

# Resource Summary Report

Generated by [NIF](#) on Sep 1, 2026

## UMAKE

RRID:SCR\_009093

Type: Tool

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### Proper Citation

UMAKE (RRID:SCR\_009093)

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### Resource Information

**URL:** <http://genome.sph.umich.edu/wiki/UMAKE>

**Proper Citation:** UMAKE (RRID:SCR\_009093)

**Description:** Software pipeline to detect SNPs and call their genotypes from a list of BAM files. UMAKE pipeline has been successfully applied in detecting SNPs from many large-scale next-generation sequencing studies. (entry from Genetic Analysis Software)

**Abbreviations:** UMAKE

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

**Keywords:** gene, genetic, genomic

**Resource Name:** UMAKE

**Resource ID:** SCR\_009093

**Alternate IDs:** nlx\_154110

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

**Record Last Update:** 20260829T183103+0000

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### Ratings and Alerts

No rating or validation information has been found for UMAKE.

No alerts have been found for UMAKE.

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### Data and Source Information

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

## Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Hu Y, et al. (2013) Accurate local-ancestry inference in exome-sequenced admixed individuals via off-target sequence reads. American journal of human genetics, 93(5), 891.

Orr V, et al. (2013) Genetic variants regulating immune cell levels in health and disease. Cell, 155(1), 242.

Zhan X, et al. (2013) Identification of a rare coding variant in complement 3 associated with age-related macular degeneration. Nature genetics, 45(11), 1375.