# Resource Summary Report

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## QTDT

RRID:SCR_013391
Type: Tool

### Proper Citation

QTDT (RRID:SCR_013391)

### Resource Information

**URL:** http://csg.sph.umich.edu//abecasis/QTDT/

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**Description:** Software application that performs linkage disequilibrium (TDT) and association analysis for quantitative traits. Includes support for the methods of Abecasis et al. (2000), Fulker et al. (1999), Monks et al. (1998), Allison (TDTQ5, 1997) and Rabinowitz (1997). Supports families of any size, with or without parental information. Includes simple variance components modelling. Interfaces with SimWalk2 for IBD estimation. (entry from Genetic Analysis Software)

**Abbreviations:** QTDT

**Synonyms:** Quantitative (Trait) Transmission/Disequilibrium Test

**Resource Type:** software resource, software application

**Keywords:** gene, genetic, genomic, c++, unix, solaris, linux, ms-windows

**Funding:**

**Resource Name:** QTDT

**Resource ID:** SCR_013391

**Alternate IDs:** nlx_154101

**Record Creation Time:** 20220129T080315+0000

**Record Last Update:** 20250416T063641+0000

## Ratings and Alerts

No rating or validation information has been found for QTDT.

No alerts have been found for QTDT.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 34 mentions in open access literature.

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


Cretin J, et al. (2023) A Non-Coding Fc Gamma Receptor Cis-Regulatory Variant within the 1q23 Gene Cluster Is Associated with Plasmodium falciparum Infection in Children Residing in Burkina Faso. International journal of molecular sciences, 24(21).

Qi L, et al. (2021) The rs1634330 Polymorphisms in the SOST Gene Are Associated with Body Composition in Chinese Nuclear Families with Male Offspring. International journal of endocrinology, 2021, 6698822.

McGurk KA, et al. (2020) Heritability of haemodynamics in the ascending aorta. Scientific reports, 10(1), 14356.

Nudel R, et al. (2020) Quantitative genome-wide association analyses of receptive language in the Danish High Risk and Resilience Study. BMC neuroscience, 21(1), 30.

Nersisyan L, et al. (2019) WGS-based telomere length analysis in Dutch family trios implicates stronger maternal inheritance and a role for RRM1 gene. Scientific reports, 9(1), 18758.

Dwivedi OP, et al. (2019) Loss of ZnT8 function protects against diabetes by enhanced insulin secretion. Nature genetics, 51(11), 1596.

Nethononda RM, et al. (2019) Marked variation in heritability estimates of left ventricular mass depending on modality of measurement. Scientific reports, 9(1), 13556.

Ashton DT, et al. (2019) High-Density Linkage Map and QTLs for Growth in Snapper (Chrysophrys auratus). G3 (Bethesda, Md.), 9(4), 1027.

Tremblay BL, et al. (2018) Familial resemblances in human whole blood transcriptome. BMC genomics, 19(1), 300.

Tremblay BL, et al. (2018) Genetic and Common Environmental Contributions to Familial

Resemblances in Plasma Carotenoid Concentrations in Healthy Families. Nutrients, 10(8).

Sarnowski C, et al. (2018) Investigation of parent-of-origin effects induced by fenofibrate treatment on triglycerides levels. BMC genetics, 19(Suppl 1), 83.

Wang S, et al. (2017) Rs12970134 near MC4R is associated with appetite and beverage intake in overweight and obese children: A family-based association study in Chinese population. PloS one, 12(5), e0177983.

Shakhbazov K, et al. (2016) Shared genetic control of expression and methylation in peripheral blood. BMC genomics, 17, 278.

Pettigrew KA, et al. (2016) Further evidence for a parent-of-origin effect at the NOP9 locus on language-related phenotypes. Journal of neurodevelopmental disorders, 8, 24.

Pinto R, et al. (2016) Testing for the mediating role of endophenotypes using molecular genetic data in a twin study of ADHD traits. American journal of medical genetics. Part B, Neuropsychiatric genetics : the official publication of the International Society of Psychiatric Genetics, 171(7), 982.

Chen G, et al. (2015) Aggregate blood pressure responses to serial dietary sodium and potassium intervention: defining responses using independent component analysis. BMC genetics, 16, 64.

Anderson D, et al. (2015) First genome-wide association study in an Australian aboriginal population provides insights into genetic risk factors for body mass index and type 2 diabetes. PloS one, 10(3), e0119333.

Marioni RE, et al. (2015) DNA methylation age of blood predicts all-cause mortality in later life. Genome biology, 16(1), 25.

Hochner H, et al. (2015) Parent-of-Origin Effects of the APOB Gene on Adiposity in Young Adults. PLoS genetics, 11(10), e1005573.

Jaiswal P, et al. (2015) SLC6A4 markers modulate platelet 5-HT level and specific behaviors of autism: a study from an Indian population. Progress in neuro-psychopharmacology & biological psychiatry, 56, 196.