Resource Summary Report

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Michigan Imputation Server

RRID:SCR_017579
Type: Tool

Proper Citation

Michigan Imputation Server (RRID:SCR_017579)

Resource Information

URL: https://imputationserver.sph.umich.edu/

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Description: Web server to implement whole genotype imputation workflow for efficient parallelization of computationally intensive tasks. Service for imputation that facilitates access to new reference panels and greatly improves user experience and productivity. Used to find haplotype segments and reference panel of sequenced genomes, assign genotypes at untyped markers, improve genome coverage, facilitate comparison and combination of studies that use different marker panels, increase power to detect genetic association, and guide fine mapping.

Synonyms: Next Generation Genotype Imputation Service

Resource Type: data access protocol, service resource, software resource, web service

Defining Citation: PMID:27571263

Keywords: Whole, genotype, imputation, workflow, parallelization, task, find, haplotype, segment, reference, panel, sequence, genome, mapping

Funding: Austrian Science Fund ;
European Community Seventh Framework Programme ;
NHGRI HG000376;
NHGRI HG007022;
NHLBI HL117626;
NIA ;
NIDA R01 DA037904

Availability: Restricted

Resource Name: Michigan Imputation Server

Resource ID: SCR_017579

Alternate URLs: https://github.com/genepi/imputationserver

Record Creation Time: 20220129T080335+0000

Record Last Update: 20260912T195854+0000

Ratings and Alerts

No rating or validation information has been found for Michigan Imputation Server.

No alerts have been found for Michigan Imputation Server.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 196 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Wang Z, et al. (2026) Identifying Plasma Proteins Associated with Risk of Solid Cancers: A 25-Year Prospective Analysis of 4,712 Circulating Proteins in the ARIC Study. medRxiv : the preprint server for health sciences.

Wagner L, et al. (2026) Functional Connectivity of the Neonatal Cerebellum is Impacted by Sex and Polygenic Liability for Autism. medRxiv : the preprint server for health sciences.

Martínez-López J, et al. (2026) Distinct Effects of Complement C4A and C4B Copy Numbers in Systemic Sclerosis Serological and Clinical Subtypes. Arthritis & rheumatology (Hoboken, N.J.), 78(4), 904.

Tzvi-Minker E, et al. (2026) Polygenic risk modulates myocardial repolarization and T-wave geometry in congenital long-QT syndrome type 1: evidence from digital ECG phenotyping. Frontiers in cardiovascular medicine, 13, 1736409.

Revanna JS, et al. (2026) Impaired lipoprotein secretion by APOE4 leads to lysosomal and mitochondrial dysfunction in human microglia. bioRxiv : the preprint server for biology.

Justice CM, et al. (2026) Combined family-based association and linkage analyses in families affected by attention-deficit hyperactivity disorder. Human genetics, 145(1).

Li Z, et al. (2026) A reference panel for linkage disequilibrium and genotype imputation using whole-genome sequencing data from 2,680 participants across India. HGG advances, 7(2), 100579.

Hu N, et al. (2026) Genetic variations interact with polybrominated diphenyl ether exposure to alter lipid homeostasis. Nature communications, 17(1).

Kitoh R, et al. (2026) Inflammation and Oxidative-Stress Pathways Are Associated with Idiopathic Sudden Hearing Loss: A Genome-Wide Association Study in 15,494 Japanese Individuals. International journal of molecular sciences, 27(4).

Rout M, et al. (2026) Identification of lipid quantitative trait loci linked with cardiometabolic disease in Asian Indians and Europeans: A genome-wide association study and Mendelian randomization. PLoS medicine, 23(4), e1005039.

Jin Y, et al. (2026) Risk factors underlying brain structure change rate in cognitive decline: Results from genomewide and phenomewide investigations. Alzheimer's & dementia : the journal of the Alzheimer's Association, 22(4), e71411.

Wang Z, et al. (2026) Estimation of direct and indirect polygenic effects and gene-environment interactions using polygenic scores in case-parent trio studies. Nature genetics, 58(6), 1237.

De Marco R, et al. (2026) Novel Potential Risk Loci for Migraine in the Portuguese Population. International journal of molecular sciences, 27(12).

Zafrilla-López M, et al. (2026) Circadian and Sleep-Related Polygenic Scores in Relation to Lithium Treatment Response in Bipolar Disorder. Neuropsychobiology, 1.

Miyahara K, et al. (2026) Upregulation of DNA repair-related genes in the prefrontal cortex of patients with schizophrenia with low genetic risk. Schizophrenia (Heidelberg, Germany), 12(1).

Kranz TM, et al. (2026) Adult ADHD with comorbid major depression shows a distinguishable polygenic pattern and negative cognitive style. Translational psychiatry, 16(1).

Ding K, et al. (2025) Admixture Mapping of Lipid Traits in Hispanic Americans. Journal of the American Heart Association, 14(21), e036650.

Audam TN, et al. (2025) The 9p21.3 Coronary Artery Disease Risk Locus Modulates Vascular Cell-State Transitions via Enhancer-Driven Regulation of MTAP. bioRxiv : the preprint server for biology.

Ruiz M, et al. (2025) Exploring the Impact of Mitonuclear Discordance on Disease in Latin American Admixed Populations. Genes, 16(6).

de Santana MBR, et al. (2025) Chromosome 21 variants tied to severe asthma exacerbations: A genome-wide association study in a Brazilian population. The journal of allergy and clinical immunology. Global, 4(3), 100507.