

Resource Summary Report

Generated by [dkNET](#) on Aug 18, 2026

powereQTL

RRID:SCR_021653

Type: Tool

Proper Citation

powereQTL (RRID:SCR_021653)

Resource Information

URL: <https://bwhbioinfo.shinyapps.io/powerEQTL/>

Proper Citation: powereQTL (RRID:SCR_021653)

Description: Software R package and shiny application for sample size and power calculation of bulk tissue and single-cell eQTL analysis.

Resource Type: data processing software, software resource, data analytics software, data analysis software, software toolkit, software application

Defining Citation: [DOI:10.1093/bioinformatics/btab385](https://doi.org/10.1093/bioinformatics/btab385)

Keywords: sample size calculation, bulk tissue, calculation, single-cell eQTL analysis

Funding: NINDS U01 NS120637;
American Parkinson Disease Association ;
NINDS R01 NS115144;
NINDS U01 NS095736;
NINDS U01 NS10 0603;
Michael J. Fox Foundation for Parkinson Research

Availability: Free, Available for download, Freely available

Resource Name: powereQTL

Resource ID: SCR_021653

Alternate URLs: <https://cran.r-project.org/web/packages/powerEQTL/index.html>,
<https://github.com/sterding/powerEQTL>

License: GPL v3

Record Creation Time: 20220129T080356+0000

Record Last Update: 20260818T043653+0000

Ratings and Alerts

No rating or validation information has been found for powereQTL.

No alerts have been found for powereQTL.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Tutino M, et al. (2025) Genetics of circulating proteins in newborn babies at high risk of type 1 diabetes. Nature communications, 16(1), 3750.

Cote AC, et al. (2024) Critical reasoning on the co-expression module QTL in the dorsolateral prefrontal cortex. HGG advances, 5(3), 100311.

Dong X, et al. (2021) powerEQTL: an R package and shiny application for sample size and power calculation of bulk tissue and single-cell eQTL analysis. Bioinformatics (Oxford, England), 37(22), 4269.