

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

[QCGWAS](#)

RRID:SCR_006408

Type: Tool

Proper Citation

QCGWAS (RRID:SCR_006408)

Resource Information

URL: <http://cran.r-project.org/web/packages/QCGWAS/>

Proper Citation: QCGWAS (RRID:SCR_006408)

Description: Software tools for (automated and manual) quality control of the results of Genome Wide Association Studies.

Abbreviations: QCGWAS

Synonyms: QCGWAS: Quality Control of Genome Wide Association Study results, Quality Control of Genome Wide Association Study

Resource Type: software resource

Defining Citation: [PMID:24395754](#)

Keywords: quality control, genome wide association study, windows, os x, r, bio.tools

Availability: GNU General Public License, v3 or later

Resource Name: QCGWAS

Resource ID: SCR_006408

Alternate IDs: OMICS_02203, biotools:qcgwas

Alternate URLs: <https://bio.tools/qcgwas>

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260801T190309+0000

Ratings and Alerts

No rating or validation information has been found for QCGWAS.

No alerts have been found for QCGWAS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Flint JP, et al. (2024) Multi-polygenic prediction of frailty highlights chronic pain and educational attainment as key risk and protective factors. medRxiv : the preprint server for health sciences.

Flint JP, et al. (2024) Validation of a polygenic risk score for frailty in the Lothian Birth Cohort 1936 and English longitudinal study of ageing. Scientific reports, 14(1), 12586.

Zhao JH, et al. (2023) Genetics of circulating inflammatory proteins identifies drivers of immune-mediated disease risk and therapeutic targets. Nature immunology, 24(9), 1540.

Flint JP, et al. (2023) Validation of a polygenic risk score for Frailty in the Lothian Birth Cohort and English Longitudinal Study of Ageing. medRxiv : the preprint server for health sciences.

Lahti J, et al. (2022) Genome-wide meta-analyses reveal novel loci for verbal short-term memory and learning. Molecular psychiatry, 27(11), 4419.

Ahluwalia TS, et al. (2021) Genome-wide association study of circulating interleukin 6 levels identifies novel loci. Human molecular genetics, 30(5), 393.

Nolte IM, et al. (2017) Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature communications, 8, 15805.