Resource Summary Report

Generated by SPARC SAWG on Sep 12, 2026

QUANTO

RRID:SCR_009084
Type: Tool

Proper Citation

QUANTO (RRID:SCR_009084)

Resource Information

URL: http://hydra.usc.edu/GxE

Proper Citation: QUANTO (RRID:SCR_009084)

Description: Software program that computes sample size or power for association studies of genes, environmental factors, gene-environment interaction, or gene-gene interaction. Available study designs for a disease (binary) outcome include the unmatched case-control, matched case-control, case-sibling, case-parent, and case-only designs. Study designs for a quantitative tra it include independent individuals and case parent designs. Quanto is a 32-bit Windows application requiring Windows 95, 98, NT, 2000, ME or XP to run. The graphical user interface allows th e user to easily change the model and view the results without having to edit an input file and rerun the program for every model. The results of a session are stored to a log file. This log can be printed or saved to a file for reviewing at a later date. An option is included to create a text file of the log that can be imported into other documents. (entry from Genetic Analysis Software)

Abbreviations: QUANTO

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, c++, ms-windows, (98/nt/2000/..)

Resource Name: QUANTO

Resource ID: SCR_009084

Alternate IDs: nlx_154095

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260912T200240+0000

Ratings and Alerts

No rating or validation information has been found for QUANTO.

No alerts have been found for QUANTO.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 927 mentions in open access literature.

Listed below are recent publications. The full list is available at SPARC SAWG .

Nacer NE, et al. (2026) Population-Specific Exploration of MIR146A Gene Polymorphism in Acute Renal Rejection: A Cross-Sectional, Case-Control Study. International journal of molecular sciences, 27(11).

Fu Y, et al. (2026) GP6 polymorphisms and venous thromboembolism: a Chinese case-control study with cross-population assessment. BMC cardiovascular disorders, 26(1), 110.

Park YC, et al. (2026) Regular exercise modifies the effects of 12 LDL-C SNPs on cardiovascular disease risk: KoGES. Lipids in health and disease, 25(1).

Gilyazova I, et al. (2026) MicroRNA Biogenesis Pathway Gene Variants Are Associated with Prostate Cancer Susceptibility. International journal of molecular sciences, 27(12).

Fang Z, et al. (2026) Association between MEF2A variants and ischemic stroke risk: a case-control study and two prospective cohort studies in a Chinese population. BMC cardiovascular disorders, 26(1), 172.

Naaman C, et al. (2026) Mapping shared genetic determinants of eGFR and albuminuria with a focus on type 2 diabetes: a large-scale European study. BMJ open diabetes research & care, 14(3).

Ma X, et al. (2026) Research note: An Adaptive Lasso-based genome-wide association study of blood and meat spots in chicken eggs. Poultry science, 105(5), 106639.

Vollenbrock CE, et al. (2026) Association of genetic variation with age at diagnosis in type 1 diabetes. BMJ open diabetes research & care, 14(1).

Churnosov V, et al. (2026) BMI-Dependent Correlations of Sex Hormone Genes with Simple Endometrial Hyperplasia. Life (Basel, Switzerland), 16(6).

Yang Y, et al. (2026) m6A-SNPs identified by integrating genomic data are associated with the occurrence and prognosis of HCC. Scientific reports, 16(1).

Chor??ziak-Michalak A, et al. (2025) Association of endothelial nitric oxide synthase (NOS3) rs2070744 variant with advanced retinopathy of prematurity: a case-control study

and meta-analysis. Scientific reports, 15(1), 329.

Gauderman WJ, et al. (2025) Pathway polygenic risk scores (pPRS) for the analysis of gene-environment interaction. PLoS genetics, 21(8), e1011543.

Afzal MU, et al. (2025) Investigating the role of genetic variations of ABCB1 (rs1045642) and CYP7A1 (rs3808607) genes on serum lipid level among Malaysian male patients treated with atorvastatin. Saudi medical journal, 46(8), 898.

Han Y, et al. (2025) Genome-wide analysis identifies susceptibility loci for heart failure and nonischemic cardiomyopathy subtype in the East Asian populations. PLoS genetics, 21(10), e1011897.

Cabrera-Serrano AJ, et al. (2025) Identification of 4 autophagy-related genetic variants as risk factors for chronic lymphocytic leukemia. Blood advances, 9(23), 6076.

Yoshikawa A, et al. (2025) Genetic markers of early response to lurasidone in acute schizophrenia. The pharmacogenomics journal, 25(2), 3.

Bidi S, et al. (2025) Association of SLC14A1C/T Polymorphisms in Patients with Bladder Cancer in Comparison with Healthy Controls. South Asian journal of cancer, 14(4), 810.

Zimmermann FB, et al. (2025) Association between Cardiovascular Risk Factors and Carotid Plaques in a Population-Based Study - The SHIP-Brazil Study. Arquivos brasileiros de cardiologia, 122(3), e20240546.

Durska A, et al. (2025) Association of ACE and AGTR1 variants with retinopathy of prematurity: a case-control study and meta-analysis. Journal of applied genetics, 66(4), 911.

Nyamupangedengu K, et al. (2025) Genetic Variation in Hydrochlorothiazide Response-Related Genes Among Hypertensive Individuals in Soweto, South Africa. Clinical and translational science, 18(7), e70302.