

Antonio Augusto Franco Garcia

List of Publications by Year in descending order

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Version: 2024-02-01

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	OneMap: software for genetic mapping in outcrossing species. <i>Hereditas</i> , 2007, 144, 78-79.	1.4	326
2	Linking rhizosphere microbiome composition of wild and domesticated <i>Phaseolus vulgaris</i> to genotypic and root phenotypic traits. <i>ISME Journal</i> , 2017, 11, 2244-2257.	9.8	298
3	Comparison of RAPD, RFLP, AFLP and SSR markers for diversity studies in tropical maize inbred lines. <i>Genetics and Molecular Biology</i> , 2004, 27, 579-588.	1.3	162
4	AGHmatrix: R Package to Construct Relationship Matrices for Autotetraploid and Diploid Species: A Blueberry Example. <i>Plant Genome</i> , 2016, 9, plantgenome2016.01.0009.	2.8	158
5	Genotyping Polyploids from Messy Sequencing Data. <i>Genetics</i> , 2018, 210, 789-807.	2.9	157
6	Analysis of genetic similarity detected by AFLP and coefficient of parentage among genotypes of sugar cane (<i>Saccharum</i> spp.). <i>Theoretical and Applied Genetics</i> , 2002, 104, 30-38.	3.6	141
7	Quantitative Trait Loci Mapping and The Genetic Basis of Heterosis in Maize and Rice. <i>Genetics</i> , 2008, 180, 1707-1724.	2.9	141
8	Efficiency of multi-trait, indirect, and trait-assisted genomic selection for improvement of biomass sorghum. <i>Theoretical and Applied Genetics</i> , 2018, 131, 747-755.	3.6	139
9	Building the sugarcane genome for biotechnology and identifying evolutionary trends. <i>BMC Genomics</i> , 2014, 15, 540.	2.8	136
10	Efficient Exact Maximum a Posteriori Computation for Bayesian SNP Genotyping in Polyploids. <i>PLoS ONE</i> , 2012, 7, e30906.	2.5	129
11	SNP genotyping allows an in-depth characterisation of the genome of sugarcane and other complex autopolyploids. <i>Scientific Reports</i> , 2013, 3, 3399.	3.3	129
12	De Novo Assembly and Transcriptome Analysis of Contrasting Sugarcane Varieties. <i>PLoS ONE</i> , 2014, 9, e88462.	2.5	129
13	Duplicate and Conquer: Multiple Homologs of <i>PHOSPHORUS-STARVATION TOLERANCE1</i> Enhance Phosphorus Acquisition and Sorghum Performance on Low-Phosphorus Soils. <i>Plant Physiology</i> , 2014, 166, 659-677.	4.8	117
14	Survey in the sugarcane expressed sequence tag database (SUCEST) for simple sequence repeats. <i>Genome</i> , 2004, 47, 795-804.	2.0	113
15	Comparison of similarity coefficients used for cluster analysis with dominant markers in maize (<i>Zea mays</i>) inbred lines. <i>Genetics</i> , 2004, 167, 1041-1049.	1.3	104
16	Development of an integrated genetic map of a sugarcane (<i>Saccharum</i> spp.) commercial cross, based on a maximum-likelihood approach for estimation of linkage and linkage phases. <i>Theoretical and Applied Genetics</i> , 2006, 112, 298-314.	3.6	101
17	Studying the genetic basis of drought tolerance in sorghum by managed stress trials and adjustments for phenological and plant height differences. <i>Theoretical and Applied Genetics</i> , 2012, 124, 1389-1402.	3.6	98
18	Sugarcane improvement: how far can we go?. <i>Current Opinion in Biotechnology</i> , 2012, 23, 265-270.	6.6	92

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19	GBS-based single dosage markers for linkage and QTL mapping allow gene mining for yield-related traits in sugarcane. <i>BMC Genomics</i> , 2017, 18, 72.	2.8	91
20	Genome-Wide Association Studies of Anthracnose and Angular Leaf Spot Resistance in Common Bean (<i>Phaseolus vulgaris</i> L.). <i>PLoS ONE</i> , 2016, 11, e0150506.	2.5	89
21	Characterization of new polymorphic functional markers for sugarcane. <i>Genome</i> , 2009, 52, 191-209.	2.0	87
22	Characterization of novel sugarcane expressed sequence tag microsatellites and their comparison with genomic SSRs. <i>Plant Breeding</i> , 2006, 125, 378-384.	1.9	84
23	Biological activity of nine recombinant AtRALF peptides: Implications for their perception and function in <i>Arabidopsis</i> . <i>Plant Physiology and Biochemistry</i> , 2014, 75, 45-54.	5.8	81
24	Functional integrated genetic linkage map based on EST-markers for a sugarcane (<i>Saccharum</i> spp.) commercial cross. <i>Molecular Breeding</i> , 2007, 20, 189-208.	2.1	79
25	Molecular mapping in tropical maize (<i>Zea mays</i> L.) using microsatellite markers. 2. Quantitative trait loci (QTL) for grain yield, plant height, ear height and grain moisture. <i>Hereditas</i> , 2004, 139, 107-115.	1.4	77
26	Linkage Analysis and Haplotype Phasing in Experimental Autopolyploid Populations with High Ploidy Level Using Hidden Markov Models. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3297-3314.	1.8	75
27	A mixed model QTL analysis for sugarcane multiple-harvest-location trial data. <i>Theoretical and Applied Genetics</i> , 2012, 124, 835-849.	3.6	73
28	QTL Mapping of Growth-Related Traits in a Full-Sib Family of Rubber Tree (<i>Hevea brasiliensis</i>) Evaluated in a Sub-Tropical Climate. <i>PLoS ONE</i> , 2013, 8, e61238.	2.5	72
29	Genetic diversity in tropical maize inbred lines: heterotic group assignment and hybrid performance determined by RFLP markers. <i>Plant Breeding</i> , 2000, 119, 491-496.	1.9	70
30	Tropical maize germplasm: what can we say about its genetic diversity in the light of molecular markers?. <i>Theoretical and Applied Genetics</i> , 2005, 111, 1288-1299.	3.6	69
31	Improving accuracies of genomic predictions for drought tolerance in maize by joint modeling of additive and dominance effects in multi-environment trials. <i>Heredity</i> , 2018, 121, 24-37.	2.6	68
32	The Biotechnology Roadmap for Sugarcane Improvement. <i>Tropical Plant Biology</i> , 2010, 3, 75-87.	1.9	62
33	A fully automated pipeline for quantitative genotype calling from next generation sequencing data in autopolyploids. <i>BMC Bioinformatics</i> , 2018, 19, 398.	2.6	62
34	Title is missing!. <i>Euphytica</i> , 2003, 130, 87-99.	1.2	57
35	Genomic Selection with Allele Dosage in <i>Panicum maximum</i> Jacq.. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2463-2475.	1.8	57
36	A genome-wide association study identified loci for yield component traits in sugarcane (<i>Saccharum</i>) Tj ETQq0 0 0 ggBT /Overlock 10 Tf	2.5	54

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37	Multiple interval QTL mapping and searching for PSTOL1 homologs associated with root morphology, biomass accumulation and phosphorus content in maize seedlings under low-P. <i>BMC Plant Biology</i> , 2015, 15, 172.	3.6	53
38	Functional markers for gene mapping and genetic diversity studies in sugarcane. <i>BMC Research Notes</i> , 2011, 4, 264.	1.4	51
39	QTL mapping for yield components in a tropical maize population using microsatellite markers. <i>Hereditas</i> , 2008, 145, 194-203.	1.4	49
40	Mapping of angular leaf spot resistance QTL in common bean (<i>Phaseolus vulgaris</i> L.) under different environments. <i>BMC Genetics</i> , 2012, 13, 50.	2.7	48
41	Common bean cultivars and lines interactions with environments. <i>Scientia Agricola</i> , 2004, 61, 169-177.	1.2	46
42	Analysis of genomic and functional RFLP derived markers associated with sucrose content, fiber and yield QTLs in a sugarcane (<i>Saccharum</i> spp.) commercial cross. <i>Euphytica</i> , 2010, 172, 313-327.	1.2	46
43	Mapping of QTLs associated with biological nitrogen fixation traits in soybean. <i>Hereditas</i> , 2013, 150, 17-25.	1.4	45
44	Identification of QTLs associated with citrus resistance to <i>Phytophthora gummosis</i> . <i>Journal of Applied Genetics</i> , 2006, 47, 23-28.	1.9	44
45	An Integrated Molecular Map of Yellow Passion Fruit Based on Simultaneous Maximum-likelihood Estimation of Linkage and Linkage Phases. <i>Journal of the American Society for Horticultural Science</i> , 2008, 133, 35-41.	1.0	44
46	Mapping QTLs for kernel oil content in a tropical maize population. <i>Euphytica</i> , 2004, 137, 251-259.	1.2	43
47	Evaluation of algorithms used to order markers on genetic maps. <i>Heredity</i> , 2009, 103, 494-502.	2.6	41
48	QTL mapping including codominant SNP markers with ploidy level information in a sugarcane progeny. <i>Euphytica</i> , 2016, 211, 1-16.	1.2	39
49	Evidence of Allopolyploidy in <i>Urochloa humidicola</i> Based on Cytological Analysis and Genetic Linkage Mapping. <i>PLoS ONE</i> , 2016, 11, e0153764.	2.5	39
50	Molecular mapping in tropical maize (<i>Zea mays</i> L.) using microsatellite markers. 1. Map construction and localization of loci showing distorted segregation. <i>Hereditas</i> , 2004, 139, 96-106.	1.4	37
51	Accurate genomic prediction of <i>Coffea canephora</i> in multiple environments using whole-genome statistical models. <i>Heredity</i> , 2019, 122, 261-275.	2.6	36
52	Quantitative analysis of race-specific resistance to <i>Colletotrichum lindemuthianum</i> in common bean. <i>Molecular Breeding</i> , 2014, 34, 1313-1329.	2.1	35
53	A novel linkage map of sugarcane with evidence for clustering of retrotransposon-based markers. <i>BMC Genetics</i> , 2012, 13, 51.	2.7	34
54	A model for quantitative trait loci mapping, linkage phase, and segregation pattern estimation for a full-sib progeny. <i>Tree Genetics and Genomes</i> , 2014, 10, 791-801.	1.6	34

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55	Mixed Modeling of Yield Components and Brown Rust Resistance in Sugarcane Families. <i>Agronomy Journal</i> , 2016, 108, 1824-1837.	1.8	34
56	Inheritance of growth habit detected by genetic linkage analysis using microsatellites in the common bean (<i>Phaseolus vulgaris</i> L.). <i>Molecular Breeding</i> , 2011, 27, 549-560.	2.1	33
57	Genetic Architecture of Phosphorus Use Efficiency in Tropical Maize Cultivated in a Low-€ Soil. <i>Crop Science</i> , 2014, 54, 1530-1538.	1.8	33
58	Genetic diversity in cultivated carioca common beans based on molecular marker analysis. <i>Genetics and Molecular Biology</i> , 2011, 34, 88-102.	1.3	32
59	Evidence for Strong Kinship Influence on the Extent of Linkage Disequilibrium in Cultivated Common Beans. <i>Genes</i> , 2019, 10, 5.	2.4	32
60	Genetic Mapping With Allele Dosage Information in Tetraploid <i>Urochloa decumbens</i> (Stapf) R. D. Webster Reveals Insights Into Spittlebug (<i>Notozulia entreriana</i> Berg) Resistance. <i>Frontiers in Plant Science</i> , 2019, 10, 92.	3.6	32
61	Seleção de descritores botânico-agronômicos para caracterização de germoplasma de cupuaçuzeiro. <i>Pesquisa Agropecuária Brasileira</i> , 2003, 38, 807-818.	0.9	31
62	Characterization of rust, early and late leaf spot resistance in wild and cultivated peanut germplasm. <i>Scientia Agricola</i> , 2009, 66, 110-117.	1.2	31
63	Molecular polymorphism and linkage analysis in sweet passion fruit, an outcrossing species. <i>Annals of Applied Biology</i> , 2013, 162, 347-361.	2.5	29
64	Developing a common bean core collection suitable for association mapping studies. <i>Genetics and Molecular Biology</i> , 2015, 38, 67-78.	1.3	29
65	The Relationship between Population Structure and Aluminum Tolerance in Cultivated Sorghum. <i>PLoS ONE</i> , 2011, 6, e20830.	2.5	29
66	Combining ability of inbred lines of maize and stability of their respective single-crosses. <i>Scientia Agricola</i> , 2003, 60, 83-89.	1.2	27
67	High-Resolution Genetic Map and QTL Analysis of Growth-Related Traits of <i>Hevea brasiliensis</i> Cultivated Under Suboptimal Temperature and Humidity Conditions. <i>Frontiers in Plant Science</i> , 2018, 9, 1255.	3.6	27
68	Evaluating genetic relationships between tropical maize inbred lines by means of AFLP profiling. <i>Hereditas</i> , 2004, 140, 24-33.	1.4	26
69	Genotypic characterization of microsatellite markers in broiler and layer selected chicken lines and their reciprocal F1s. <i>Scientia Agricola</i> , 2009, 66, 150-158.	1.2	26
70	Quantitative trait loci analysis of citrus leprosis resistance in an interspecific backcross family of (<i>Citrus reticulata</i> Blanco × <i>C. sinensis</i> L. Osbeck) × <i>C. sinensis</i> L. Osb. <i>Euphytica</i> , 2009, 169, 101-111.	1.2	25
71	Novel Bayesian Networks for Genomic Prediction of Developmental Traits in Biomass Sorghum. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 769-781.	1.8	25
72	A mixed model to multiple harvest-location trials applied to genomic prediction in <i>Coffea canephora</i> . <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	1.6	23

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73	Gene Duplication in the Sugarcane Genome: A Case Study of Allele Interactions and Evolutionary Patterns in Two Genic Regions. <i>Frontiers in Plant Science</i> , 2019, 10, 553.	3.6	23
74	Sugarcane Underground Organs: Going Deep for Sustainable Production. <i>Tropical Plant Biology</i> , 2011, 4, 22-30.	1.9	22
75	QTL mapping and identification of corresponding genomic regions for black pod disease resistance to three <i>Phytophthora</i> species in <i>Theobroma cacao</i> L.. <i>Euphytica</i> , 2018, 214, 1.	1.2	22
76	Novel strategies for genomic prediction of untested single-cross maize hybrids using unbalanced historical data. <i>Theoretical and Applied Genetics</i> , 2020, 133, 443-455.	3.6	22
77	High-Resolution Linkage Map With Allele Dosage Allows the Identification of Regions Governing Complex Traits and Apospory in Guinea Grass (<i>Megathyrsus maximus</i>). <i>Frontiers in Plant Science</i> , 2020, 11, 15.	3.6	22
78	Comparaçãõ de Índices de seleçãõ nãõ paramã©tricos para a seleçãõ de cultivares. <i>Bragantia</i> , 1999, 58, 253-267.	1.3	22
79	Influênciã do sistema de criaçãõ sobre o desempenho, a condiçãõ fisiol³gica e o comportamento de linhagens de frangos para corte. <i>Revista Brasileira De Zootecnia</i> , 2003, 32, 208-213.	0.8	20
80	Linkage Disequilibrium and Population Structure in Wild and Cultivated Populations of Rubber Tree (<i>Hevea brasiliensis</i>). <i>Frontiers in Plant Science</i> , 2018, 9, 815.	3.6	20
81	Multi-trait multi-environment quantitative trait loci mapping for a sugarcane commercial cross provides insights on the inheritance of important traits. <i>Molecular Breeding</i> , 2015, 35, 175.	2.1	19
82	QTL detection for growth and latex production in a full-sib rubber tree population cultivated under suboptimal climate conditions. <i>BMC Plant Biology</i> , 2018, 18, 223.	3.6	18
83	Improving yield and fruit quality traits in sweet passion fruit: Evidence for genotype by environment interaction and selection of promising genotypes. <i>PLoS ONE</i> , 2020, 15, e0232818.	2.5	16
84	Boosting predictive ability of tropical maize hybrids via genotypeã©byã©environment interaction under multivariate GBLUP models. <i>Crop Science</i> , 2020, 60, 3049-3065.	1.8	15
85	Marker-trait association and epistasis for brown rust resistance in sugarcane. <i>Euphytica</i> , 2015, 203, 533-547.	1.2	13
86	Estimation of Molecular Pairwise Relatedness in Autopolyploid Crops. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 4579-4589.	1.8	11
87	Angular Leaf Spot Resistance Loci Associated With Different Plant Growth Stages in Common Bean. <i>Frontiers in Plant Science</i> , 2021, 12, 647043.	3.6	11
88	Development of a genetic linkage map of rubber tree (<i>Hevea brasiliensis</i>) based on microsatellite markers. <i>BMC Proceedings</i> , 2011, 5, .	1.6	10
89	Alocaçãõ de linhagens de milho derivadas das populaçãões BR-105 e BR-106 em grupos heterã³ticos. <i>Scientia Agricola</i> , 2001, 58, 541-548.	1.2	9
90	Genetic Variability, Correlation among Agronomic Traits, and Genetic Progress in a Sugarcane Diversity Panel. <i>Agriculture (Switzerland)</i> , 2021, 11, 533.	3.1	9

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91	Leveraging probability concepts for cultivar recommendation in multi-environment trials. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1385-1399.	3.6	8
92	The Sweet Passion Fruit (<i>Passiflora alata</i>) Crop: Genetic and Phenotypic Parameter Estimates and QTL Mapping for Fruit Traits. <i>Tropical Plant Biology</i> , 2017, 10, 18-29.	1.9	7
93	A first genetic map of <i>Acca sellowiana</i> based on ISSR, AFLP and SSR markers. <i>Scientia Horticulturae</i> , 2014, 169, 138-146.	3.6	6
94	Ascertainment bias from imputation methods evaluation in wheat. <i>BMC Genomics</i> , 2016, 17, 773.	2.8	5
95	New Developments in Sugarcane Genetics and Genomics. , 2017, , 159-174.		5
96	A molecular linkage map for <i>Drosophila mediopunctata</i> confirms synteny with <i>Drosophila melanogaster</i> and suggests a region that controls the variation in the number of abdominal spots. <i>Insect Molecular Biology</i> , 2012, 21, 89-95.	2.0	4
97	Genomic Selection: State of the Art. , 2017, , 19-54.		4
98	Comparison of different selection methods in the seedling stage of sugarcane breeding. <i>Agronomy Journal</i> , 2020, 112, 4879-4897.	1.8	4
99	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. <i>Genetics and Molecular Research</i> , 2010, 9, 1357-1376.	0.2	4
100	Genetic mapping reveals complex architecture and candidate genes involved in common bean response to <i>Meloidogyne incognita</i> infection. <i>Plant Genome</i> , 2022, 15, e20161.	2.8	4
101	Genome-wide association studies dissect the genetic architecture of seed shape and size in common bean. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	4
102	Significance of linkage disequilibrium and epistasis on genetic variances in noninbred and inbred populations. <i>BMC Genomics</i> , 2022, 23, 286.	2.8	4
103	Phenotypic recurrent selection to improve protein quality in non-opaque maize populations. <i>Scientia Agricola</i> , 2002, 59, 743-748.	1.2	3
104	Decomposição ortogonal de graus de liberdade de tratamentos utilizando variáveis auxiliares e o PROC GLM do SAS. <i>Bragantia</i> , 2005, 64, 157-167.	1.3	3
105	Construction of a High-Density Genetic Map of <i>Acca sellowiana</i> (Berg.) Burret, an Outcrossing Species, Based on Two Connected Mapping Populations. <i>Frontiers in Plant Science</i> , 2021, 12, 626811.	3.6	3
106	QTL mapping for bioenergy traits in sweet sorghum recombinant inbred lines. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	3
107	Regiões genômicas associadas a características de desempenho e carcaça no cromossomo 5 de linhagens Brasileiras de galinha. <i>Pesquisa Agropecuária Brasileira</i> , 2011, 46, 229-238.	0.9	2
108	Composite interval mapping and mixed models reveal QTL associated with performance and carcass traits on chicken chromosomes 1, 3, and 4. <i>Journal of Applied Genetics</i> , 2014, 55, 97-103.	1.9	1

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109	Compara��o dos algoritmos delinea��o r�pida em cadeia e serializa��o, para a constru��o de mapas gen�ticos. Pesquisa Agropecuaria Brasileira, 2008, 43, 505-512.	0.9	1
110	Allele expression biases in mixed-ploid sugarcane accessions. Scientific Reports, 2022, 12, .	3.3	1