

Resource Summary Report

Generated by [kravitz2](#) on Sep 17, 2026

UMAKE

RRID:SCR_009093

Type: Tool

Proper Citation

UMAKE (RRID:SCR_009093)

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: 20260912T200240+0000

Ratings and Alerts

No rating or validation information has been found for UMAKE.

No alerts have been found for UMAKE.

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 [kravitz2](#) .

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.