

Resource Summary Report

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eQTL Visualization Tool

RRID:SCR_013413

Type: Tool

Proper Citation

eQTL Visualization Tool (RRID:SCR_013413)

Resource Information

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

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on June 1, 2023. eQTL Explorer was developed as a computational resource to visualize and explore data from combined genome-wide expression and linkage studies is essential for the development of testable hypotheses. This visualization tool stores expression profiles, linkage data and information from external sources in a relational database and enables simultaneous visualization and intuitive interpretation of the combined data via a Java graphical interface. eQTL Explorer also provides a new and powerful tool to interrogate these very large and complex datasets. eQTLExplorer allows users to mine and understand data from a repository of genetical genomics experiments. It will graphically display eQTL information based on a certain number of selection criteria, including: tissue type, p-value, cis/trans, probeset Affymetrix id and PQTL type. Sponsors: This work was funded by the MRC Clinical Sciences Centre and the Wellcome Trust programme for Cardiovascular Functional Genomics.

Synonyms: eQTLExplorer

Resource Type: data visualization software, software application, data processing software, software resource

Keywords: experiment, explore, expression, genome, genetic, genetical, cis, computational, data, database, genomic, grafical, interface, linkage, mine, pqtI type, p-value, repository, tissue, tissue type, trans, visualization, visualize

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: eQTL Visualization Tool

Resource ID: SCR_013413

Alternate IDs: nif-0000-10222

Record Creation Time: 20220129T080316+0000

Record Last Update: 20260801T042717+0000

Ratings and Alerts

No rating or validation information has been found for eQTL Visualization Tool.

No alerts have been found for eQTL Visualization Tool.

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 [kravitz2](#) .

Morrissey C, et al. (2011) Integrated genomic approaches to identification of candidate genes underlying metabolic and cardiovascular phenotypes in the spontaneously hypertensive rat. Physiological genomics, 43(21), 1207.