

Carlos Alonso-Blanco

List of Publications by Year in descending order

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87
papers

12,789
citations

36303

51
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53230

85
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89
all docs

89
docs citations

89
times ranked

11844
citing authors

#	ARTICLE	IF	CITATIONS
1	A role of flowering genes in the tolerance of <i>Arabidopsis thaliana</i> to cucumber mosaic virus. <i>Molecular Plant Pathology</i> , 2022, 23, 175-187.	4.2	3
2	Differential environmental and genomic architectures shape the natural diversity for trichome patterning and morphology in different <i>Arabidopsis</i> organs. <i>Plant, Cell and Environment</i> , 2022, 45, 3018-3035.	5.7	2
3	An oxygen-sensing mechanism for angiosperm adaptation to altitude. <i>Nature</i> , 2022, 606, 565-569.	27.8	31
4	MYB transcription factors drive evolutionary innovations in <i>Arabidopsis</i> fruit trichome patterning. <i>Plant Cell</i> , 2021, 33, 548-565.	6.6	12
5	Analyses of Natural Variation: Field Experiments and Nucleotide Diversity for Your Favorite Gene. <i>Methods in Molecular Biology</i> , 2021, 2200, 93-112.	0.9	1
6	An ecological history of the relict genetic lineage of <i>Arabidopsis thaliana</i> . <i>Environmental and Experimental Botany</i> , 2020, 170, 103800.	4.2	15
7	Root microbiota assembly and adaptive differentiation among European <i>Arabidopsis</i> populations. <i>Nature Ecology and Evolution</i> , 2020, 4, 122-131.	7.8	157
8	Ecological, genetic and evolutionary drivers of regional genetic differentiation in <i>Arabidopsis thaliana</i> . <i>BMC Evolutionary Biology</i> , 2020, 20, 71.	3.2	18
9	Cucumber mosaic virus infection as a potential selective pressure on <i>Arabidopsis thaliana</i> populations. <i>PLoS Pathogens</i> , 2019, 15, e1007810.	4.7	35
10	Genetic Interactions and Molecular Evolution of the Duplicated Genes <i>ICARUS2</i> and <i>ICARUS1</i> Help <i>Arabidopsis</i> Plants Adapt to Different Ambient Temperatures. <i>Plant Cell</i> , 2019, 31, 1222-1237.	6.6	3
11	A hierarchical Bayesian Beta regression approach to study the effects of geographical genetic structure and spatial autocorrelation on species distribution range shifts. <i>Molecular Ecology Resources</i> , 2019, 19, 929-943.	4.8	6
12	A Genetic Dissection of Natural Variation for Stomatal Abundance Traits in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1392.	3.6	6
13	Genome-wide signatures of flowering adaptation to climate temperature: Regional analyses in a highly diverse native range of <i>Arabidopsis thaliana</i> . <i>Plant, Cell and Environment</i> , 2018, 41, 1806-1820.	5.7	49
14	Temperature fine-tunes Mediterranean <i>Arabidopsis thaliana</i> life-cycle phenology geographically. <i>Plant Biology</i> , 2018, 20, 148-156.	3.8	20
15	Quantifying temporal change in plant population attributes: insights from a resurrection approach. <i>AoB PLANTS</i> , 2018, 10, ply063.	2.3	14
16	Spatio-temporal variation in fitness responses to contrasting environments in <i>Arabidopsis thaliana</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 1570-1586.	2.3	34
17	On the post-glacial spread of human commensal <i>Arabidopsis thaliana</i> . <i>Nature Communications</i> , 2017, 8, 14458.	12.8	83
18	African genomes illuminate the early history and transition to selfing in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5213-5218.	7.1	142

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19	Environmental and genetic interactions reveal <i>FLOWERING LOCUS C</i> as a modulator of the natural variation for the plasticity of flowering in Arabidopsis. <i>Plant, Cell and Environment</i> , 2016, 39, 282-294.	5.7	29
20	Tackling intraspecific genetic structure in distribution models better reflects species geographical range. <i>Ecology and Evolution</i> , 2016, 6, 2084-2097.	1.9	59
21	Epigenomic Diversity in a Global Collection of Arabidopsis thaliana Accessions. <i>Cell</i> , 2016, 166, 492-505.	28.9	594
22	Altitudinal and climatic associations of seed dormancy and flowering traits evidence adaptation of annual life cycle timing in Arabidopsis thaliana. <i>Plant, Cell and Environment</i> , 2016, 39, 1737-1748.	5.7	90
23	1,135 Genomes Reveal the Global Pattern of Polymorphism in Arabidopsis thaliana. <i>Cell</i> , 2016, 166, 481-491.	28.9	1,107
24	Genome expansion of Arabis alpina linked with retrotransposition and reduced symmetric DNA methylation. <i>Nature Plants</i> , 2015, 1, 14023.	9.3	156
25	<i>FE</i> , a phloem-specific Myb-related protein, promotes flowering through transcriptional activation of <i>FLOWERING LOCUS T</i> and <i>FLOWERING LOCUS T INTERACTING PROTEIN 1</i> . <i>Plant Journal</i> , 2015, 83, 1059-1068.	5.7	53
26	Natural Variation Identifies ICARUS1, a Universal Gene Required for Cell Proliferation and Growth at High Temperatures in Arabidopsis thaliana. <i>PLoS Genetics</i> , 2015, 11, e1005085.	3.5	34
27	The genetic structure of Arabidopsis thaliana in the south-western Mediterranean range reveals a shared history between North Africa and southern Europe. <i>BMC Plant Biology</i> , 2014, 14, 17.	3.6	53
28	Natural variation in arsenate tolerance identifies an arsenate reductase in Arabidopsis thaliana. <i>Nature Communications</i> , 2014, 5, 4617.	12.8	136
29	Genetic architecture of naturally occurring quantitative traits in plants: an updated synthesis. <i>Current Opinion in Plant Biology</i> , 2014, 18, 37-43.	7.1	68
30	Deciphering the Adjustment between Environment and Life History in Annuals: Lessons from a Geographically-Explicit Approach in Arabidopsis thaliana. <i>PLoS ONE</i> , 2014, 9, e87836.	2.5	57
31	The Flowering Repressor SVP Underlies a Novel Arabidopsis thaliana QTL Interacting with the Genetic Background. <i>PLoS Genetics</i> , 2013, 9, e1003289.	3.5	58
32	Among- and within-population variation in flowering time of Iberian Arabidopsis thaliana estimated in field and glasshouse conditions. <i>New Phytologist</i> , 2013, 197, 1332-1343.	7.3	56
33	Arabidopsis 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.	7.1	79
34	Natural Arabidopsis brx Loss-of-Function Alleles Confer Root Adaptation to Acidic Soil. <i>Current Biology</i> , 2012, 22, 1962-1968.	3.9	66
35	GENETIC BASIS OF ADAPTATION IN ARABIDOPSIS THALIANA: LOCAL ADAPTATION AT THE SEED DORMANCY QTL DOG1. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 2287-2302.	2.3	103
36	Novel natural alleles at <i>FLC</i> and <i>LVR</i> loci account for enhanced vernalization responses in Arabidopsis thaliana. <i>Plant, Cell and Environment</i> , 2012, 35, 1672-1684.	5.7	45

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37	Whole-genome sequencing of multiple <i>Arabidopsis thaliana</i> populations. <i>Nature Genetics</i> , 2011, 43, 956-963.	21.4	910
38	Temporal variation in genetic diversity and effective population size of Mediterranean and subalpine <i>Arabidopsis thaliana</i> populations. <i>Molecular Ecology</i> , 2011, 20, no-no.	3.9	47
39	Altitudinal and Climatic Adaptation Is Mediated by Flowering Traits and <i>FRI</i> , <i>FLC</i> , and <i>PHYC</i> Genes in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2011, 157, 1942-1955.	4.8	171
40	Natural variation in stomatal abundance of <i>Arabidopsis thaliana</i> includes cryptic diversity for different developmental processes. <i>Annals of Botany</i> , 2011, 107, 1247-1258.	2.9	58
41	Natural Variation in <i>Arabidopsis thaliana</i> . , 2011, , 123-151.		6
42	Site and plant species are important determinants of the <i>Methylobacterium</i> community composition in the plant phyllosphere. <i>ISME Journal</i> , 2010, 4, 719-728.	9.8	297
43	Natural variation for seed dormancy in <i>Arabidopsis</i> is regulated by additive genetic and molecular pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4264-4269.	7.1	194
44	Temporal analysis of natural variation for the rate of leaf production and its relationship with flowering initiation in <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2010, 61, 1611-1623.	4.8	56
45	<i>Arabidopsis thaliana</i> as a model for the study of plant-virus co-evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 1983-1995.	4.0	92
46	Differential Tolerance to Direct and Indirect Density-Dependent Costs of Viral Infection in <i>Arabidopsis thaliana</i> . <i>PLoS Pathogens</i> , 2009, 5, e1000531.	4.7	33
47	A high-density collection of EMS-induced mutations for TILLING in <i>Landsberg erecta</i> genetic background of <i>Arabidopsis</i> . <i>BMC Plant Biology</i> , 2009, 9, 147.	3.6	57
48	Control of perennial flowering and perenniality in <i>Arabis alpina</i> , a relative of <i>Arabidopsis thaliana</i> . <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2009, 153, S195-S196.	1.8	2
49	PEP1 regulates perennial flowering in <i>Arabis alpina</i> . <i>Nature</i> , 2009, 459, 423-427.	27.8	325
50	What Has Natural Variation Taught Us about Plant Development, Physiology, and Adaptation?. <i>Plant Cell</i> , 2009, 21, 1877-1896.	6.6	401
51	Demographic and Genetic Patterns of Variation among Populations of <i>Arabidopsis thaliana</i> from Contrasting Native Environments. <i>PLoS ONE</i> , 2009, 4, e7213.	2.5	77
52	Host Responses in Life-History Traits and Tolerance to Virus Infection in <i>Arabidopsis thaliana</i> . <i>PLoS Pathogens</i> , 2008, 4, e1000124.	4.7	68
53	Natural Genetic Variation of <i>Arabidopsis thaliana</i> Is Geographically Structured in the Iberian Peninsula. <i>Genetics</i> , 2008, 180, 1009-1021.	2.9	116
54	Development of a Near-Isogenic Line Population of <i>Arabidopsis thaliana</i> and Comparison of Mapping Power With a Recombinant Inbred Line Population. <i>Genetics</i> , 2007, 175, 891-905.	2.9	214

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55	Quantitative genetic analysis of flowering time in tomato. <i>Genome</i> , 2007, 50, 303-315.	2.0	36
56	The Relationship of Within-Host Multiplication and Virulence in a Plant-Virus System. <i>PLoS ONE</i> , 2007, 2, e786.	2.5	69
57	QTL Analysis. , 2006, 323, 79-100.		19
58	Gene function beyond the single trait: natural variation, gene effects, and evolutionary ecology in <i>Arabidopsis thaliana</i> . <i>Plant, Cell and Environment</i> , 2005, 28, 2-20.	5.7	103
59	ERECTA receptor-like kinase and heterotrimeric G protein from <i>Arabidopsis</i> are required for resistance to the necrotrophic fungus <i>Plectosphaerella cucumerina</i> . <i>Plant Journal</i> , 2005, 43, 165-180.	5.7	303
60	From phenotypic to molecular polymorphisms involved in naturally occurring variation of plant development. <i>International Journal of Developmental Biology</i> , 2005, 49, 717-732.	0.6	78
61	Environmental regulation of flowering. <i>International Journal of Developmental Biology</i> , 2005, 49, 689-705.	0.6	149
62	Genetic and Molecular Analyses of Natural Variation Indicate CBF2 as a Candidate Gene for Underlying a Freezing Tolerance Quantitative Trait Locus in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2005, 139, 1304-1312.	4.8	149
63	Regulation of flowering time by FVE, a retinoblastoma-associated protein. <i>Nature Genetics</i> , 2004, 36, 162-166.	21.4	347
64	Pleiotropic Effects of the <i>Arabidopsis</i> Cryptochrome 2 Allelic Variation Underlie Fruit Trait-Related QTL. <i>Plant Biology</i> , 2004, 6, 370-374.	3.8	28
65	NATURALLY OCCURRING GENETIC VARIATION IN <i>ARABIDOPSIS THALIANA</i> . <i>Annual Review of Plant Biology</i> , 2004, 55, 141-172.	18.7	610
66	The Cape Verde Islands Allele of Cryptochrome 2 Enhances Cotyledon Unfolding in the Absence of Blue Light in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2003, 133, 1547-1556.	4.8	46
67	The Role of Cryptochrome 2 in Flowering in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2003, 133, 1504-1516.	4.8	71
68	Analysis of Natural Allelic Variation at Seed Dormancy Loci of <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2003, 164, 711-729.	2.9	359
69	A QTL for flowering time in <i>Arabidopsis</i> reveals a novel allele of CRY2. <i>Nature Genetics</i> , 2001, 29, 435-440.	21.4	387
70	Genetic Analysis of Seed-Soluble Oligosaccharides in Relation to Seed Storability of <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2000, 124, 1595-1604.	4.8	205
71	The Late Flowering Phenotype of <i>fwa</i> Mutants Is Caused by Gain-of-Function Epigenetic Alleles of a Homeodomain Gene. <i>Molecular Cell</i> , 2000, 6, 791-802.	9.7	545
72	Naturally occurring variation in <i>Arabidopsis</i> : an underexploited resource for plant genetics. <i>Trends in Plant Science</i> , 2000, 5, 22-29.	8.8	398

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73	Natural allelic variation at seed size loci in relation to other life history traits of <i>Arabidopsis thaliana</i> . Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 4710-4717.	7.1	257
74	Natural allelic variation identifies new genes in the <i>Arabidopsis</i> circadian system. Plant Journal, 1999, 20, 67-77.	5.7	171
75	Cytogenetics for the model system <i>Arabidopsis thaliana</i> . Plant Journal, 1998, 13, 867-876.	5.7	304
76	Development of an AFLP based linkage map of Ler, Col and Cvi <i>Arabidopsis thaliana</i> ecotypes and construction of a Ler/Cvi recombinant inbred line population. Plant Journal, 1998, 14, 259-271.	5.7	355
77	GENETIC CONTROL OF FLOWERING TIME IN ARABIDOPSIS. Annual Review of Plant Biology, 1998, 49, 345-370.	14.3	445
78	The Use of Recombinant Inbred Lines (RILs) for Genetic Mapping. , 1998, 82, 137-146.		13
79	Analysis of Natural Allelic Variation at Flowering Time Loci in the Landsberg erecta and Cape Verde Islands Ecotypes of <i>Arabidopsis thaliana</i> . Genetics, 1998, 149, 749-764.	2.9	225
80	QTL analysis of seed dormancy in <i>Arabidopsis</i> using recombinant inbred lines and MQM mapping. Heredity, 1997, 79, 190-200.	2.6	31
81	QTL analysis of seed dormancy in <i>Arabidopsis</i> using recombinant inbred lines and MQM mapping. Heredity, 1997, 79, 190-200.	2.6	139
82	Genetic approaches in plant physiology. New Phytologist, 1997, 137, 1-8.	7.3	65
83	High-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
84	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
85	Physical mapping of translocation breakpoints in rye by means of synaptonemal complex analysis. Theoretical and Applied Genetics, 1994, 89, 33-41.	3.6	5
86	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
87	Genetic linkage between cytological markers and the seed storage protein loci Sec2[Gli-R2] and Sec3[Glu-R1] in rye. Theoretical and Applied Genetics, 1993, 87, 321-327.	3.6	14