1.0	0
38	Dissecting the Phenotypic Components of Crop Plant Growth and Drought Responses Based on High-Throughput Image Analysis Å. Plant Cell, 2015, 26, 4636-4655.	3.1	329
39	AtRD22 and AtUSPL1, Members of the Plant-Specific BURP Domain Family Involved in Arabidopsis thaliana Drought Tolerance. PLoS ONE, 2014, 9, e110065.	1.1	74
40	Cold Tolerance in Two Large Maize Inbred Panels Adapted to European Climates. Crop Science, 2014, 54, 1981-1991.	0.8	30
41	Bridging Genomics and Phenomics. , 2014, , 299-333.		16
42	Transcription Factor Sensor System for Parallel Quantification of Metabolites On-Chip. Analytical Chemistry, 2014, 86, 12152-12158.	3.2	4
43	Recovering Power in Association Mapping Panels with Variable Levels of Linkage Disequilibrium. Genetics, 2014, 197, 375-387.	1.2	89
44	Optimizing experimental procedures for quantitative evaluation of crop plant performance in high throughput phenotyping systems. Frontiers in Plant Science, 2014, 5, 770.	1.7	187
45	Intraspecific variation of recombination rate in maize. Genome Biology, 2013, 14, R103.	13.9	176
46	PIN2 Turnover in Arabidopsis Root Epidermal Cells Explored by the Photoconvertible Protein Dendra2. PLoS ONE, 2013, 8, e61403.	1.1	37
47	Genome-wide association mapping of leaf metabolic profiles for dissecting complex traits in maize. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8872-8877.	3.3	340
48	Hybrid Incompatibility in Arabidopsis Is Determined by a Multiple-Locus Genetic Network Å Å. Plant Physiology, 2012, 158, 801-812.	2.3	42
49	Genomic and metabolic prediction of complex heterotic traits in hybrid maize. Nature Genetics, 2012, 44, 217-220.	9.4	532
50	Natural Variation in Biogenesis Efficiency of Individual Arabidopsis thaliana MicroRNAs. Current Biology, 2012, 22, 166-170.	1.8	42
51	Heterosis manifestation during early Arabidopsis seedling development is characterized by intermediate gene expression and enhanced metabolic activity in the hybrids. Plant Journal, 2012, 71, 669-683.	2.8	117
52	A tyrosine aminotransferase involved in tocopherol synthesis in Arabidopsis. Plant Journal, 2012, 71, 850-859.	2.8	82
53	Integration of a Systems Biological Network Analysis and QTL Results for Biomass Heterosis in Arabidopsis thaliana. PLoS ONE, 2012, 7, e49951.	1.1	6
54	Use of TILLING and robotised enzyme assays to generate an allelic series of Arabidopsis thaliana mutants with altered ADP-glucose pyrophosphorylase activity. Journal of Plant Physiology, 2011, 168, 1395-1405.	1.6	23

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55	Identification of enzymatic and regulatory genes of plant metabolism through QTL analysis in <i>Arabidopsis</i> . <i>Journal of Plant Physiology</i> , 2011, 168, 1387-1394.	1.6	37
56	Dynamic <sup>13</sup> C/ <sup>1</sup> H NMR imaging uncovers sugar allocation in the living seed. <i>Plant Biotechnology Journal</i> , 2011, 9, 1022-1037.	4.1	69
57	A RESTORER OF FERTILITY-like PPR gene is required for 5' end processing of the <i>nad4</i> mRNA in mitochondria of <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2011, 65, 737-744.	2.8	68
58	Subtissue-Specific Evaluation of Promoter Efficiency by Quantitative Fluorometric Assay in Laser Microdissected Tissues of Rapeseed. <i>Plant Physiology</i> , 2011, 157, 563-573.	2.3	9
59	QTL analysis of early stage heterosis for biomass in <i>Arabidopsis</i> . <i>Theoretical and Applied Genetics</i> , 2010, 120, 227-237.	1.8	90
60	Prediction of hybrid biomass in <i>Arabidopsis thaliana</i> by selected parental SNP and metabolic markers. <i>Theoretical and Applied Genetics</i> , 2010, 120, 239-247.	1.8	46
61	Enriched partial correlations in genome-wide gene expression profiles of hybrids ( <i>A. thaliana</i> ): a systems biological approach towards the molecular basis of heterosis. <i>Theoretical and Applied Genetics</i> , 2010, 120, 249-259.	1.8	26
62	Single feature polymorphism (SFP)-based selective sweep identification and association mapping of growth-related metabolic traits in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2010, 11, 188.	1.2	11
63	Constitutive salicylic acid defences do not compromise seed yield, drought tolerance and water productivity in the <i>Arabidopsis</i> accession C24. <i>Plant, Cell and Environment</i> , 2010, 33, 1959-1973.	2.8	67
64	Network Analysis of Enzyme Activities and Metabolite Levels and Their Relationship to Biomass in a Large Panel of <i>Arabidopsis</i> Accessions. <i>Plant Cell</i> , 2010, 22, 2872-2893.	3.1	131
65	Starch as a major integrator in the regulation of plant growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 10348-10353.	3.3	467
66	Towards Systems Biology of Heterosis: A Hypothesis about Molecular Network Structure Applied for the <i>Arabidopsis</i> Metabolome. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2009, 2009, 1-12.	1.4	9
67	The Metabolic Role of the Legume Endosperm: A Noninvasive Imaging Study. <i>Plant Physiology</i> , 2009, 151, 1139-1154.	2.3	56
68	Unraveling Epistasis With Triple Testcross Progenies of Near-Isogenic Lines. <i>Genetics</i> , 2009, 181, 247-257.	1.2	28
69	SNP identification in crop plants. <i>Current Opinion in Plant Biology</i> , 2009, 12, 211-217.	3.5	379
70	Identification of heterotic metabolite QTL in <i>Arabidopsis thaliana</i> RIL and IL populations. <i>Plant Journal</i> , 2009, 59, 777-788.	2.8	95
71	Analysis of <i>Arabidopsis</i> natural variation in biomass accumulation and metabolism. <i>New Biotechnology</i> , 2009, 25, S307.	2.4	2
72	Improved Heterosis Prediction by Combining Information on DNA- and Metabolic Markers. <i>PLoS ONE</i> , 2009, 4, e5220.	1.1	57

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73	Identification of metabolic and biomass QTL in <i>Arabidopsis thaliana</i> in a parallel analysis of RIL and IL populations. <i>Plant Journal</i> , 2008, 53, 960-972.	2.8	211
74	A subtilisin-like serine protease essential for mucilage release from <i>Arabidopsis</i> seed coats. <i>Plant Journal</i> , 2008, 54, 466-480.	2.8	159
75	Construction and Analysis of 2 Reciprocal <i>Arabidopsis</i> Introgression Line Populations. <i>Journal of Heredity</i> , 2008, 99, 396-406.	1.0	40
76	The metabolic signature related to high plant growth rate in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 4759-4764.	3.3	377
77	Analysis of a Triple Testcross Design With Recombinant Inbred Lines Reveals a Significant Role of Epistasis in Heterosis for Biomass-Related Traits in <i>Arabidopsis</i> . <i>Genetics</i> , 2007, 175, 2009-2017.	1.2	65
78	Genetic Basis of Heterosis for Growth-Related Traits in <i>Arabidopsis</i> Investigated by Testcross Progenies of Near-Isogenic Lines Reveals a Significant Role of Epistasis. <i>Genetics</i> , 2007, 177, 1827-1837.	1.2	95
79	Heterosis for Biomass-Related Traits in <i>Arabidopsis</i> Investigated by Quantitative Trait Loci Analysis of the Triple Testcross Design With Recombinant Inbred Lines. <i>Genetics</i> , 2007, 177, 1839-1850.	1.2	55
80	Description and applications of a rapid and sensitive non-radioactive microplate-based assay for maximum and initial activity of D-ribulose-1,5-bisphosphate carboxylase/oxygenase. <i>Plant, Cell and Environment</i> , 2007, 30, 1163-1175.	2.8	82
81	The AtNFXL1 gene encodes a NF-X1 type zinc finger protein required for growth under salt stress. <i>FEBS Letters</i> , 2006, 580, 4851-4856.	1.3	53
82	Stomatal aperture can compensate altered stomatal density in <i>Arabidopsis thaliana</i> at growth light conditions. <i>Functional Plant Biology</i> , 2006, 33, 1037.	1.1	82
83	Metabolic changes in fruits of the tomato dx mutant. <i>Phytochemistry</i> , 2006, 67, 2232-2238.	1.4	68
84	Evidence for a large-scale population structure of <i>Arabidopsis thaliana</i> from genome-wide single nucleotide polymorphism markers. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1104-1114.	1.8	109
85	Segregation distortion in <i>Arabidopsis</i> C24/Col-0 and Col-0/C24 recombinant inbred line populations is due to reduced fertility caused by epistatic interaction of two loci. <i>Theoretical and Applied Genetics</i> , 2006, 113, 1551-1561.	1.8	71
86	Variation of Enzyme Activities and Metabolite Levels in 24 <i>Arabidopsis</i> Accessions Growing in Carbon-Limited Conditions. <i>Plant Physiology</i> , 2006, 142, 1574-1588.	2.3	270
87	Inferring Hypotheses on Functional Relationships of Genes: Analysis of the <i>Arabidopsis thaliana</i> Subtilase Gene Family. <i>PLoS Computational Biology</i> , 2005, 1, e40.	1.5	157
88	Identification of brassinosteroid-related genes by means of transcript co-response analyses. <i>Nucleic Acids Research</i> , 2005, 33, 2685-2696.	6.5	64
89	Genome-Wide Identification and Testing of Superior Reference Genes for Transcript Normalization in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2005, 139, 5-17.	2.3	2,835
90	Heterosis of Biomass Production in <i>Arabidopsis</i> . Establishment during Early Development. <i>Plant Physiology</i> , 2004, 134, 1813-1823.	2.3	159

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91	Versatile Gene-Specific Sequence Tags for Arabidopsis Functional Genomics: Transcript Profiling and Reverse Genetics Applications. <i>Genome Research</i> , 2004, 14, 2176-2189.	2.4	282
92	EXORDIUM regulates brassinosteroid-responsive genes. <i>FEBS Letters</i> , 2004, 563, 82-86.	1.3	73
93	Changes in gene expression in response to altered SHL transcript levels. <i>Plant Molecular Biology</i> , 2003, 53, 805-820.	2.0	10
94	Genomic Brassinosteroid Effects. <i>Journal of Plant Growth Regulation</i> , 2003, 22, 313-324.	2.8	30
95	Photosynthetic performance of an Arabidopsis mutant with elevated stomatal density (sdd1-1) under different light regimes. <i>Journal of Experimental Botany</i> , 2003, 54, 867-874.	2.4	140
96	Brassinosteroids Promote Root Growth in Arabidopsis. <i>Plant Physiology</i> , 2003, 133, 1261-1271.	2.3	265
97	Large-Scale Identification and Analysis of Genome-Wide Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana. <i>Genome Research</i> , 2003, 13, 1250-1257.	2.4	184
98	Brassinosteroid-Regulated Gene Expression. <i>Plant Physiology</i> , 2002, 129, 1241-1251.	2.3	246
99	Evidence for a Ustilago maydis Steroid 5 $\alpha$ -Reductase by Functional Expression in Arabidopsis det2-1 Mutants. <i>Plant Physiology</i> , 2002, 129, 717-732.	2.3	9
100	Application of metabolomics to plant genotype discrimination using statistics and machine learning. <i>Bioinformatics</i> , 2002, 18, S241-S248.	1.8	229
101	Using array hybridization to monitor gene expression at the single cell level. <i>Journal of Experimental Botany</i> , 2002, 53, 2315-2323.	2.4	73
102	The Subtilisin-Like Serine Protease SDD1 Mediates Cell-to-Cell Signaling during Arabidopsis Stomatal Development. <i>Plant Cell</i> , 2002, 14, 1527-1539.	3.1	271
103	Novel Aspects of Symbiotic Nitrogen Fixation Uncovered by Transcript Profiling with cDNA Arrays. <i>Molecular Plant-Microbe Interactions</i> , 2002, 15, 411-420.	1.4	129
104	Wie mit Microarrays die AktivitÄt vieler Gene erfasst wird: Methodik der funktionellen Genomanalyse. <i>Biologie in Unserer Zeit</i> , 2002, 32, 20-29.	0.3	0
105	Integrated studies on plant biology using multiparallel techniques. <i>Current Opinion in Biotechnology</i> , 2001, 12, 82-86.	3.3	112
106	Phosphate acquisition heterosis in Arabidopsis thaliana: a morphological and physiological analysis. <i>Plant and Soil</i> , 2001, 234, 91-97.	1.8	30
107	Stomatal cell biology. <i>Current Opinion in Plant Biology</i> , 2001, 4, 555-560.	3.5	34
108	Response of Arabidopsis to Iron Deficiency Stress as Revealed by Microarray Analysis. <i>Plant Physiology</i> , 2001, 127, 1030-1043.	2.3	226

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109	Metabolite profiling for plant functional genomics. <i>Nature Biotechnology</i> , 2000, 18, 1157-1161.	9.4	1,936
110	12-Oxophytodienoate reductase 3 (OPR3) is the isoenzyme involved in jasmonate biosynthesis. <i>Planta</i> , 2000, 210, 979-984.	1.6	357
111	Analysis of Phosphate Acquisition Efficiency in Different Arabidopsis Accessions. <i>Plant Physiology</i> , 2000, 124, 1786-1799.	2.3	148
112	A novel stress-inducible 12-oxophytodienoate reductase from Arabidopsis thaliana provides a potential link between Brassinosteroid-action and Jasmonic-acid synthesis. <i>Journal of Plant Physiology</i> , 2000, 157, 143-152.	1.6	110
113	A subtilisin-like serine protease involved in the regulation of stomatal density and distribution in Arabidopsis thaliana. <i>Genes and Development</i> , 2000, 14, 1119-1131.	2.7	374
114	Physiology and molecular mode of action of brassinosteroids. <i>Plant Physiology and Biochemistry</i> , 1999, 37, 363-372.	2.8	49
115	A complete BAC-based physical map of the Arabidopsis thaliana genome. <i>Nature Genetics</i> , 1999, 22, 271-275.	9.4	155
116	Molecular physiology of brassinosteroids revealed by the analysis of mutants. <i>Planta</i> , 1999, 208, 1-11.	1.6	121
117	A tale of dwarfs and drugs: brassinosteroids to the rescue. <i>Trends in Genetics</i> , 1998, 14, 490-495.	2.9	27
118	Recent advances in brassinosteroid molecular genetics. <i>Current Opinion in Plant Biology</i> , 1998, 1, 378-383.	3.5	57
119	Use of the IGF BAC library for physical mapping of the Arabidopsis thaliana genome. <i>Plant Journal</i> , 1998, 16, 377-384.	2.8	42
120	Inactivation of a Glycyl-tRNA Synthetase Leads to an Arrest in Plant Embryo Development. <i>Plant Cell</i> , 1998, 10, 1277-1294.	3.1	112
121	Brassinosteroids from seeds of Arabidopsis thaliana. <i>Phytochemistry</i> , 1997, 45, 1325-1327.	1.4	45
122	Brassinosteroids Rescue the Deficiency of CYP90, a Cytochrome P450, Controlling Cell Elongation and De-etiolation in Arabidopsis. <i>Cell</i> , 1996, 85, 171-182.	13.5	963
123	Genetic evidence for an essential role of brassinosteroids in plant development. <i>Plant Journal</i> , 1996, 9, 701-713.	2.8	338
124	Characterization of waldmeister, a novel developmental mutant in Arabidopsis thaliana. <i>Journal of Experimental Botany</i> , 1996, 47, 1007-1017.	2.4	16
125	Ac/Ds transposon mutagenesis in Arabidopsis thaliana: mutant spectrum and frequency of Ds insertion mutants. <i>Molecular Genetics and Genomics</i> , 1995, 247, 646-652.	2.4	41
126	Easy determination of ploidy level in Arabidopsis thaliana plants by means of pollen size measurement. <i>Plant Cell Reports</i> , 1994, 13, 652-6.	2.8	46



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127	Non-destructive assay systems for detection of $\beta$ -glucuronidase activity in higher plants. Plant Molecular Biology Reporter, 1992, 10, 37-46.	1.0	29
128	Deep Learning Based Greenhouse Image Segmentation and Shoot Phenotyping (DeepShoot). Frontiers in Plant Science, 0, 13, .	1.7	5