

Resource Summary Report

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MACH 1.0

RRID:SCR_001759

Type: Tool

Proper Citation

MACH 1.0 (RRID:SCR_001759)

Resource Information

URL: <http://csg.sph.umich.edu/abecasis/MACH/index.html>

Proper Citation: MACH 1.0 (RRID:SCR_001759)

Description: A Markov Chain based software tool for haplotyping, genotype imputation and disease association analysis that can resolve long haplotypes or infer missing genotypes in samples of unrelated individuals.

Synonyms: MArkov Chain Haplotyper MINIMAC, MArkov Chain Haplotyping

Resource Type: data processing software, software application, data analysis software, software resource

Defining Citation: [PMID:21058334](#), [PMID:19715440](#)

Keywords: gene, genetic, genomic, haplotype, genotype, genomic analysis, imaging genomics, imputation, snp, gene, haplotyping, sequence

Availability: Free

Resource Name: MACH 1.0

Resource ID: SCR_001759

Alternate IDs: nlx_154202, OMICS_00064

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260731T042622+0000

Ratings and Alerts

No rating or validation information has been found for MACH 1.0.

No alerts have been found for MACH 1.0.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 58 mentions in open access literature.

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

Akiyama M, et al. (2023) Genome-wide association study reveals BET1L associated with survival time in the 137,693 Japanese individuals. *Communications biology*, 6(1), 143.

Akiyama M, et al. (2019) Characterizing rare and low-frequency height-associated variants in the Japanese population. *Nature communications*, 10(1), 4393.

Bhatnagar V, et al. (2016) Analysis of ABCG2 and other urate transporters in uric acid homeostasis in chronic kidney disease: potential role of remote sensing and signaling. *Clinical kidney journal*, 9(3), 444.

Finkel TH, et al. (2016) Variants in CXCR4 associate with juvenile idiopathic arthritis susceptibility. *BMC medical genetics*, 17, 24.

Keaton JM, et al. (2016) Genome-Wide Interaction with Insulin Secretion Loci Reveals Novel Loci for Type 2 Diabetes in African Americans. *PloS one*, 11(7), e0159977.

Lu AT, et al. (2016) Genetic variants near MLST8 and DHX57 affect the epigenetic age of the cerebellum. *Nature communications*, 7, 10561.

Chahal HS, et al. (2016) Genome-wide association study identifies 14 novel risk alleles associated with basal cell carcinoma. *Nature communications*, 7, 12510.

Chahal HS, et al. (2016) Genome-wide association study identifies novel susceptibility loci for cutaneous squamous cell carcinoma. *Nature communications*, 7, 12048.

van Nistelrooij AM, et al. (2015) Single nucleotide polymorphisms in CRTC1 and BARX1 are associated with esophageal adenocarcinoma. *Journal of carcinogenesis*, 14, 5.

Cao S, et al. (2015) Genome-wide Association Study on Platinum-induced Hepatotoxicity in Non-Small Cell Lung Cancer Patients. *Scientific reports*, 5, 11556.

Huang T, et al. (2015) Genetic Predisposition to Central Obesity and Risk of Type 2 Diabetes: Two Independent Cohort Studies. *Diabetes care*, 38(7), 1306.

Michailidou K, et al. (2015) Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. *Nature genetics*, 47(4), 373.

Corvol H, et al. (2015) Genome-wide association meta-analysis identifies five modifier loci of lung disease severity in cystic fibrosis. *Nature communications*, 6, 8382.

Kim YJ, et al. (2015) A new strategy for enhancing imputation quality of rare variants from next-generation sequencing data via combining SNP and exome chip data. *BMC genomics*, 16, 1109.

Nakano M, et al. (2014) Novel common variants and susceptible haplotype for exfoliation glaucoma specific to Asian population. *Scientific reports*, 4, 5340.

Cai Q, et al. (2014) Genome-wide association analysis in East Asians identifies breast cancer susceptibility loci at 1q32.1, 5q14.3 and 15q26.1. *Nature genetics*, 46(8), 886.

Orozco G, et al. (2014) Novel rheumatoid arthritis susceptibility locus at 22q12 identified in an extended UK genome-wide association study. *Arthritis & rheumatology* (Hoboken, N.J.), 66(1), 24.

Rafiq S, et al. (2014) A genome wide meta-analysis study for identification of common variation associated with breast cancer prognosis. *PloS one*, 9(12), e101488.

Wang Y, et al. (2014) Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. *Nature genetics*, 46(7), 736.

Gialluisi A, et al. (2014) Genome-wide screening for DNA variants associated with reading and language traits. *Genes, brain, and behavior*, 13(7), 686.