

Resource Summary Report

Generated by [NIF](#) on Sep 14, 2026

IMPUTE2

RRID:SCR_013055

Type: Tool

Proper Citation

IMPUTE2 (RRID:SCR_013055)

Resource Information

URL: http://mathgen.stats.ox.ac.uk/impute/impute_v2.html

Proper Citation: IMPUTE2 (RRID:SCR_013055)

Description: A computer program for phasing observed genotypes and imputing missing genotypes.

Abbreviations: IMPUTE2

Resource Type: software resource

Resource Name: IMPUTE2

Resource ID: SCR_013055

Alternate IDs: OMICS_00062

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260912T195758+0000

Ratings and Alerts

No rating or validation information has been found for IMPUTE2.

No alerts have been found for IMPUTE2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1317 mentions in open access literature.

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

Sánchez-Maldonado JM, et al. (2026) ULK4 and CDKN2A polymorphisms influence the risk of developing monoclonal gammopathy of undetermined significance. *International journal of cancer*, 159(2), 410.

Vince N, et al. (2026) HLA Class II Protein Expression Regulation Is Strongly Linked to Cis-Acting SNPs. *HLA*, 107(4), e70669.

Fang X, et al. (2026) Protocol for identifying cell-type-specific genes associated with disease risk using single-cell eQTL data. *STAR protocols*, 7(2), 104545.

Cheng CF, et al. (2026) Comparative polygenic predispositions of treatment-resistant depression in East Asian and European populations. *Neuropsychopharmacology* : official publication of the American College of Neuropsychopharmacology, 51(4), 753.

Hwang LD, et al. (2026) Biologically informed instrument selection for dietary Mendelian randomization using chemosensory receptor variants. *medRxiv* : the preprint server for health sciences.

Olin A, et al. (2026) Demographic and genetic factors shape the epitope specificity of the human antibody repertoire against viruses. *Nature immunology*, 27(3), 600.

Toda N, et al. (2026) Genetic and Social Determinants of Renin-Angiotensin-Aldosterone System Inhibitor-Induced Angioedema: A Precision Medicine Health Equity Study. *medRxiv* : the preprint server for health sciences.

Ng JY, et al. (2026) A genome-wide association study identifies that SAMD5 interacts with regular Sun exposure to influence nasolabial folds development. *Journal of physiological anthropology*, 45(1).

Mollon J, et al. (2026) Gene × sex interactions on cognition in the Philadelphia neurodevelopmental cohort. *Biology of sex differences*, 17(1).

Trudel L, et al. (2026) Eligibility for anti-amyloid treatment in a multiethnic community-based study. *Alzheimer's & dementia (Amsterdam, Netherlands)*, 18(2), e70314.

Fu J, et al. (2026) Genome-wide association studies of brain diffusion kurtosis imaging phenotypes. *EBioMedicine*, 127, 106261.

Gerstner N, et al. (2026) Schizophrenia risk variants modulate transcription factor binding and gene expression in cortical cell types. *Cellular and molecular life sciences : CMLS*, 83(1).

Vollenbrock CE, et al. (2026) Association of genetic variation with age at diagnosis in type 1 diabetes. *BMJ open diabetes research & care*, 14(1).

Witonsky D, et al. (2026) Genomic profiling of active vitamin D colonic responses in African- and European-Americans identifies an ancestry-related regulatory variant of POLB. *PLoS genetics*, 22(1), e1011983.

Lee MP, et al. (2026) Lp(a) Has Specific Effects on Coronary Artery Disease Independent of LDL-C: A Mendelian Randomization Study. *JACC. Advances*, 5(5), 102697.

Ye L, et al. (2026) Mendelian randomization facilitates identification of schizophrenia risk enhancer RNAs. *Molecular psychiatry*, 31(4), 2133.

Wang G, et al. (2026) Distinct genetic profiles influence body mass index between infancy and adolescence. *Nature communications*, 17(1), 1594.

Feitosa M, et al. (2026) Discovery of gene-alcohol interaction loci influencing blood pressure in 1.1 million individuals from multiple populations. *Research square*.

Geng JH, et al. (2026) Development and Validation of a Genome-Wide Association Study Based Polygenic Risk Score for Prostate Cancer in an Asian Population. *The world journal of men's health*, 44(2), 402.

Wang X, et al. (2026) Mapping Genetic Regulation of Transcription to Identify Functional Variants and Genes Associated with Pancreatic Cancer Risk. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(29), e17184.