

Resource Summary Report

Generated by T1D on Aug 1, 2026

QUTIE

RRID:SCR_009098

Type: Tool

Proper Citation

QUTIE (RRID:SCR_009098)

Resource Information

URL: <http://www.sanger.ac.uk/resources/software/rarevariant/>

Proper Citation: QUTIE (RRID:SCR_009098)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on May 16,2023. Software application for enabling the analysis of rare variants in large-scale case control and quantitative trait association studies. CCRaVAT (Case-Control Rare Variant Analysis Tool) and QuTie (Quantitative Trait) are software packages that enable efficient large-scale analysis of rare variants across specific regions or genome-wide. These programs implement a rare variant super-locus or collapsing method that investigates the accumulation of rare variant alleles in either a case-control or quantitative trait study design. (entry from Genetic Analysis Software)

Abbreviations: QUTIE

Synonyms: Case-Control RAre Variant Analysis Tool CCRAVAT

Resource Type: software resource, software application

Keywords: gene, genetic, genomic

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: QUTIE

Resource ID: SCR_009098

Alternate IDs: nlx_154191

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260731T042759+0000

Ratings and Alerts

No rating or validation information has been found for QUTIE.

No alerts have been found for QUTIE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Moutsianas L, et al. (2014) Methodology for the analysis of rare genetic variation in genome-wide association and re-sequencing studies of complex human traits. *Briefings in functional genomics*, 13(5), 362.