Resource Summary Report

Generated by dkNET on Apr 16, 2025

QUANTO

RRID:SCR_009084
Type: Tool

Proper Citation

QUANTO (RRID:SCR_009084)

Resource Information

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

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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/..)

Funding:

Resource Name: QUANTO

Resource ID: SCR_009084

Alternate IDs: nlx_154095

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250416T063536+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 894 mentions in open access literature.

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

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.

Lara LDS, et al. (2024) Exploring the role of the WNT5A rs566926 polymorphism and its interactions in non-syndromic orofacial cleft: a multicenter study in Brazil. Journal of applied oral science : revista FOB, 32, e20230353.

Alves de Oliveira H, et al. (2024) Impact of genetic background as a risk factor for atherosclerotic cardiovascular disease: A protocol for a nationwide genetic case-control (CV-GENES) study in Brazil. PloS one, 19(3), e0289439.

Lv S, et al. (2024) Association of RIPK1 and RIPK2 Gene Polymorphisms with Rheumatoid Arthritis in a Chinese Han Population. The application of clinical genetics, 17, 159.

Patel RS, et al. (2024) Estrogen Receptor 1 Gene Polymorphism and its Association with Idiopathic Short Stature in a North Indian Population. Journal of clinical research in pediatric endocrinology, 16(3), 279.

Lin F, et al. (2024) Replication of previous autism-GWAS hits suggests the association between NAA1, SORCS3, and GSDME and autism in the Han Chinese population. Heliyon, 10(1), e23677.

Uittenbogaard P, et al. (2024) FCGR2/3 polymorphisms are associated with susceptibility to Kawasaki disease but do not predict intravenous immunoglobulin resistance and coronary artery aneurysms. Frontiers in immunology, 15, 1323171.

Song J, et al. (2024) Variants in PPARD-GLP1R are related to diabetic kidney disease in Chinese Han patients with type 2 diabetes mellitus. Heliyon, 10(15), e35289.

Errigo A, et al. (2024) Lack of association between common polymorphisms associated with successful aging and longevity in the population of Sardinian Blue Zone. Scientific reports, 14(1), 30773.

Quansah E, et al. (2024) Low nucleotide diversity of the Plasmodium falciparum AP2-EXP2 gene among clinical samples from Ghana. Parasites & vectors, 17(1), 453.

Liang P, et al. (2024) Association between Mir-17-92 gene promoter polymorphisms and depression in a Chinese population. BMC medical genomics, 17(1), 123.

Kim J, et al. (2024) Consumption of dietary fiber and APOA5 genetic variants in metabolic syndrome: baseline data from the Korean Medicine Daejeon Citizen Cohort Study. Nutrition & metabolism, 21(1), 19.

Pereira DA, et al. (2024) Functional polymorphisms of NOS3 and GUCY1A3 affect both nitric oxide formation and association with hypertensive disorders of pregnancy. Frontiers in genetics, 15, 1293082.

Paniri A, et al. (2024) Genetic variations in IKZF3, LET7-a2, and CDKN2B-AS1: Exploring associations with metabolic syndrome susceptibility and clinical manifestations. Journal of clinical laboratory analysis, 38(1-2), e24999.

Upmale-Engela S, et al. (2024) Genetic and Environmental Factors in Autoimmune Thyroid Disease: Exploring Associations with Selenium Levels and Novel Loci in a Latvian Cohort. Current issues in molecular biology, 46(3), 2553.

Peng X, et al. (2024) Peripheral amyloid-? clearance mediates cognitive impairment in non-alcoholic fatty liver disease. EBioMedicine, 102, 105079.

Novakov V, et al. (2024) Polymorphism rs143384 GDF5 reduces the risk of knee osteoarthritis development in obese individuals and increases the disease risk in non-obese population. Arthroplasty (London, England), 6(1), 12.

Wuni R, et al. (2024) Interaction between genetic risk score and dietary fat intake on lipid-related traits in Brazilian young adults. The British journal of nutrition, 132(5), 575.

León-Reyes G, et al. (2023) Interaction between SIDT2 and ABCA1 Variants with Nutrients on HDL-c Levels in Mexican Adults. Nutrients, 15(2).

Han JM, et al. (2023) Association between SLCO1B1 genetic polymorphisms and bleeding risk in patients treated with edoxaban. Scientific reports, 13(1), 15967.