Resource Summary Report

Generated by T1D on Jul 31, 2026

openSNP

RRID:SCR_001636
Type: Tool

Proper Citation

openSNP (RRID:SCR_001636)

Resource Information

URL: http://opensnp.org/

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Description: Database of raw data from people who have shared their direct-to-customer (DTC) genetic results from 23andMe, deCODEme or FamilyTreeDNA. Logged-In users can search the database for users with specific phenotypes and mass-download all corresponding SNP-datasets. This allows you to get datasets like All genotyping files of openSNP-users that have Alzheimer and the corresponding control group. They are currently working on providing API-access. You can also use JSON to get access to openSNP-data and some other ways: If you want to automate the file-downloads for a given phenotype the RSS-feeds could help you. Inside the RSS-XML there are 2 flags you could use to automatically create correct genotype-groups: gives you the variation of this user at the phenotype you are looking at and gives you the download link. If you were genotyped by 23andMe, deCODEme or FamilyTreeDNA (contact them regarding others) you can upload the raw genotype data which you can download from your DTC test provider. The data will then be openly available for the world to see and download. They also parse these SNPs and annotate them. For annotation they include the manually curated SNPedia and find Open Access primary publications which appear in the journals of The Public Library of Science (PLoS), an Open Access publishing group. Additionally they screen Mendeley, a crowd-sourced repository of scientific publications. You can also publish some of your phenotypes so some day it might get possible to associate some SNPs with phenotypes. You can also share your knowledge about SNPs and phenotypes with other users and can socialize.

Abbreviations: openSNP

Resource Type: service resource, data repository, source code, software resource, data or information resource, database, storage service resource

Defining Citation: PMID:24647222

Keywords: SNP, genotype, phenotype, snp, genetic variation, disease, trait, genetics, genome wide association study, crowdsourcing, data set

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: openSNP

Resource ID: SCR_001636

Alternate IDs: nlx_153904

License: MIT License

License URLs: https://github.com/gedankenstuecke/snpr/blob/master/LICENSE.md

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260731T042620+0000

Ratings and Alerts

No rating or validation information has been found for openSNP.

No alerts have been found for openSNP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Namazi M, et al. (2025) Privacy-preserving framework for genomic computations via multi-key homomorphic encryption. Bioinformatics (Oxford, England), 41(3).

Muflikhah L, et al. (2025) Feature Selection for Hypertension Risk Prediction Using XGBoost on Single Nucleotide Polymorphism Data. Healthcare informatics research, 31(1), 16.

Saleem K, et al. (2025) Beacon Reconstruction Attack: Reconstruction of genomes in genomic data-sharing beacons using summary statistics. Bioinformatics (Oxford, England), 41(6).

Pe??a MJ, et al. (2024) Frequency of Gene Polymorphisms in Admixed Venezuelan Women with Recurrent Pregnancy Loss: Microsomal Epoxy Hydroxylase (rs1051740) and Enos (rs1799983). Current issues in molecular biology, 46(4), 3460.

Slosarek T, et al. (2023) Implementation and evaluation of personal genetic testing as part of genomics analysis courses in German universities. BMC medical genomics, 16(1), 73.

Chung HC, et al. (2023) Responsiveness to endurance training can be partly explained by the number of favorable single nucleotide polymorphisms an individual possesses. PloS one, 18(7), e0288996.

Huang J, et al. (2022) PAGEANT: personal access to genome and analysis of natural traits. Nucleic acids research, 50(7), e39.

Muneeb M, et al. (2021) Eye-color and Type-2 diabetes phenotype prediction from genotype data using deep learning methods. BMC bioinformatics, 22(1), 198.

Bedford FL, et al. (2021) Re-analysis of Genetic Risks for Chronic Fatigue Syndrome From 23andMe Data Finds Few Remain. Frontiers in pediatrics, 9, 590040.

Gaudillo J, et al. (2019) Machine learning approach to single nucleotide polymorphism-based asthma prediction. PloS one, 14(12), e0225574.

Fadda M, et al. (2018) User Perspectives of a Web-Based Data-Sharing Platform (Open Humans) on Ethical Oversight in Participant-Led Research: Protocol for a Quantitative Study. JMIR research protocols, 7(11), e10939.

Gershman SJ, et al. (2018) Dopaminergic genes are associated with both directed and random exploration. Neuropsychologia, 120, 97.

Nadeali Z, et al. (2017) UGT1A1 gene linkage analysis: application of polymorphic markers rs4148326/rs4124874 in the Iranian population. Iranian journal of basic medical sciences, 20(8), 880.

Vayena E, et al. (2016) Between Openness and Privacy in Genomics. PLoS medicine, 13(1), e1001937.

Turrini M, et al. (2016) Beyond clinical utility: The multiple values of DTC genetics. Applied & translational genomics, 8, 4.

Greshake B, et al. (2014) openSNP--a crowdsourced web resource for personal genomics. PloS one, 9(3), e89204.

Corpas M, et al. (2012) A genome blogger manifesto. GigaScience, 1(1), 15.