

Resource Summary Report

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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 SNPTTEST and IMPUTE. (entry from Genetic Analysis Software)

Abbreviations: GTOOL

Resource Type: software resource, software application

Keywords: gene, genetic, genomic

Resource Name: GTOOL

Resource ID: SCR_009215

Alternate IDs: nlx_154368

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260813T054952+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 [ASWG](#) .

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

Valentini S, et al. (2022) Polym pact: 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.

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.

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.

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.

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

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.

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.