Resource Summary Report

Generated by dkNET on Apr 18, 2025

BEAGLECALL

RRID:SCR_013301
Type: Tool

Proper Citation

BEAGLECALL (RRID:SCR_013301)

Resource Information

URL: http://faculty.washington.edu/browning/beaglecall/beaglecall.html

Proper Citation: BEAGLECALL (RRID:SCR_013301)

Description: Software package for simultaneous genotype calling and haplotype phasing for unrelated individuals. BEAGLECALL produces output posterior genotype probabilities and output phased haplotypes. BEAGLECALL generates extremely accurate genotype calls because it uses both allele signal intensity data and inter-marker correlation to call genotypes. BEAGLECALL is designed for use with high-density SNP arrays, and it uses the BEAGLE haplotype frequency model to model inter-marker correlation. (entry from Genetic Analysis Software)

Abbreviations: BEAGLECALL

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, java, ms-windows, unix, linux, macos

Funding:

Resource Name: BEAGLECALL

Resource ID: SCR_013301

Alternate IDs: nlx_154239

Record Creation Time: 20220129T080315+0000

Record Last Update: 20250416T063639+0000

Ratings and Alerts

No rating or validation information has been found for BEAGLECALL.

No alerts have been found for BEAGLECALL.

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 dkNET.

Guo T, et al. (2017) Genome-Wide Association Study to Find Modifiers for Tetralogy of Fallot in the 22q11.2 Deletion Syndrome Identifies Variants in the GPR98 Locus on 5q14.3. Circulation. Cardiovascular genetics, 10(5), e001690.