Resource Summary Report

Generated by PRECISE-TBI on Sep 19, 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 PRECISE-TBI .

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.

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.

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

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.

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.

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).

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.

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.

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.

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).

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.

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

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.