

Resource Summary Report

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GRIDQTL

RRID:SCR_013397

Type: Tool

Proper Citation

GRIDQTL (RRID:SCR_013397)

Resource Information

URL: <http://www.gridqtl.org.uk/>

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Description: Publicly available Web-based application that can perform QTL mapping on a variety of population types. GridQTL will extend the functionality of QTLEXPRESS by adding new and advanced approaches for modelling QTL analysis in simple and complex populations. These new methods will be available on a Grid system that will offer flexible workflow management, resource allocation, data persistence, detached execution of simulations and the scalability required for the increase in data volume, data sources and complexity required by the new models. (entry from Genetic Analysis Software)

Abbreviations: GRIDQTL

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, web-based

Availability: Public

Resource Name: GRIDQTL

Resource ID: SCR_013397

Alternate IDs: nlx_154215

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260905T133255+0000

Ratings and Alerts

No rating or validation information has been found for GRIDQTL.

No alerts have been found for GRIDQTL.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 28 mentions in open access literature.

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

Ashton DT, et al. (2019) High-Density Linkage Map and QTLs for Growth in Snapper (*Chrysophrys auratus*). *G3* (Bethesda, Md.), 9(4), 1027.

de Carvalho LR, et al. (2019) Genetic Predisposition to Hepatocarcinogenesis in Inbred and Outbred Mouse Lines Selected for High or Low Inflammatory Response. *Journal of immunology research*, 2019, 5298792.

Cho IC, et al. (2019) A functional regulatory variant of MYH3 influences muscle fiber-type composition and intramuscular fat content in pigs. *PLoS genetics*, 15(10), e1008279.

Jin S, et al. (2018) Identification of quantitative trait loci for the fatty acid composition in Korean native chicken. *Asian-Australasian journal of animal sciences*, 31(8), 1134.

Park HB, et al. (2017) Genome scan linkage analysis identifies a major quantitative trait loci for fatty acid composition in longissimus dorsi muscle in an F2 intercross between Landrace and Korean native pigs. *Asian-Australasian journal of animal sciences*, 30(8), 1061.

Lv W, et al. (2016) QTL variations for growth-related traits in eight distinct families of common carp (*Cyprinus carpio*). *BMC genetics*, 17(1), 65.

Knaust J, et al. (2016) Epistatic interactions between at least three loci determine the "rat-tail" phenotype in cattle. *Genetics, selection, evolution : GSE*, 48, 26.

Jin S, et al. (2016) A Major Locus for Quantitatively Measured Shank Skin Color Traits in Korean Native Chicken. *Asian-Australasian journal of animal sciences*, 29(11), 1555.

Kuang YY, et al. (2016) The genetic map of goldfish (*Carassius auratus*) provided insights to the divergent genome evolutions in the Cyprinidae family. *Scientific reports*, 6, 34849.

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

Babbucci M, et al. (2016) An integrated genomic approach for the study of mandibular prognathism in the European seabass (*Dicentrarchus labrax*). *Scientific reports*, 6, 38673.

Gonen S, et al. (2015) Mapping and validation of a major QTL affecting resistance to pancreas disease (salmonid alphavirus) in Atlantic salmon (*Salmo salar*). *Heredity*, 115(5), 405.

Palti Y, et al. (2015) Detection and Validation of QTL Affecting Bacterial Cold Water Disease Resistance in Rainbow Trout Using Restriction-Site Associated DNA Sequencing. PloS one, 10(9), e0138435.

Johnson JL, et al. (2015) Genotyping-By-Sequencing (GBS) Detects Genetic Structure and Confirms Behavioral QTL in Tame and Aggressive Foxes (*Vulpes vulpes*). PloS one, 10(6), e0127013.

Tsai HY, et al. (2015) The genetic architecture of growth and fillet traits in farmed Atlantic salmon (*Salmo salar*). BMC genetics, 16, 51.

Palaiokostas C, et al. (2015) A novel sex-determining QTL in Nile tilapia (*Oreochromis niloticus*). BMC genomics, 16(1), 171.

Palaiokostas C, et al. (2015) A new SNP-based vision of the genetics of sex determination in European sea bass (*Dicentrarchus labrax*). Genetics, selection, evolution : GSE, 47(1), 68.

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.

Gutierrez AP, et al. (2014) Detection of quantitative trait loci (QTL) related to grilsing and late sexual maturation in Atlantic salmon (*Salmo salar*). Marine biotechnology (New York, N.Y.), 16(1), 103.

Richardson CJ, et al. (2014) Phenotypic and QTL allelic associations among embryonic developmental rate, body size, and precocious maturation in male rainbow trout. Marine genomics, 18 Pt A, 31.