Resource Summary Report

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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 resource, software application

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: 20260731T042806+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 915 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

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.

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.

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.

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

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.

Standl M, et al. (2025) Gene-Environment Interaction Affects Risk of Atopic Eczema: Population and In Vitro Studies. Allergy, 80(8), 2201.

Zeng Q, et al. (2025) MTNR1B variants increase gestational diabetes mellitus risk in young Chinese pregnant women. Scientific reports, 15(1), 19643.

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.

Standl M, et al. (2025) Gene-environment interaction analysis in atopic eczema: evidence from large population datasets and modelling in vitro. medRxiv : the preprint server for health sciences.

Guad RM, et al. (2025) Association of intercellular adhesion molecule 1 (ICAM-1) (rs5498) genetic polymorphism and dengue in Sabah East Malaysia population. Molecular biology reports, 53(1), 138.

Li N, et al. (2025) Association of maternal VDR and VDBP gene polymorphisms with spontaneous preterm birth risks: a nested case-control study in China. BMC pregnancy and childbirth, 26(1), 18.

Bidi SR, et al. (2025) Association of rs2294008 (PSCA) Gene polymorphism in Urothelial Bladder Cancer of South Indian Population. Asian Pacific journal of cancer prevention : APJCP, 26(4), 1441.

Rosa-Baez C, et al. (2025) Assessing the MUC5B promoter variant in a large cohort of systemic sclerosis-associated interstitial lung disease. RMD open, 11(3).

Liu X, et al. (2025) Gene polymorphisms of miR-323b and miR-1343 that regulate kininogen L are associated with schizophrenia susceptibility: A preliminary population? based study. Biomolecules & biomedicine, 25(6), 1293.

Chmielarz-Czarnoci?ska A, et al. (2025) Association of the ADRB2 rs1042714 variant with retinopathy of prematurity highlights the importance of the renin-angiotensin-aldosterone system. Scientific reports, 15(1), 11232.

Sharif M, et al. (2025) Effect of genetic polymorphism of rosuvastatin transporter gene rs2231137 on its clinical efficacy and safety. Scientific reports, 15(1), 38811.

Al-Barazenji T, et al. (2025) Association Between Vitamin D Receptor BsmI Polymorphism and Low Bone Mineral Density in Postmenopausal Women in the MENA Region. Pathophysiology : the official journal of the International Society for Pathophysiology, 32(1).