## **Resource Summary Report**

Generated by NIF on Apr 8, 2025

# **GeneCruiser**

RRID:SCR\_003153

Type: Tool

## **Proper Citation**

GeneCruiser (RRID:SCR\_003153)

#### **Resource Information**

**URL:** <a href="http://genecruiser.broadinstitute.org/genecruiser3/">http://genecruiser.broadinstitute.org/genecruiser3/</a>

**Proper Citation:** GeneCruiser (RRID:SCR\_003153)

**Description:** A web service and web application for the annotation of microarray data providing integrated access to genomic information freely available from public data sources.

Abbreviations: GeneCruiser

Resource Type: service resource, data access protocol, software resource, web service

**Defining Citation:** PMID:16030072

**Keywords:** gene, genetic variation, probe, variation, annotation

**Funding:** 

Availability: Acknowledgement requested, Account required

Resource Name: GeneCruiser

Resource ID: SCR\_003153

Alternate IDs: OMICS\_00760

**Record Creation Time:** 20220129T080217+0000

**Record Last Update:** 20250407T215342+0000

### **Ratings and Alerts**

No rating or validation information has been found for GeneCruiser.

No alerts have been found for GeneCruiser.

### **Data and Source Information**

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 4 mentions in open access literature.

**Listed below are recent publications.** The full list is available at NIF.

Robiou-du-Pont S, et al. (2015) Should we have blind faith in bioinformatics software? Illustrations from the SNAP web-based tool. PloS one, 10(3), e0118925.

Vaughan LK, et al. (2015) Linkage and association analysis of obesity traits reveals novel loci and interactions with dietary n-3 fatty acids in an Alaska Native (Yup'ik) population. Metabolism: clinical and experimental, 64(6), 689.

Faino A, et al. (2014) Identifying rare variants associated with hypertension using the C-alpha test. BMC proceedings, 8(Suppl 1 Genetic Analysis Workshop 18Vanessa Olmo), S56.

Vaughan LK, et al. (2013) Where in the genome are we? A cautionary tale of database use in genomics research. Frontiers in genetics, 4, 38.