Antonio Augusto Franco Garcia

List of Publications by Year
in descending order

110 papers	5,680 citations	66343 42 h-index	95266 68 g-index
137 all docs	137 docs citations	137 times ranked	5121 citing authors

#	Article	IF	Citations
1	Genetic mapping reveals complex architecture and candidate genes involved in common bean response to *Meloidogyne incognita* infection. Plant Genome, 2022, 15, e20161.	2.8	4
2	Leveraging probability concepts for cultivar recommendation in multi-environment trials. Theoretical and Applied Genetics, 2022, 135, 1385-1399.	3.6	8
3	Genome-wide association studies dissect the genetic architecture of seed shape and size in common bean. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	4
4	Significance of linkage disequilibrium and epistasis on genetic variances in noninbred and inbred populations. BMC Genomics, 2022, 23, 286.	2.8	4
5	Allele expression biases in mixed-ploid sugarcane accessions. Scientific Reports, 2022, 12, .	3.3	1
6	Construction of a High-Density Genetic Map of Acca sellowiana (Berg.) Burret, an Outcrossing Species, Based on Two Connected Mapping Populations. Frontiers in Plant Science, 2021, 12, 626811.	3.6	3
7	Angular Leaf Spot Resistance Loci Associated With Different Plant Growth Stages in Common Bean. Frontiers in Plant Science, 2021, 12, 647043.	3.6	11
8	Genetic Variability, Correlation among Agronomic Traits, and Genetic Progress in a Sugarcane Diversity Panel. Agriculture (Switzerland), 2021, 11, 533.	3.1	9
9	QTL mapping for bioenergy traits in sweet sorghum recombinant inbred lines. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	3
10	Novel strategies for genomic prediction of untested single-cross maize hybrids using unbalanced historical data. Theoretical and Applied Genetics, 2020, 133, 443-455.	3.6	22
11	Novel Bayesian Networks for Genomic Prediction of Developmental Traits in Biomass Sorghum. G3: Genes, Genomes, Genetics, 2020, 10, 769-781.	1.8	25
12	Comparison of different selection methods in the seedling stage of sugarcane breeding. Agronomy Journal, 2020, 112, 4879-4897.	1.8	4
13	Estimation of Molecular Pairwise Relatedness in Autopolyploid Crops. G3: Genes, Genomes, Genetics, 2020, 10, 4579-4589.	1.8	11
14	Improving yield and fruit quality traits in sweet passion fruit: Evidence for genotype by environment interaction and selection of promising genotypes. PLoS ONE, 2020, 15, e0232818.	2.5	16
15	High-Resolution Linkage Map With Allele Dosage Allows the Identification of Regions Governing Complex Traits and Apospory in Guinea Grass (Megathyrsus maximus). Frontiers in Plant Science, 2020, 11, 15.	3.6	22
16	Boosting predictive ability of tropical maize hybrids via genotype‐by‐environment interaction under multivariate GBLUP models. Crop Science, 2020, 60, 3049-3065.	1.8	15
17	Accurate genomic prediction of Coffea canephora in multiple environments using whole-genome statistical models. Heredity, 2019, 122, 261-275.	2.6	36
18	A genome-wide association study identified loci for yield component traits in sugarcane (Saccharum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.5	54

#	ARTICLE	IF	CITATIONS
19	Evidence for Strong Kinship Influence on the Extent of Linkage Disequilibrium in Cultivated Common Beans. Genes, 2019, 10, 5.	2.4	32
20	Gene Duplication in the Sugarcane Genome: A Case Study of Allele Interactions and Evolutionary Patterns in Two Genic Regions. Frontiers in Plant Science, 2019, 10, 553.	3.6	23
21	Genetic Mapping With Allele Dosage Information in Tetraploid Urochloa decumbens (Stapf) R. D. Webster Reveals Insights Into Spittlebug (Notozulia entreriana Berg) Resistance. Frontiers in Plant Science, 2019, 10, 92.	3.6	32
22	Linkage Analysis and Haplotype Phasing in Experimental Autopolyploid Populations with High Ploidy Level Using Hidden Markov Models. G3: Genes, Genomes, Genetics, 2019, 9, 3297-3314.	1.8	75
23	Genomic Selection with Allele Dosage in *Panicum maximum* Jacq.. G3: Genes, Genomes, Genetics, 2019, 9, 2463-2475.	1.8	57
24	Improving accuracies of genomic predictions for drought tolerance in maize by joint modeling of additive and dominance effects in multi-environment trials. Heredity, 2018, 121, 24-37.	2.6	68
25	Efficiency of multi-trait, indirect, and trait-assisted genomic selection for improvement of biomass sorghum. Theoretical and Applied Genetics, 2018, 131, 747-755.	3.6	139
26	A fully automated pipeline for quantitative genotype calling from next generation sequencing data in autopolyploids. BMC Bioinformatics, 2018, 19, 398.	2.6	62
27	Genotyping Polyploids from Messy Sequencing Data. Genetics, 2018, 210, 789-807.	2.9	157
28	QTL mapping and identification of corresponding genomic regions for black pod disease resistance to three Phytophthora species in Theobroma cacao L.. Euphytica, 2018, 214, 1.	1.2	22
29	QTL detection for growth and latex production in a full-sib rubber tree population cultivated under suboptimal climate conditions. BMC Plant Biology, 2018, 18, 223.	3.6	18
30	Linkage Disequilibrium and Population Structure in Wild and Cultivated Populations of Rubber Tree (Hevea brasiliensis). Frontiers in Plant Science, 2018, 9, 815.	3.6	20
31	High-Resolution Genetic Map and QTL Analysis of Growth-Related Traits of Hevea brasiliensis Cultivated Under Suboptimal Temperature and Humidity Conditions. Frontiers in Plant Science, 2018, 9, 1255.	3.6	27
32	GBS-based single dosage markers for linkage and QTL mapping allow gene mining for yield-related traits in sugarcane. BMC Genomics, 2017, 18, 72.	2.8	91
33	New Developments in Sugarcane Genetics and Genomics. , 2017, , 159-174.		5
34	A mixed model to multiple harvest-location trials applied to genomic prediction in Coffea canephora. Tree Genetics and Genomes, 2017, 13, 1.	1.6	23
35	Genomic Selection: State of the Art. , 2017, , 19-54.		4
36	Linking rhizosphere microbiome composition of wild and domesticated *Phaseolus vulgaris* to genotypic and root phenotypic traits. ISME Journal, 2017, 11, 2244-2257.	9.8	298

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37	The Sweet Passion Fruit (Passiflora alata) Crop: Genetic and Phenotypic Parameter Estimates and QTL Mapping for Fruit Traits. Tropical Plant Biology, 2017, 10, 18-29.	1.9	7
38	AGHmatrix: R Package to Construct Relationship Matrices for Autotetraploid and Diploid Species: A Blueberry Example. Plant Genome, 2016, 9, plantgenome2016.01.0009.	2.8	158
39	Ascertainment bias from imputation methods evaluation in wheat. BMC Genomics, 2016, 17, 773.	2.8	5
40	Mixed Modeling of Yield Components and Brown Rust Resistance in Sugarcane Families. Agronomy Journal, 2016, 108, 1824-1837.	1.8	34
41	QTL mapping including codominant SNP markers with ploidy level information in a sugarcane progeny. Euphytica, 2016, 211, 1-16.	1.2	39
42	Genome-Wide Association Studies of Anthracnose and Angular Leaf Spot Resistance in Common Bean (Phaseolus vulgaris L.). PLoS ONE, 2016, 11, e0150506.	2.5	89
43	Evidence of Allopolyploidy in Urochloa humidicola Based on Cytological Analysis and Genetic Linkage Mapping. PLoS ONE, 2016, 11, e0153764.	2.5	39
44	Developing a common bean core collection suitable for association mapping studies. Genetics and Molecular Biology, 2015, 38, 67-78.	1.3	29
45	Multi-trait multi-environment quantitative trait loci mapping for a sugarcane commercial cross provides insights on the inheritance of important traits. Molecular Breeding, 2015, 35, 175.	2.1	19
46	Multiple interval QTL mapping and searching for PSTOL1 homologs associated with root morphology, biomass accumulation and phosphorus content in maize seedlings under low-P. BMC Plant Biology, 2015, 15, 172.	3.6	53
47	Marker-trait association and epistasis for brown rust resistance in sugarcane. Euphytica, 2015, 203, 533-547.	1.2	13
48	De Novo Assembly and Transcriptome Analysis of Contrasting Sugarcane Varieties. PLoS ONE, 2014, 9, e88462.	2.5	129
49	Genetic Architecture of Phosphorus Use Efficiency in Tropical Maize Cultivated in a Low€P Soil. Crop Science, 2014, 54, 1530-1538.	1.8	33
50	Quantitative analysis of race-specific resistance to Colletotrichum lindemuthianum in common bean. Molecular Breeding, 2014, 34, 1313-1329.	2.1	35
51	Duplicate and Conquer: Multiple Homologs of<i>PHOSPHORUS-STARVATION TOLERANCE1</i>Enhance Phosphorus Acquisition and Sorghum Performance on Low-Phosphorus Soils Â Â Â. Plant Physiology, 2014, 166, 659-677.	4.8	117
52	Biological activity of nine recombinant AtRALF peptides: Implications for their perception and function in Arabidopsis. Plant Physiology and Biochemistry, 2014, 75, 45-54.	5.8	81
53	Composite interval mapping and mixed models reveal QTL associated with performance and carcass traits on chicken chromosomes 1, 3, and 4. Journal of Applied Genetics, 2014, 55, 97-103.	1.9	1
54	A first genetic map of Acca sellowiana based on ISSR, AFLP and SSR markers. Scientia Horticulturae, 2014, 169, 138-146.	3.6	6

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55	Building the sugarcane genome for biotechnology and identifying evolutionary trends. BMC Genomics, 2014, 15, 540.	2.8	136
56	A model for quantitative trait loci mapping, linkage phase, and segregation pattern estimation for a full-sib progeny. Tree Genetics and Genomes, 2014, 10, 791-801.	1.6	34
57	Mapping of QTLs associated with biological nitrogen fixation traits in soybean. Hereditas, 2013, 150, 17-25.	1.4	45
58	Molecular polymorphism and linkage analysis in sweet passion fruit, an outcrossing species. Annals of Applied Biology, 2013, 162, 347-361.	2.5	29
59	SNP genotyping allows an in-depth characterisation of the genome of sugarcane and other complex autopolyploids. Scientific Reports, 2013, 3, 3399.	3.3	129
60	QTL Mapping of Growth-Related Traits in a Full-Sib Family of Rubber Tree (Hevea brasiliensis) Evaluated in a Sub-Tropical Climate. PLoS ONE, 2013, 8, e61238.	2.5	72
61	Mapping of angular leaf spot resistance QTL in common bean (Phaseolus vulgaris L.) under different environments. BMC Genetics, 2012, 13, 50.	2.7	48
62	A novel linkage map of sugarcane with evidence for clustering of retrotransposon-based markers. BMC Genetics, 2012, 13, 51.	2.7	34
63	Efficient Exact Maximum a Posteriori Computation for Bayesian SNP Genotyping in Polyploids. PLoS ONE, 2012, 7, e30906.	2.5	129
64	Studying the genetic basis of drought tolerance in sorghum by managed stress trials and adjustments for phenological and plant height differences. Theoretical and Applied Genetics, 2012, 124, 1389-1402.	3.6	98
65	A molecular linkage map for *Drosophila mediopunctata* confirms synteny with *Drosophila melanogaster* and suggests a region that controls the variation in the number of abdominal spots. Insect Molecular Biology, 2012, 21, 89-95.	2.0	4
66	Sugarcane improvement: how far can we go?. Current Opinion in Biotechnology, 2012, 23, 265-270.	6.6	92
67	A mixed model QTL analysis for sugarcane multiple-harvest-location trial data. Theoretical and Applied Genetics, 2012, 124, 835-849.	3.6	73
68	Genetic diversity in cultivated carioca common beans based on molecular marker analysis. Genetics and Molecular Biology, 2011, 34, 88-102.	1.3	32
69	Functional markers for gene mapping and genetic diversity studies in sugarcane. BMC Research Notes, 2011, 4, 264.	1.4	51
70	Inheritance of growth habit detected by genetic linkage analysis using microsatellites in the common bean (Phaseolus vulgaris L.). Molecular Breeding, 2011, 27, 549-560.	2.1	33
71	Sugarcane Underground Organs: Going Deep for Sustainable Production. Tropical Plant Biology, 2011, 4, 22-30.	1.9	22
72	Development of a genetic linkage map of rubber tree (Hevea braziliensis) based on microsatellite markers. BMC Proceedings, 2011, 5, .	1.6	10

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73	The Relationship between Population Structure and Aluminum Tolerance in Cultivated Sorghum. PLoS ONE, 2011, 6, e20830.	2.5	29
74	RegiÃµes genÃ´micas associadas a caracterÃsticas de desempenho e carcaÃ§a no cromossomo 5 de linhagens Brasileiras de galinha. Pesquisa Agropecuaria Brasileira, 2011, 46, 229-238.	0.9	2
75	The Biotechnology Roadmap for Sugarcane Improvement. Tropical Plant Biology, 2010, 3, 75-87.	1.9	62
76	Analysis of genomic and functional RFLP derived markers associated with sucrose content, fiber and yield QTLs in a sugarcane (Saccharum spp.) commercial cross. Euphytica, 2010, 172, 313-327.	1.2	46
77	Precision of distances and ordering of microsatellite markers in consensus linkage maps of chromosomes 1, 3 and 4 from two reciprocal chicken populations using bootstrap sampling. Genetics and Molecular Research, 2010, 9, 1357-1376.	0.2	4
78	Genotypic characterization of microsatellite markers in broiler and layer selected chicken lines and their reciprocal F1s. Scientia Agricola, 2009, 66, 150-158.	1.2	26
79	Characterization of rust, early and late leaf spot resistance in wild and cultivated peanut germplasm. Scientia Agricola, 2009, 66, 110-117.	1.2	31
80	Quantitative trait loci analysis of citrus leprosis resistance in an interspecific backcross family of (Citrus reticulata BlancoÃÂ—ÂC. sinensis L. Osbeck)ÃÂ—ÂC. sinensis L. Osb. Euphytica, 2009, 169, 101-111.	1.2	25
81	Evaluation of algorithms used to order markers on genetic maps. Heredity, 2009, 103, 494-502.	2.6	41
82	Characterization of new polymorphic functional markers for sugarcane. Genome, 2009, 52, 191-209.	2.0	87
83	QTL mapping for yield components in a tropical maize population using microsatellite markers. Hereditas, 2008, 145, 194-203.	1.4	49
84	Quantitative Trait Loci Mapping and The Genetic Basis of Heterosis in Maize and Rice. Genetics, 2008, 180, 1707-1724.	2.9	141
85	An Integrated Molecular Map of Yellow Passion Fruit Based on Simultaneous Maximum-likelihood Estimation of Linkage and Linkage Phases. Journal of the American Society for Horticultural Science, 2008, 133, 35-41.	1.0	44
86	ComparaÃ§Ã£o dos algoritmos delineaÃ§Ã£o rÃ¡pida em cadeia e seriaÃ§Ã£o, para a construÃ§Ã£o de mapas genÃ©ticos. Pesquisa Agropecuaria Brasileira, 2008, 43, 505-512.	0.9	1
87	OneMap: software for genetic mapping in outcrossing species. Hereditas, 2007, 144, 78-79.	1.4	326
88	Functional integrated genetic linkage map based on EST-markers for a sugarcane (Saccharum spp.) commercial cross. Molecular Breeding, 2007, 20, 189-208.	2.1	79
89	Characterization of novel sugarcane expressed sequence tag microsatellites and their comparison with genomic SSRs. Plant Breeding, 2006, 125, 378-384.	1.9	84
90	Identification of QTLs associated with citrus resistance toPhytophthora gummosis. Journal of Applied Genetics, 2006, 47, 23-28.	1.9	44

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91	Development of an integrated genetic map of a sugarcane (Saccharum spp.) commercial cross, based on a maximum-likelihood approach for estimation of linkage and linkage phases. Theoretical and Applied Genetics, 2006, 112, 298-314.	3.6	101
92	Tropical maize germplasm: what can we say about its genetic diversity in the light of molecular markers?. Theoretical and Applied Genetics, 2005, 111, 1288-1299.	3.6	69
93	Decomposição ortogonal de graus de liberdade de tratamentos utilizando variáveis auxiliares e o PROC GLM do SAS. Bragantia, 2005, 64, 157-167.	1.3	3
94	Common bean cultivars and lines interactions with environments. Scientia Agricola, 2004, 61, 169-177.	1.2	46
95	Comparison of similarity coefficients used for cluster analysis with dominant markers in maize (Zea) Tj ETQq1 1 0.784314 rgBT /Overlo	1.3	104
96	Comparison of RAPD, RFLP, AFLP and SSR markers for diversity studies in tropical maize inbred lines. Genetics and Molecular Biology, 2004, 27, 579-588.	1.3	162
97	Molecular mapping in tropical maize (Zea mays L.) using microsatellite markers. 1. Map construction and localization of loci showing distorted segregation. Hereditas, 2004, 139, 96-106.	1.4	37
98	Molecular mapping in tropical maize (Zea mays L.) using microsatellite markers. 2. Quantitative trait loci (QTL) for grain yield, plant heigth, ear height and grain moisture. Hereditas, 2004, 139, 107-115.	1.4	77
99	Evaluating genetic relationships between tropical maize inbred lines by means of AFLP profiling. Hereditas, 2004, 140, 24-33.	1.4	26
100	Mapping QTLs for kernel oil content in a tropical maize population. Euphytica, 2004, 137, 251-259.	1.2	43
101	Survey in the sugarcane expressed sequence tag database (SUCEST) for simple sequence repeats. Genome, 2004, 47, 795-804.	2.0	113
102	Title is missing!. Euphytica, 2003, 130, 87-99.	1.2	57
103	Combining ability of inbred lines of maize and stability of their respective single-crosses. Scientia Agricola, 2003, 60, 83-89.	1.2	27
104	Seleção de descritores botânico-agronômicos para caracterização de germoplasma de cupuaçuzeiro. Pesquisa Agropecuaria Brasileira, 2003, 38, 807-818.	0.9	31
105	Influência do sistema de criação sobre o desempenho, a condição fisiológica e o comportamento de linhagens de frangos para corte. Revista Brasileira De Zootecnia, 2003, 32, 208-213.	0.8	20
106	Phenotypic recurrent selection to improve protein quality in non-opaque maize populations. Scientia Agricola, 2002, 59, 743-748.	1.2	3
107	Analysis of genetic similarity detected by AFLP and coefficient of parentage among genotypes of sugar cane (Saccharum spp.). Theoretical and Applied Genetics, 2002, 104, 30-38.	3.6	141
108	Alocação de linhagens de milho derivadas das populações BR-105 e BR-106 em grupos heteróticos. Scientia Agricola, 2001, 58, 541-548.	1.2	9

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109	Genetic diversity in tropical maize inbred lines: heterotic group assignment and hybrid performance determined by RFLP markers. Plant Breeding, 2000, 119, 491-496.	1.9	70
110	Comparação de índices de seleção não paramétricos para a seleção de cultivares. Bragantia, 1999, 58, 253-267.	1.3	22