

# Joost J B Keurentjes

## List of Publications by Year in descending order

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Version: 2024-02-01

80  
papers

8,462  
citations

57631

44  
h-index

62479

80  
g-index

89  
all docs

89  
docs citations

89  
times ranked

11408  
citing authors

#	ARTICLE	IF	CITATIONS
1	Untargeted large-scale plant metabolomics using liquid chromatography coupled to mass spectrometry. <i>Nature Protocols</i> , 2007, 2, 778-791.	5.5	803
2	Sucrose-Specific Induction of Anthocyanin Biosynthesis in Arabidopsis Requires the MYB75/PAP1 Gene. <i>Plant Physiology</i> , 2005, 139, 1840-1852.	2.3	593
3	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
4	The genetics of plant metabolism. <i>Nature Genetics</i> , 2006, 38, 842-849.	9.4	454
5	What Has Natural Variation Taught Us about Plant Development, Physiology, and Adaptation?. <i>Plant Cell</i> , 2009, 21, 1877-1896.	3.1	401
6	Regulatory network construction in Arabidopsis by using genome-wide gene expression quantitative trait loci. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1708-1713.	3.3	329
7	System-wide molecular evidence for phenotypic buffering in Arabidopsis. <i>Nature Genetics</i> , 2009, 41, 166-167.	9.4	249
8	Development of a Near-Isogenic Line Population of Arabidopsis thaliana and Comparison of Mapping Power With a Recombinant Inbred Line Population. <i>Genetics</i> , 2007, 175, 891-905.	1.2	214
9	The genomic landscape of meiotic crossovers and gene conversions in Arabidopsis thaliana. <i>ELife</i> , 2013, 2, e01426.	2.8	197
10	A cheminformatics approach to characterize metabolomes in stable-isotope-labeled organisms. <i>Nature Methods</i> , 2019, 16, 295-298.	9.0	194
11	Marker-Based Estimation of Heritability in Immortal Populations. <i>Genetics</i> , 2015, 199, 379-398.	1.2	192
12	Rhizobacteria-mediated Induced Systemic Resistance: Triggering, Signalling and Expression. <i>European Journal of Plant Pathology</i> , 2001, 107, 51-61.	0.8	181
13	Epigenetic Basis of Morphological Variation and Phenotypic Plasticity in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2015, 27, 337-348.	3.1	178
14	Control of Fusarium Wilt of Radish by Combining Pseudomonas putida Strains that have Different Disease-Suppressive Mechanisms. <i>Phytopathology</i> , 2003, 93, 626-632.	1.1	172
15	Vacuolar invertase regulates elongation of Arabidopsis thaliana roots as revealed by QTL and mutant analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2994-2999.	3.3	171
16	Improved batch correction in untargeted MS-based metabolomics. <i>Metabolomics</i> , 2016, 12, 88.	1.4	167
17	Identification and characterization of QTL underlying whole-plant physiology in Arabidopsis thaliana: delta13C, stomatal conductance and transpiration efficiency. <i>Plant, Cell and Environment</i> , 2005, 28, 697-708.	2.8	162
18	Genetic Components of Root Architecture Remodeling in Response to Salt Stress. <i>Plant Cell</i> , 2017, 29, 3198-3213.	3.1	156

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19	Metabolic Networks: How to Identify Key Components in the Regulation of Metabolism and Growth. <i>Plant Physiology</i> , 2010, 152, 428-444.	2.3	155
20	Genetic architecture of plant stress resistance: multi-trait genome-wide association mapping. <i>New Phytologist</i> , 2017, 213, 1346-1362.	3.5	144
21	Genetical metabolomics: closing in on phenotypes. <i>Current Opinion in Plant Biology</i> , 2009, 12, 223-230.	3.5	136
22	Metabolomics: the chemistry between ecology and genetics. <i>Molecular Ecology Resources</i> , 2010, 10, 583-593.	2.2	136
23	Accelerating Climate Resilient Plant Breeding by Applying Next-Generation Artificial Intelligence. <i>Trends in Biotechnology</i> , 2019, 37, 1217-1235.	4.9	134
24	Untargeted Metabolic Quantitative Trait Loci Analyses Reveal a Relationship between Primary Metabolism and Potato Tuber Quality. <i>Plant Physiology</i> , 2012, 158, 1306-1318.	2.3	119
25	Mapping the Arabidopsis Metabolic Landscape by Untargeted Metabolomics at Different Environmental Conditions. <i>Molecular Plant</i> , 2018, 11, 118-134.	3.9	116
26	Genetic analysis of metabolome-phenotype interactions: from model to crop species. <i>Trends in Genetics</i> , 2013, 29, 41-50.	2.9	111
27	Reverse breeding in <i>Arabidopsis thaliana</i> generates homozygous parental lines from a heterozygous plant. <i>Nature Genetics</i> , 2012, 44, 467-470.	9.4	97
28	Parental DNA Methylation States Are Associated with Heterosis in Epigenetic Hybrids. <i>Plant Physiology</i> , 2018, 176, 1627-1645.	2.3	93
29	Integrative analyses of genetic variation in enzyme activities of primary carbohydrate metabolism reveal distinct modes of regulation in <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2008, 9, R129.	13.9	90
30	Genome-Wide Association Mapping of Fertility Reduction upon Heat Stress Reveals Developmental Stage-Specific QTLs in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2015, 27, 1857-1874.	3.1	82
31	Genome-wide association mapping of growth dynamics detects time-specific and general quantitative trait loci. <i>Journal of Experimental Botany</i> , 2015, 66, 5567-5580.	2.4	80
32	<i>Arabidopsis</i> semidwarfs evolved from independent mutations in <i>GA20ox1</i> , ortholog to green revolution dwarf alleles in rice and barley. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15818-15823.	3.3	79
33	Genome-Wide Association Mapping and Genomic Prediction Elucidate the Genetic Architecture of Morphological Traits in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2016, 170, 2187-2203.	2.3	77
34	Grass root decomposition is retarded when grass has been grown under elevated CO <sub>2</sub> . <i>Soil Biology and Biochemistry</i> , 1995, 27, 117-120.	4.2	76
35	Converging phenomics and genomics to study natural variation in plant photosynthetic efficiency. <i>Plant Journal</i> , 2019, 97, 112-133.	2.8	75
36	Redefining plant systems biology: from cell to ecosystem. <i>Trends in Plant Science</i> , 2011, 16, 183-190.	4.3	70

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37	Quantitative genetics in the age of omics. <i>Current Opinion in Plant Biology</i> , 2008, 11, 123-128.	3.5	69
38	Combined Use of Genome-Wide Association Data and Correlation Networks Unravels Key Regulators of Primary Metabolism in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2016, 12, e1006363.	1.5	67
39	Genome-wide association mapping of time-dependent growth responses to moderate drought stress in <i>Arabidopsis</i> . <i>Plant, Cell and Environment</i> , 2016, 39, 88-102.	2.8	67
40	Colonization of the <i>Arabidopsis</i> rhizosphere by fluorescent <i>Pseudomonas</i> spp. activates a root-specific, ethylene-responsive PR-5 gene in the vascular bundle. <i>Plant Molecular Biology</i> , 2005, 57, 731-748.	2.0	62
41	Identifying Genotype-by-Environment Interactions in the Metabolism of Germinating <i>Arabidopsis</i> Seeds Using Generalized Genetical Genomics. <i>Plant Physiology</i> , 2013, 162, 553-566.	2.3	61
42	Regulatory Network Identification by Genetical Genomics: Signaling Downstream of the <i>Arabidopsis</i> Receptor-Like Kinase ERECTA. <i>Plant Physiology</i> , 2010, 154, 1067-1078.	2.3	59
43	Multi-dimensional regulation of metabolic networks shaping plant development and performance. <i>Journal of Experimental Botany</i> , 2012, 63, 3353-3365.	2.4	58
44	Effects of Multi-Generational Stress Exposure and Offspring Environment on the Expression and Persistence of Transgenerational Effects in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2016, 11, e0151566.	1.1	53
45	Advances in Genetical Genomics of Plants. <i>Current Genomics</i> , 2009, 10, 540-549.	0.7	49
46	Development and characterization of microsatellite markers in the sexual-apomictic complex <i>Taraxacum officinale</i> (dandelion). <i>Theoretical and Applied Genetics</i> , 1998, 97, 283-292.	1.8	46
47	Reciprocal cybrids reveal how organellar genomes affect plant phenotypes. <i>Nature Plants</i> , 2020, 6, 13-21.	4.7	40
48	Hybrid recreation by reverse breeding in <i>Arabidopsis thaliana</i> . <i>Nature Protocols</i> , 2014, 9, 761-772.	5.5	37
49	De novo assembly, functional annotation, and analysis of the giant reed ( <i>Arundo donax</i> L.) leaf transcriptome provide tools for the development of a biofuel feedstock. <i>Biotechnology for Biofuels</i> , 2017, 10, 138.	6.2	37
50	Biomass traits and candidate genes for bioenergy revealed through association genetics in coppiced European <i>Populus nigra</i> (L.). <i>Biotechnology for Biofuels</i> , 2016, 9, 195.	6.2	36
51	Genes and gene clusters related to genotype and drought-induced variation in saccharification potential, lignin content and wood anatomical traits in <i>Populus nigra</i> . <i>Tree Physiology</i> , 2018, 38, 320-339.	1.4	35
52	Genome-Wide Association Mapping Reveals That Specific and Pleiotropic Regulatory Mechanisms Fine-Tune Central Metabolism and Growth in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2017, 29, 2349-2373.	3.1	32
53	The Role of Transcriptional Regulation in Hybrid Vigor. <i>Frontiers in Plant Science</i> , 2020, 11, 410.	1.7	31
54	MetaNetwork: a computational protocol for the genetic study of metabolic networks. <i>Nature Protocols</i> , 2007, 2, 685-694.	5.5	30

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55	The genetic framework of shoot regeneration in <i>Arabidopsis</i> comprises master regulators and conditional fine-tuning factors. <i>Communications Biology</i> , 2020, 3, 549.	2.0	30
56	Histochemical Analysis Reveals Organ-Specific Quantitative Trait Loci for Enzyme Activities in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2004, 134, 237-245.	2.3	29
57	Genetic analysis of morphological traits in a new, versatile, rapid-cycling <i>Brassica rapa</i> recombinant inbred line population. <i>Frontiers in Plant Science</i> , 2012, 3, 183.	1.7	28
58	Epigenetic mapping of the <i>Arabidopsis</i> metabolome reveals mediators of the epigenotype-phenotype map. <i>Genome Research</i> , 2019, 29, 96-106.	2.4	28
59	Genetic resources for quantitative trait analysis: novelty and efficiency in design from an <i>Arabidopsis</i> perspective. <i>Current Opinion in Plant Biology</i> , 2014, 18, 103-109.	3.5	27
60	GWA Mapping of Anthocyanin Accumulation Reveals Balancing Selection of MYB90 in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2015, 10, e0143212.	1.1	26
61	AraQTL workbench and archive for systems genetics in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2017, 89, 1225-1235.	2.8	24
62	Natural variation in life history strategy of <i>Arabidopsis thaliana</i> determines stress responses to drought and insects of different feeding guilds. <i>Molecular Ecology</i> , 2017, 26, 2959-2977.	2.0	23
63	Intervessel pit membrane thickness best explains variation in embolism resistance amongst stems of <i>Arabidopsis thaliana</i> accessions. <i>Annals of Botany</i> , 2021, 128, 171-182.	1.4	23
64	Characterization of phenology, physiology, morphology and biomass traits across a broad Euro-Mediterranean ecotypic panel of the lignocellulosic feedstock <i>Arundo donax</i> . <i>GCB Bioenergy</i> , 2019, 11, 152-170.	2.5	21
65	Allelic differences in a vacuolar invertase affect <i>Arabidopsis</i> growth at early plant development. <i>Journal of Experimental Botany</i> , 2016, 67, 4091-4103.	2.4	20
66	Identification of Quantitative Trait Loci Controlling Symptom Development During Viral Infection in <i>Arabidopsis thaliana</i> . <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 198-207.	1.4	19
67	A comparison of population types used for QTL mapping in <i>Arabidopsis thaliana</i> . <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011, 9, 185-188.	0.4	17
68	Backcross Populations and Near Isogenic Lines. <i>Methods in Molecular Biology</i> , 2012, 871, 3-16.	0.4	17
69	Predictive modelling of complex agronomic and biological systems. <i>Plant, Cell and Environment</i> , 2013, 36, 1700-1710.	2.8	14
70	Identification of seed-related QTL in <i>Brassica rapa</i> . <i>Spanish Journal of Agricultural Research</i> , 2013, 11, 1085.	0.3	13
71	Epigenetic variation contributes to environmental adaptation of <i>Arabidopsis thaliana</i> . <i>Plant Signaling and Behavior</i> , 2015, 10, e1057368.	1.2	12
72	Novel Genes Affecting the Interaction between the Cabbage Whitefly and <i>Arabidopsis</i> Uncovered by Genome-Wide Association Mapping. <i>PLoS ONE</i> , 2015, 10, e0145124.	1.1	9

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73	Assessment of heterosis in two <i>Arabidopsis thaliana</i> common-reference mapping populations. <i>PLoS ONE</i> , 2018, 13, e0205564.	1.1	8
74	The role of natural variation in dissecting genetic regulation of primary metabolism. <i>Plant Signaling and Behavior</i> , 2009, 4, 244-246.	1.2	7
75	A genetical metabolomics approach for bioprospecting plant biosynthetic gene clusters. <i>BMC Research Notes</i> , 2019, 12, 194.	0.6	7
76	Meiotic crossover reduction by virus-induced gene silencing enables the efficient generation of chromosome substitution lines and reverse breeding in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2020, 104, 1437-1452.	2.8	6
77	Cross-platform comparative analyses of genetic variation in amino acid content in potato tubers. <i>Metabolomics</i> , 2014, 10, 1239-1257.	1.4	3
78	Exploiting Natural Variation in <i>Arabidopsis</i> . <i>Methods in Molecular Biology</i> , 2014, 1062, 139-153.	0.4	3
79	QTLepi Mapping in <i>Arabidopsis thaliana</i> . <i>Methods in Molecular Biology</i> , 2018, 1675, 373-394.	0.4	2
80	Genotypic and tissue-specific variation of <i>Populus nigra</i> transcriptome profiles in response to drought. <i>Scientific Data</i> , 2022, 9, .	2.4	0