Resource Summary Report

Generated by ASWG on Aug 3, 2026

IMPUTE

RRID:SCR_009245
Type: Tool

Proper Citation

IMPUTE (RRID:SCR_009245)

Resource Information

URL: https://mathgen.stats.ox.ac.uk/impute/impute.html

Proper Citation: IMPUTE (RRID:SCR_009245)

Description: Software application for estimating (imputing) unobserved genotypes in SNP association studies. The program is designed to work seamlessly with the output of the genotype calling program CHIAMO and the population genetic simulator HAPGEN, and it produces output that can be analyzed using the program SNPTEST. (entry from Genetic Analysis Software)

Abbreviations: IMPUTE

Resource Type: software resource, software application

Keywords: gene, genetic, genomic

Resource Name: IMPUTE

Resource ID: SCR_009245

Alternate IDs: nlx_154411

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260801T191058+0000

Ratings and Alerts

No rating or validation information has been found for IMPUTE.

No alerts have been found for IMPUTE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 628 mentions in open access literature.

Listed below are recent publications. The full list is available at ASWG .

Chami N, et al. (2025) Genetic subtyping of obesity reveals biological insights into the uncoupling of adiposity from its cardiometabolic comorbidities. medRxiv : the preprint server for health sciences.

Xiong Z, et al. (2025) Combined genome-wide association study of facial traits in Europeans increases explained variance and improves prediction. Nature communications, 16(1), 6562.

Hoppe R, et al. (2025) Lessons learned from a candidate gene study investigating aromatase inhibitor treatment outcome in breast cancer. NPJ breast cancer, 11(1), 18.

Shealy EP, et al. (2025) DNA methylation-based age prediction and sex-specific epigenetic aging in a lizard with female-biased longevity. Science advances, 11(5), eadq3589.

Jung HU, et al. (2025) Assessment of polygenic risk score performance in East Asian populations for ten common diseases. Communications biology, 8(1), 374.

Chami N, et al. (2025) Genetic subtyping of obesity reveals biological insights into the uncoupling of adiposity from its cardiometabolic comorbidities. Nature medicine, 31(11), 3801.

Lidani KCF, et al. (2025) Impact of AGT rs5050(T>G) variants on associations between estradiol and angiotensinogen levels: Multi-Ethnic Study of Atherosclerosis (MESA). PloS one, 20(12), e0339786.

Power GM, et al. (2025) The role of body image dissatisfaction in the relationship between body size and disordered eating and self-harm: complimentary Mendelian randomization and mediation analyses. Molecular psychiatry, 30(2), 521.

Park JM, et al. (2025) Nicotine Metabolism-Related Genetic Polymorphisms Associated with Smoking Cessation in Korean Men: A Candidate Gene Association Study in a Korean Cohort. Lifestyle genomics, 18(1), 20.

Lee SB, et al. (2025) Impact of genetic markers related to hyper-HDL cholesterol on the prevalence of myocardial infarction: a KoGES study. Journal of lipid research, 66(4), 100777.

Sharma J, et al. (2025) Genetic ancestry influences gene-environment interactions with sociocultural factors: Results from the Hispanic Community Health Study/Study of Latinos. HGG advances, 6(3), 100451.

Lau PP, et al. (2025) Genome-wide association study of the fatty liver index in the Taiwanese population reveals shared and population-specific genetic risk factors across ethnicities. Cell & bioscience, 15(1), 19.

Foco L, et al. (2025) Genomic and molecular evidence that the LncRNA DSP-AS1 modulates desmoplakin expression. Human genetics, 144(8), 843.

Foco L, et al. (2025) Genomic and molecular evidence that the lncRNA DSP-AS1 modulates Desmoplakin expression. medRxiv : the preprint server for health sciences.

Xiao H, et al. (2025) Diet as a source of the non-direct genetic effects in metabolic traits: evidence from a family-based GWAS study. Human genetics, 144(11-12), 1097.

Imtiaz MA, et al. (2025) Genome-wide association study meta-analysis uncovers novel genetic variants associated with olfactory dysfunction. BMC genomic data, 26(1), 64.

Tan H, et al. (2025) Genetic predisposition to Behcet's disease mediated by a IL10RA enhancer polymorphism. Heliyon, 11(1), e41529.

Kim S, et al. (2025) Genome-wide identification and functional validation of the WW domain containing oxidoreductase gene associated with sleep duration. Scientific reports, 15(1), 5552.

Lidani KCF, et al. (2025) Genome-wide association study of angiotensinogen levels and key single nucleotide polymorphism associations with blood pressure. Journal of hypertension, 43(9), 1500.

Tao B, et al. (2025) An inherited predisposition allele promotes gastric cancer via enhancing deubiquitination-mediated activation of epithelial-to-mesenchymal transition signaling. The Journal of clinical investigation, 135(8).