

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

QTL EXPRESS

RRID:SCR_009350

Type: Tool

Proper Citation

QTL EXPRESS (RRID:SCR_009350)

Resource Information

URL: <http://qtl.cap.ed.ac.uk/>

Proper Citation: QTL EXPRESS (RRID:SCR_009350)

Description: A web-based user-friendly package to map Quantitative Trait Loci in outbred populations. Population structures catered for are line crosses, halfsib families, nuclear families and sibpairs. Permutation tests to determine empirical significance levels and bootstrapping to estimate empirical confidence intervals of QTL locations are optional. Fixed effects/covariates can be fitted and models may include single or multiple QTL. Results are presented in tabular and graphical format. (entry from Genetic Analysis Software)

Abbreviations: QTL EXPRESS

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, java, web-based

Resource Name: QTL EXPRESS

Resource ID: SCR_009350

Alternate IDs: nlx_154565

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260727T040449+0000

Ratings and Alerts

No rating or validation information has been found for QTL EXPRESS.

No alerts have been found for QTL EXPRESS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Khamseh A, et al. (2025) Analysis of HPV-16 viral load, integration status, and p16 expression in relation to EBV co-infection and cervical lesion severity. Scientific reports, 15(1), 8329.

Newbrook K, et al. (2025) Clinical disease in British sheep infected with an emerging strain of bluetongue virus serotype 3. The Veterinary record, 196(4), e4910.

Meng SS, et al. (2023) Anisotropic flexibility and rigidification in a TPE-based Zr-MOFs with scu topology. Nature communications, 14(1), 5347.

Psifidi A, et al. (2016) The genomic architecture of resistance to Campylobacter jejuni intestinal colonisation in chickens. BMC genomics, 17, 293.

Basheer A, et al. (2015) Genetic loci inherited from hens lacking maternal behaviour both inhibit and paradoxically promote this behaviour. Genetics, selection, evolution : GSE, 47, 100.

Choi BH, et al. (2012) Detection of quantitative trait Loci affecting fat deposition traits in pigs. Asian-Australasian journal of animal sciences, 25(11), 1507.

Choi BH, et al. (2012) Porcine LMNA Is a Positional Candidate Gene Associated with Growth and Fat Deposition. Asian-Australasian journal of animal sciences, 25(12), 1649.

Laenoi W, et al. (2011) Quantitative trait loci analysis for leg weakness-related traits in a Duroc × Pietrain crossbred population. Genetics, selection, evolution : GSE, 43(1), 13.

Gutiérrez-Gil B, et al. (2010) Identification of QTL with effects on fatty acid composition of meat in a Charolais x Holstein cross population. Meat science, 85(4), 721.

Ding N, et al. (2009) Genome-wide QTL mapping for three traits related to teat number in a White Duroc x Erhualian pig resource population. BMC genetics, 10, 6.

Mao H, et al. (2008) A genome-wide scan for quantitative trait loci affecting limb bone lengths and areal bone mineral density of the distal femur in a White Duroc x Erhualian F2 population. BMC genetics, 9, 63.

Muráni E, et al. (2006) Molecular characterization and evidencing of the porcine CRH gene as a functional-positional candidate for growth and body composition. Biochemical and biophysical research communications, 342(2), 394.

Siwek M, et al. (2006) Detection of QTL for innate: non-specific antibody levels binding LPS and LTA in two independent populations of laying hens. Developmental and

comparative immunology, 30(7), 659.