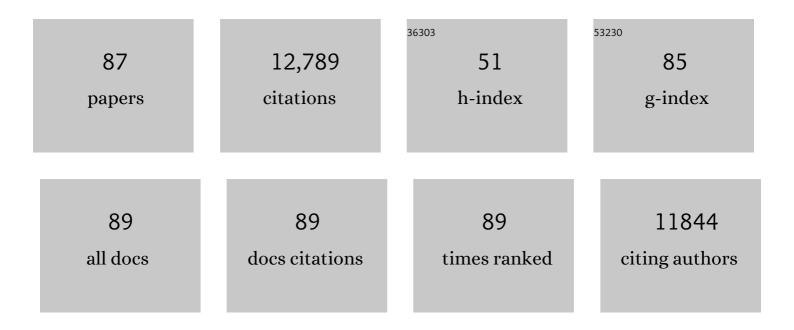
Carlos Alonso-Blanco

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	1,135 Genomes Reveal the Global Pattern of Polymorphism in Arabidopsis thaliana. Cell, 2016, 166, 481-491.	28.9	1,107
2	Whole-genome sequencing of multiple Arabidopsis thaliana populations. Nature Genetics, 2011, 43, 956-963.	21.4	910
3	NATURALLY OCCURRING GENETIC VARIATION INARABIDOPSIS THALIANA. Annual Review of Plant Biology, 2004, 55, 141-172.	18.7	610
4	Epigenomic Diversity in a Global Collection of Arabidopsis thaliana Accessions. Cell, 2016, 166, 492-505.	28.9	594
5	The Late Flowering Phenotype of fwa Mutants Is Caused by Gain-of-Function Epigenetic Alleles of a Homeodomain Gene. Molecular Cell, 2000, 6, 791-802.	9.7	545
6	GENETIC CONTROL OF FLOWERING TIME IN ARABIDOPSIS. Annual Review of Plant Biology, 1998, 49, 345-370.	14.3	445
7	What Has Natural Variation Taught Us about Plant Development, Physiology, and Adaptation?. Plant Cell, 2009, 21, 1877-1896.	6.6	401
8	Naturally occurring variation in Arabidopsis: an underexploited resource for plant genetics. Trends in Plant Science, 2000, 5, 22-29.	8.8	398
9	A QTL for flowering time in Arabidopsis reveals a novel allele of CRY2. Nature Genetics, 2001, 29, 435-440.	21.4	387
10	Analysis of Natural Allelic Variation at Seed Dormancy Loci of <i>Arabidopsis thaliana</i> . Genetics, 2003, 164, 711-729.	2.9	359
11	Development of an AFLP based linkage map of Ler, Col and Cvi Arabidopsis thaliana ecotypes and construction of a Ler/Cvi recombinant inbred line population. Plant Journal, 1998, 14, 259-271.	5.7	355
12	Regulation of flowering time by FVE, a retinoblastoma-associated protein. Nature Genetics, 2004, 36, 162-166.	21.4	347
13	PEP1 regulates perennial flowering in Arabis alpina. Nature, 2009, 459, 423-427.	27.8	325
14	Cytogenetics for the model system <i>Arabidopsis thaliana</i> . Plant Journal, 1998, 13, 867-876.	5.7	304
15	ERECTA receptor-like kinase and heterotrimeric G protein from Arabidopsis are required for resistance to the necrotrophic fungus Plectosphaerella cucumerina. Plant Journal, 2005, 43, 165-180.	5.7	303
16	Site and plant species are important determinants of the <i>Methylobacterium</i> community composition in the plant phyllosphere. ISME Journal, 2010, 4, 719-728.	9.8	297
17	Natural allelic variation at seed size loci in relation to other life history traits of Arabidopsis thaliana. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 4710-4717.	7.1	257
18	Highâ€resolution physical mapping in <i>Arabidopsis thaliana</i> and tomato by fluorescence <i>in situ</i> hybridization to extended DNA fibres. Plant Journal, 1996, 9, 421-430.	5.7	229

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19	Analysis of Natural Allelic Variation at Flowering Time Loci in the Landsberg erecta and Cape Verde Islands Ecotypes of Arabidopsis thaliana. Genetics, 1998, 149, 749-764.	2.9	225
20	Development of a Near-Isogenic Line Population of Arabidopsis thaliana and Comparison of Mapping Power With a Recombinant Inbred Line Population. Genetics, 2007, 175, 891-905.	2.9	214
21	Genetic Analysis of Seed-Soluble Oligosaccharides in Relation to Seed Storability of Arabidopsis. Plant Physiology, 2000, 124, 1595-1604.	4.8	205
22	Natural variation for seed dormancy in Arabidopsis is regulated by additive genetic and molecular pathways. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 4264-4269.	7.1	194
23	Natural allelic variation identifies new genes in the Arabidopsis circadian system. Plant Journal, 1999, 20, 67-77.	5.7	171
24	Altitudinal and Climatic Adaptation Is Mediated by Flowering Traits and <i>FRI</i> , <i>FLC</i> , and <i>PHYC</i> Genes in Arabidopsis Â. Plant Physiology, 2011, 157, 1942-1955.	4.8	171
25	Root microbiota assembly and adaptive differentiation among European Arabidopsis populations. Nature Ecology and Evolution, 2020, 4, 122-131.	7.8	157
26	Genome expansion of Arabis alpina linked with retrotransposition and reduced symmetric DNA methylation. Nature Plants, 2015, 1, 14023.	9.3	156
27	Environmental regulation of flowering. International Journal of Developmental Biology, 2005, 49, 689-705.	0.6	149
28	Genetic and Molecular Analyses of Natural Variation Indicate CBF2 as a Candidate Gene for Underlying a Freezing Tolerance Quantitative Trait Locus in Arabidopsis. Plant Physiology, 2005, 139, 1304-1312.	4.8	149
29	African genomes illuminate the early history and transition to selfing in <i>Arabidopsis thaliana</i> . Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 5213-5218.	7.1	142
30	QTL analysis of seed dormancy in Arabidopsis using recombinant inbred lines and MQM mapping. Heredity, 1997, 79, 190-200.	2.6	139
31	Natural variation in arsenate tolerance identifies an arsenate reductase in Arabidopsis thaliana. Nature Communications, 2014, 5, 4617.	12.8	136
32	Natural Genetic Variation of <i>Arabidopsis thaliana</i> Is Geographically Structured in the Iberian Peninsula. Genetics, 2008, 180, 1009-1021.	2.9	116
33	Gene function beyond the single trait: natural variation, gene effects, and evolutionary ecology in Arabidopsis thaliana. Plant, Cell and Environment, 2005, 28, 2-20.	5.7	103
34	GENETIC BASIS OF ADAPTATION IN ARABIDOPSIS THALIANA: LOCAL ADAPTATION AT THE SEED DORMANCY QTL DOG1. Evolution; International Journal of Organic Evolution, 2012, 66, 2287-2302.	2.3	103
35	<i>Arabidopsis thaliana</i> as a model for the study of plant–virus co-evolution. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 1983-1995.	4.0	92
36	Altitudinal and climatic associations of seed dormancy and flowering traits evidence adaptation of annual life cycle timing in <i>Arabidopsis thaliana</i> . Plant, Cell and Environment, 2016, 39, 1737-1748.	5.7	90

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37	On the post-glacial spread of human commensal Arabidopsis thaliana. Nature Communications, 2017, 8, 14458.	12.8	83
38	<i>Arabidopsis</i> semidwarfs evolved from independent mutations in <i>GA20ox1</i> , ortholog to green revolution dwarf alleles in rice and barley. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 15818-15823.	7.1	79
39	From phenotypic to molecular polymorphisms involved in naturally occurring variation of plant development. International Journal of Developmental Biology, 2005, 49, 717-732.	0.6	78
40	Demographic and Genetic Patterns of Variation among Populations of Arabidopsis thaliana from Contrasting Native Environments. PLoS ONE, 2009, 4, e7213.	2.5	77
41	The Role of Cryptochrome 2 in Flowering in Arabidopsis. Plant Physiology, 2003, 133, 1504-1516.	4.8	71
42	The Relationship of Within-Host Multiplication and Virulence in a Plant-Virus System. PLoS ONE, 2007, 2, e786.	2.5	69
43	Host Responses in Life-History Traits and Tolerance to Virus Infection in Arabidopsis thaliana. PLoS Pathogens, 2008, 4, e1000124.	4.7	68
44	Genetic architecture of naturally occurring quantitative traits in plants: an updated synthesis. Current Opinion in Plant Biology, 2014, 18, 37-43.	7.1	68
45	Natural Arabidopsis brx Loss-of-Function Alleles Confer Root Adaptation to Acidic Soil. Current Biology, 2012, 22, 1962-1968.	3.9	66
46	Genetic approaches in plant physiology. New Phytologist, 1997, 137, 1-8.	7.3	65
47	Tackling intraspecific genetic structure in distribution models better reflects species geographical range. Ecology and Evolution, 2016, 6, 2084-2097.	1.9	59
48	Natural variation in stomatal abundance of Arabidopsis thaliana includes cryptic diversity for different developmental processes. Annals of Botany, 2011, 107, 1247-1258.	2.9	58
49	The Flowering Repressor SVP Underlies a Novel Arabidopsis thaliana QTL Interacting with the Genetic Background. PLoS Genetics, 2013, 9, e1003289.	3.5	58
50	A high-density collection of EMS-induced mutations for TILLING in Landsberg erecta genetic background of Arabidopsis. BMC Plant Biology, 2009, 9, 147.	3.6	57
51	Deciphering the Adjustment between Environment and Life History in Annuals: Lessons from a Geographically-Explicit Approach in Arabidopsis thaliana. PLoS ONE, 2014, 9, e87836.	2.5	57
52	Temporal analysis of natural variation for the rate of leaf production and its relationship with flowering initiation in Arabidopsis thaliana. Journal of Experimental Botany, 2010, 61, 1611-1623.	4.8	56
53	Among―and withinâ€population variation in flowering time of Iberian Arabidopsis thaliana estimated in field and glasshouse conditions. New Phytologist, 2013, 197, 1332-1343.	7.3	56
54	The genetic structure of Arabidopsis thaliana in the south-western Mediterranean range reveals a shared history between North Africa and southern Europe. BMC Plant Biology, 2014, 14, 17.	3.6	53

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55	<scp>FE</scp> , a phloemâ€specific Mybâ€related protein, promotes flowering through transcriptional activation of <i><scp>FLOWERING LOCUS</scp> T</i> and <i><scp>FLOWERING LOCUS</scp> T <scp>INTERACTING PROTEIN</scp> 1</i> . Plant Journal, 2015, 83, 1059-1068.	5.7	53
56	Genomeâ€wide signatures of flowering adaptation to climate temperature: Regional analyses in a highly diverse native range of <i>Arabidopsis thaliana</i> . Plant, Cell and Environment, 2018, 41, 1806-1820.	5.7	49
57	Temporal variation in genetic diversity and effective population size of Mediterranean and subalpine Arabidopsis thaliana populations. Molecular Ecology, 2011, 20, no-no.	3.9	47
58	The Cape Verde Islands Allele of Cryptochrome 2 Enhances Cotyledon Unfolding in the Absence of Blue Light in Arabidopsis Â. Plant Physiology, 2003, 133, 1547-1556.	4.8	46
59	Novel natural alleles at <i>FLC</i> and <i>LVR</i> loci account for enhanced vernalization responses in <i>Arabidopsis thaliana</i> . Plant, Cell and Environment, 2012, 35, 1672-1684.	5.7	45
60	Quantitative genetic analysis of flowering time in tomato. Genome, 2007, 50, 303-315.	2.0	36
61	Cucumber mosaic virus infection as a potential selective pressure on Arabidopsis thaliana populations. PLoS Pathogens, 2019, 15, e1007810.	4.7	35
62	Natural Variation Identifies ICARUS1, a Universal Gene Required for Cell Proliferation and Growth at High Temperatures in Arabidopsis thaliana. PLoS Genetics, 2015, 11, e1005085.	3.5	34
63	Spatio-temporal variation in fitness responses to contrasting environments in <i>Arabidopsis thaliana</i> . Evolution; International Journal of Organic Evolution, 2018, 72, 1570-1586.	2.3	34
64	Differential Tolerance to Direct and Indirect Density-Dependent Costs of Viral Infection in Arabidopsis thaliana. PLoS Pathogens, 2009, 5, e1000531.	4.7	33
65	QTL analysis of seed dormancy in Arabidopsis using recombinant inbred lines and MQM mapping. Heredity, 1997, 79, 190-200.	2.6	31
66	An oxygen-sensing mechanism for angiosperm adaptation to altitude. Nature, 2022, 606, 565-569.	27.8	31
67	Environmental and genetic interactions reveal <i>FLOWERING LOCUSC</i> as a modulator of the natural variation for the plasticity of flowering in Arabidopsis. Plant, Cell and Environment, 2016, 39, 282-294.	5.7	29
68	Pleiotropic Effects of the Arabidopsis Cryptochrome 2 Allelic Variation Underlie Fruit Traitâ€Related QTL. Plant Biology, 2004, 6, 370-374.	3.8	28
69	Temperature fineâ€ŧunes Mediterranean <i>Arabidopsis thaliana</i> life ycle phenology geographically. Plant Biology, 2018, 20, 148-156.	3.8	20
70	A cytogenetic map on the entire length of rye chromosome 1R, including one translocation breakpoint, three isozyme loci and four C-bands. Theoretical and Applied Genetics, 1993, 85-85, 735-744.	3.6	19
71	QTL Analysis. , 2006, 323, 79-100.		19
72	Ecological, genetic and evolutionary drivers of regional genetic differentiation in Arabidopsis thaliana. BMC Evolutionary Biology, 2020, 20, 71.	3.2	18

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73	An ecological history of the relict genetic lineage of Arabidopsis thaliana. Environmental and Experimental Botany, 2020, 170, 103800.	4.2	15
74	Genetic linkage between cytological markers and the seed storage protein lociSec2[Gli-R2] andSec3[Glu-R1] in rye. Theoretical and Applied Genetics, 1993, 87, 321-327.	3.6	14
75	Quantifying temporal change in plant population attributes: insights from a resurrection approach. AoB PLANTS, 2018, 10, ply063.	2.3	14
76	The Use of Recombinant Inbred Lines (RILs) for Genetic Mapping. , 1998, 82, 137-146.		13
77	MYB transcription factors drive evolutionary innovations in Arabidopsis fruit trichome patterning. Plant Cell, 2021, 33, 548-565.	6.6	12
78	Genetic mapping of cytological and isozyme markers on chromosomes 1R, 3R, 4R and 6R of rye. Theoretical and Applied Genetics, 1994, 88, 208-214.	3.6	11
79	A hierarchical Bayesian Beta regression approach to study the effects of geographical genetic structure and spatial autocorrelation on species distribution range shifts. Molecular Ecology Resources, 2019, 19, 929-943.	4.8	6
80	A Genetic Dissection of Natural Variation for Stomatal Abundance Traits in Arabidopsis. Frontiers in Plant Science, 2019, 10, 1392.	3.6	6
81	Natural Variation in Arabidopsis thaliana. , 2011, , 123-151.		6
82	Physical mapping of translocation breakpoints in rye by means of synaptonemal complex analysis. Theoretical and Applied Genetics, 1994, 89, 33-41.	3.6	5
83	Genetic Interactions and Molecular Evolution of the Duplicated Genes <i>ICARUS2</i> and <i>ICARUS1</i> Help Arabidopsis Plants Adapt to Different Ambient Temperatures. Plant Cell, 2019, 31, 1222-1237.	6.6	3
84	A role of flowering genes in the tolerance of <i>Arabidopsis thaliana</i> to cucumber mosaic virus. Molecular Plant Pathology, 2022, 23, 175-187.	4.2	3
85	Control of perennial flowering and perenniality in Arabis alpina, a relative of Arabidopsis thaliana. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2009, 153, S195-S196.	1.8	2
86	Differential environmental and genomic architectures shape the natural diversity for trichome patterning and morphology in different Arabidopsis organs. Plant, Cell and Environment, 2022, 45, 3018-3035.	5.7	2
87	Analyses of Natural Variation: Field Experiments and Nucleotide Diversity for Your Favorite Gene. Methods in Molecular Biology, 2021, 2200, 93-112.	0.9	1