

# Resource Summary Report

Generated by [kravitz2](#) on Aug 2, 2026

## CHIAMO

RRID:SCR\_009150

Type: Tool

### Proper Citation

CHIAMO (RRID:SCR\_009150)

### Resource Information

**URL:** <http://innovation.ox.ac.uk/licence-details/chiamo/>

**Proper Citation:** CHIAMO (RRID:SCR\_009150)

**Description:** Software application for calling genotypes from the Affymetrix 500K Mapping chip. The program allows for multiple cohorts which have potentially different intensity characteristics that can lead to elevated false-positive rates in genome-wide studies. The underlying model has a hierarchical structure that allows for correlation between the parameters of each cohort. The output files produced by CHIAMO feed directly into both the programs SNPTEST and IMPUTE. CHIAMO was used to call genotypes for the 7 genome-wide association studies carried out by the Wellcome Trust Case-Control Consortium (WTCCC).

**Abbreviations:** CHIAMO

**Resource Type:** software resource, software application

**Keywords:** gene, genetic, genomic

**Resource Name:** CHIAMO

**Resource ID:** SCR\_009150

**Alternate IDs:** nlx\_154269

**Old URLs:** <http://www.stats.ox.ac.uk/~marchini/software/gwas/chiamo.html>

**Record Creation Time:** 20220129T080251+0000

**Record Last Update:** 20260801T191054+0000

### Ratings and Alerts

No rating or validation information has been found for CHIAMO.

No alerts have been found for CHIAMO.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Selzam S, et al. (2017) Predicting educational achievement from DNA. Molecular psychiatry, 22(2), 267.

López Herráez D, et al. (2009) Genetic variation and recent positive selection in worldwide human populations: evidence from nearly 1 million SNPs. PloS one, 4(11), e7888.