

Efficient Control of Population Structure in Model Orga

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Quantitative Trait Loci for Hypercalciuria in a Rat Model of Kidney Stone Disease. <i>Journal of the American Society of Nephrology: JASN</i> , 2003, 14, 1844-1850.	3.0	42
2	Multivariate analyses reveal common and drug-specific genetic influences on responses to four drugs of abuse. <i>Trends in Pharmacological Sciences</i> , 2008, 29, 537-543.	4.0	23
3	High-Resolution Mapping of Gene Expression Using Association in an Outbred Mouse Stock. <i>PLoS Genetics</i> , 2008, 4, e1000149.	1.5	53
4	Phylogenetic Dependency Networks: Inferring Patterns of CTL Escape and Codon Covariation in HIV-1 Gag. <i>PLoS Computational Biology</i> , 2008, 4, e1000225.	1.5	116
5	Accurate Discovery of Expression Quantitative Trait Loci Under Confounding From Spurious and Genuine Regulatory Hotspots. <i>Genetics</i> , 2008, 180, 1909-1925.	1.2	136
6	A semiparametric test to detect associations between quantitative traits and candidate genes in structured populations. <i>Bioinformatics</i> , 2008, 24, 2356-2362.	1.8	9
7	Identifying genetic components of drug response in mice. <i>Pharmacogenomics</i> , 2008, 9, 1323-1330.	0.6	2
8	A Multiparent Advanced Generation Inter-Cross to Fine-Map Quantitative Traits in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2009, 5, e1000551.	1.5	554
9	Association Mapping: Critical Considerations Shift from Genotyping to Experimental Design. <i>Plant Cell</i> , 2009, 21, 2194-2202.	3.1	786
10	Nonmetric Multidimensional Scaling Corrects for Population Structure in Association Mapping With Different Sample Types. <i>Genetics</i> , 2009, 182, 875-888.	1.2	102
11	Software engineering the mixed model for genome-wide association studies on large samples. <i>Briefings in Bioinformatics</i> , 2009, 10, 664-675.	3.2	96
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14	FastMap: Fast eQTL mapping in homozygous populations. <i>Bioinformatics</i> , 2009, 25, 482-489.	1.8	35
15	Recombinational Landscape and Population Genomics of <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2009, 5, e1000419.	1.5	381
16	Genetic Architecture of Tameness in a Rat Model of Animal Domestication. <i>Genetics</i> , 2009, 182, 541-554.	1.2	111
17	Identification of <i>Las2</i> , a Major Modifier Gene Affecting the <i>Pas1</i> Mouse Lung Tumor Susceptibility Locus. <i>Cancer Research</i> , 2009, 69, 6290-6298.	0.4	6
18	Searching genetic risk factors for schizophrenia and bipolar disorder: learn from the past and back to the future. <i>Human Mutation</i> , 2009, 30, 1139-1152.	1.1	49

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19	An experimental assessment of in silico haplotype association mapping in laboratory mice. <i>BMC Genetics</i> , 2009, 10, 81.	2.7	19
20	Detection and interpretation of expression quantitative trait loci (eQTL). <i>Methods</i> , 2009, 48, 265-276.	1.9	115
22	Association Studies Identify Natural Variation at <i>PHYC</i> Linked to Flowering Time and Morphological Variation in Pearl Millet. <i>Genetics</i> , 2009, 182, 899-910.	1.2	80
23	Analytical Approaches and Population Types for Finding and Utilizing QTL in Complex Plant Populations. <i>Crop Science</i> , 2009, 49, 363-380.	0.8	53
24	Population Structure and Cryptic Relatedness in Genetic Association Studies. <i>Statistical Science</i> , 2009, 24, .	1.6	372
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28	Serious limitations of the QTL/Microarray approach for QTL gene discovery. <i>BMC Biology</i> , 2010, 8, 96.	1.7	29
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30	Genetic variants cis-regulating <i>Xrn2</i> expression contribute to the risk of spontaneous lung tumor. <i>Oncogene</i> , 2010, 29, 1041-1049.	2.6	26
31	Genome-wide association study of 107 phenotypes in <i>Arabidopsis thaliana</i> inbred lines. <i>Nature</i> , 2010, 465, 627-631.	13.7	1,651
32	Mixed linear model approach adapted for genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 355-360.	9.4	2,022
33	Variance component model to account for sample structure in genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 348-354.	9.4	2,287
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52	Genome-wide association mapping reveals a rich genetic architecture of complex traits in <i>Oryza sativa</i> . <i>Nature Communications</i> , 2011, 2, 467.	5.8	1,230
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55	Voxelwise gene-wide association study (vGeneWAS): Multivariate gene-based association testing in 731 elderly subjects. <i>NeuroImage</i> , 2011, 56, 1875-1891.	2.1	116
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66	The Genetics of Winterhardiness in Barley: Perspectives from Genome-wide Association Mapping. <i>Plant Genome</i> , 2011, 4, .	1.6	62
67	Dark Matter: Are Mice the Solution to Missing Heritability?. <i>Frontiers in Genetics</i> , 2011, 2, 32.	1.1	49
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69	Association Study of Resistance to <i>Soilborne wheat mosaic virus</i> in U.S. Winter Wheat. <i>Phytopathology</i> , 2011, 101, 1322-1329.	1.1	15
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87	Gene networks associated with conditional fear in mice identified using a systems genetics approach. <i>BMC Systems Biology</i> , 2011, 5, 43.	3.0	71
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90	Altered Structural Brain Connectivity in Healthy Carriers of the Autism Risk Gene, <i>CNTNAP2</i> . <i>Brain Connectivity</i> , 2011, 1, 447-459.	0.8	98
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112	A Genome-Wide Association Study Identifies Variants Underlying the Arabidopsis thaliana Shade Avoidance Response. PLoS Genetics, 2012, 8, e1002589.	1.5	95
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132	Genetic control of susceptibility to infection with <i>Plasmodium chabaudi chabaudi</i> AS in inbred mouse strains. <i>Genes and Immunity</i> , 2012, 13, 155-163.	2.2	25
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145	Genome-Wide Association and Fine Mapping of Genetic Loci Predisposing to Colon Carcinogenesis in Mice. <i>Molecular Cancer Research</i> , 2012, 10, 66-74.	1.5	24
146	Genetics of Climate Change Adaptation. <i>Annual Review of Genetics</i> , 2012, 46, 185-208.	3.2	365
147	Robustness of Bayesian Multilocus Association Models to Cryptic Relatedness. <i>Annals of Human Genetics</i> , 2012, 76, 510-523.	0.3	31

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154	Genetic adaptation to high altitude in the Ethiopian highlands. <i>Genome Biology</i> , 2012, 13, R1.	13.9	327
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164	A mixed-model approach for genome-wide association studies of correlated traits in structured populations. <i>Nature Genetics</i> , 2012, 44, 1066-1071.	9.4	380
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167	Rapid variance components-based method for whole-genome association analysis. <i>Nature Genetics</i> , 2012, 44, 1166-1170.	9.4	193
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171	Genome-wide association mapping of flowering time and northern corn leaf blight (<i>Setosphaeria</i>) Tj ETQq1 1 0.784314 rgBT /Overloc	1.6	70
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188	A Candidate-Gene Association Study for Berry Colour and Anthocyanin Content in <i>Vitis vinifera</i> L.. <i>PLoS ONE</i> , 2012, 7, e46021.	1.1	35
189	Genome-Wide Association Study Heterogeneous Cohort Homogenization via Subject Weight Knock-Down. <i>PLoS ONE</i> , 2012, 7, e48653.	1.1	1
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498	Mapping small-effect and linked quantitative trait loci for complex traits in backcross or DH populations via a multi-locus GWAS methodology. <i>Scientific Reports</i> , 2016, 6, 29951.	1.6	51
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522	Molecular, genetic and evolutionary analysis of a paracentric inversion in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2016, 88, 159-178.	2.8	81
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559	Statistical Analysis of GWAS. <i>Computational Biology</i> , 2016, , 105-161.	0.1	0
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564	Sporadic, Global Linkage Disequilibrium Between Unlinked Segregating Sites. <i>Genetics</i> , 2016, 202, 427-437.	1.2	18
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604	Genome-wide Association Studies in Maize: Praise and Stargaze. <i>Molecular Plant</i> , 2017, 10, 359-374.	3.9	334
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618	From Hype to Hope: Genome-Wide Association Studies in Soybean. <i>Compendium of Plant Genomes</i> , 2017, , 95-109.	0.3	0
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641	Multiplex confounding factor correction for genomic association mapping with squared sparse linear mixed model. , 2017, , .		0
642	A unified framework for variance component estimation with summary statistics in genome-wide association studies. <i>Annals of Applied Statistics</i> , 2017, 11, 2027-2051.	0.5	98
643	Mathematical and Statistical Applications in Life Sciences and Engineering. , 2017, , .		0
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647	Association Mapping Reveals Novel Genetic Loci Contributing to Flooding Tolerance during Germination in Indica Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 678.	1.7	53
648	Genetic Architecture of Anther Extrusion in Spring and Winter Wheat. <i>Frontiers in Plant Science</i> , 2017, 8, 754.	1.7	53
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