Resource Summary Report

Generated by T1D on Aug 10, 2026

GTOOL

RRID:SCR_009215
Type: Tool

Proper Citation

GTOOL (RRID:SCR_009215)

Resource Information

URL: http://www.stats.ox.ac.uk/~marchini/software/gwas/gtool.html

Proper Citation: GTOOL (RRID:SCR_009215)

Description: Software application for transforming sets of genotype data for use with the programs SNPTEST and IMPUTE. (entry from Genetic Analysis Software)

Abbreviations: GTOOL

Resource Type: software application, software resource

Keywords: gene, genetic, genomic

Resource Name: GTOOL

Resource ID: SCR_009215

Alternate IDs: nlx_154368

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260810T040458+0000

Ratings and Alerts

No rating or validation information has been found for GTOOL.

No alerts have been found for GTOOL.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 42 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Yang CH, et al. (2022) Independent phenotypic plasticity axes define distinct obesity subtypes. Nature metabolism, 4(9), 1150.

Valentini S, et al. (2022) Polympact: exploring functional relations among common human genetic variants. Nucleic acids research, 50(3), 1335.

Jung JO, et al. (2022) Clinical Relevance of Gastroesophageal Cancer Associated SNPs for Oncologic Outcome After Curative Surgery. Annals of surgical oncology, 29(2), 1453.

Li J, et al. (2022) Schizophrenia risk loci from xMHC region were associated with antipsychotic response in chronic schizophrenic patients with persistent positive symptom. Translational psychiatry, 12(1), 92.

Xin J, et al. (2021) Systematic evaluation of the effects of genetic variants on PIWI-interacting RNA expression across 33 cancer types. Nucleic acids research, 49(1), 90.

Pechlivanis S, et al. (2021) Pharmacogenetic association of diabetes-associated genetic risk score with rapid progression of coronary artery calcification following treatment with HMG-CoA-reductase inhibitors -results of the Heinz Nixdorf Recall Study. Naunyn-Schmiedeberg's archives of pharmacology, 394(8), 1713.

Curtis SW, et al. (2021) The PAX1 locus at 20p11 is a potential genetic modifier for bilateral cleft lip. HGG advances, 2(2).

Pechlivanis S, et al. (2020) Risk prediction for coronary heart disease by a genetic risk score - results from the Heinz Nixdorf Recall study. BMC medical genetics, 21(1), 178.

Liu H, et al. (2020) Analysis of zebrafish periderm enhancers facilitates identification of a regulatory variant near human KRT8/18. eLife, 9.

Pechlivanis S, et al. (2020) Association between lipoprotein(a) (Lp(a)) levels and Lp(a) genetic variants with coronary artery calcification. BMC medical genetics, 21(1), 62.

Hsieh AR, et al. (2020) Lack of association of genetic variants for diabetic retinopathy in Taiwanese patients with diabetic nephropathy. BMJ open diabetes research & care, 8(1).

Pechlivanis S, et al. (2020) Genetic risk scores for coronary artery disease and its traditional risk factors: Their role in the progression of coronary artery calcification-Results of the Heinz Nixdorf Recall study. PloS one, 15(5), e0232735.

Ali AT, et al. (2020) Analysis of mitochondrial m1A/G RNA modification reveals links to nuclear genetic variants and associated disease processes. Communications biology, 3(1), 147.

Pechlivanis S, et al. (2019) Male-pattern baldness and incident coronary heart disease and risk factors in the Heinz Nixdorf Recall Study. PloS one, 14(11), e0225521.

Zhao J, et al. (2019) Meta-analysis of genome-wide association studies provides insights into genetic control of tomato flavor. Nature communications, 10(1), 1534.

Misganaw B, et al. (2019) Polygenic risk associated with post-traumatic stress disorder onset and severity. Translational psychiatry, 9(1), 165.

Schurz H, et al. (2019) Evaluating the Accuracy of Imputation Methods in a Five-Way Admixed Population. Frontiers in genetics, 10, 34.

López-Isac E, et al. (2019) GWAS for systemic sclerosis identifies multiple risk loci and highlights fibrotic and vasculopathy pathways. Nature communications, 10(1), 4955.

Bonàs-Guarch S, et al. (2018) Re-analysis of public genetic data reveals a rare X-chromosomal variant associated with type 2 diabetes. Nature communications, 9(1), 321.

Tsai PC, et al. (2018) Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health. Clinical epigenetics, 10(1), 126.