

Resource Summary Report

Generated by [NIF](#) on Sep 2, 2026

EQTL EXPLORER

RRID:SCR_001123

Type: Tool

Proper Citation

EQTL EXPLORER (RRID:SCR_001123)

Resource Information

URL: <http://web.bioinformatics.ic.ac.uk/eqtlexplorer/>

Proper Citation: EQTL EXPLORER (RRID:SCR_001123)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 23,2022. An eQTL visualization tool that allows users to mine and understand data from a repository of genetical genomics experiments (entry from Genetic Analysis Software)

Abbreviations: EQTL EXPLORER

Resource Type: software application, software resource

Defining Citation: [PMID:16357031](#)

Keywords: gene, genetic, genomic, java

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: EQTL EXPLORER

Resource ID: SCR_001123

Alternate IDs: nlx_154018

Record Creation Time: 20220129T080205+0000

Record Last Update: 20260829T183051+0000

Ratings and Alerts

No rating or validation information has been found for EQTL EXPLORER.

No alerts have been found for EQTL EXPLORER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Pashos EE, et al. (2017) Large, Diverse Population Cohorts of hiPSCs and Derived Hepatocyte-like Cells Reveal Functional Genetic Variation at Blood Lipid-Associated Loci. Cell stem cell, 20(4), 558.

Patnala R, et al. (2013) Candidate gene association studies: a comprehensive guide to useful in silico tools. BMC genetics, 14, 39.