Resource Summary Report

Generated by RRID on Sep 17, 2026

SNPnexus

RRID:SCR_005192
Type: Tool

Proper Citation

SNPnexus (RRID:SCR_005192)

Resource Information

URL: http://www.snp-nexus.org/

Proper Citation: SNPnexus (RRID:SCR_005192)

Description: A web server for functional annotation of novel and publicly known genetic variants that was developed to assess the potential significance of known and novel SNPs on the major transcriptome, proteome, regulatory and structural variation models in order to identify the phenotypically important variants. A broader range of variations have been incorporated such as insertions / deletions, block substitutions, IUPAC codes submission and region-based analysis, expanding the query size limit, and most importantly including additional categories for the assessment of functional impact. SNPnexus provides a comprehensive set of annotations for genomic variation data by characterizing related functional consequences at the transcriptome/proteome levels of seven major annotation systems with in-depth analysis of potential deleterious effects, inferring physical and cytogenetic mapping, reporting information on HapMap genotype/allele data, finding overlaps with potential regulatory elements, structural variations and conserved elements, and retrieving links with previously reported genetic disease studies.

Abbreviations: SNPnexus

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Defining Citation: PMID:23395730, PMID:22544707, PMID:19098027

Keywords: single nucleotide polymorphism, genetic variant, gene, variant, insertion, deletion, block substitution, functional annotation, genotyping, phenotype, disease, regulatory element, conservation, non-synonymous coding snp, gene, protein, hapmap, population, structural variation

Availability: Acknowledgement requested

Resource Name: SNPnexus

Resource ID: SCR_005192

Alternate IDs: OMICS_00188

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260912T200136+0000

Ratings and Alerts

No rating or validation information has been found for SNPnexus.

No alerts have been found for SNPnexus.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 177 mentions in open access literature.

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

Li SX, et al. (2026) Interactions between genetic predisposition to obesity, insulin resistance and type 2 diabetes risk, and food or beverage intake for incident type 2 diabetes: European Prospective Investigation into Cancer and Nutrition (EPIC) InterAct case-cohort study. The American journal of clinical nutrition, 123(3), 101198.

Kaushik A, et al. (2026) Comparative GWAS using global and Indian Reference Panels reveals non-coding drivers of COVID-19 severity and mortality. PLoS neglected tropical diseases, 20(3), e0014020.

Liu D, et al. (2026) Shared genetic architecture between obesity and psychiatric disorders reveals comorbid etiology and therapeutic targets. Life medicine, 5(3), lnag015.

Yu H, et al. (2026) Coupling and Uncoupling Pleiotropy Between Hypertension and Type 2 Diabetes Contribute to Exploring Potential Heterogeneity in Cardiovascular Risk in East Asian Population. Biomedicines, 14(6).

Li X, et al. (2026) Causal role of serum metabolites in chronic periodontitis: A bidirectional Mendelian randomization and multi-omics integration study. Medicine, 105(19), e48615.

Tang S, et al. (2026) Multivariable genome-wide analysis elucidates the shared genetic architecture, immunosenescence features, and gut-origin therapeutic targets of ulcerative colitis-associated multisystem inflammation. Inflammation research : official journal of the European Histamine Research Society ... [et al.], 75(1).

Abbatangelo CL, et al. (2026) A comparative GWAS of eye colour in light and dark eye genetic backgrounds defined by HERC2 rs12913832 polymorphism in a Canadian cohort

of European ancestry. Scientific reports, 16(1).

Lteif C, et al. (2026) The role of Id genes on pulmonary hypertension development in left heart failure. American heart journal plus : cardiology research and practice, 61, 100692.

Liu Y, et al. (2026) Integrating Bidirectional Mendelian Randomization with Multi-Omics Reveals Causal Serum Metabolites and Novel Metabolic Drivers of Multiple Myeloma. International journal of molecular sciences, 27(4).

Yu EY, et al. (2026) Trans-ethnic estimation and implications of genetic impact on continuous glycemic profiles. Cell discovery, 12(1).

Yin K, et al. (2026) Multi-omics uncovers the pleiotropic genetic mechanisms linking MASLD and cardiometabolic syndromes. Cardiovascular diabetology, 25(1).

Li J, et al. (2026) Circulating metabolites, genetics and lifestyle factors in relation to future risk of type 2 diabetes. Nature medicine, 32(2), 660.

Wang X, et al. (2026) Combining single cell and bulk transcriptomics with Mendelian randomization identifies gut microbiota related prognostic genes and mechanisms in thyroid cancer. Discover oncology, 17(1).

Danelakis A, et al. (2026) Diagnosing migraine from genome-wide genotype data: a machine learning analysis. Brain : a journal of neurology, 149(1), 290.

Mei T, et al. (2026) Genome-Wide Association Study of Genetic Variants Associated with Serum Albumin Levels in Chinese Winter Sports Athletes. Biology, 15(4).

Shi X, et al. (2025) Shared Plasma Metabolites Mediate Causal Effects of Metabolic Diseases on Colorectal Cancer: A Two-Step Mendelian Randomization Study. Biomedicines, 13(10).

Esposito M, et al. (2025) Regulatory polymorphisms of MSH6, MSH2, FBXO11, and PPP1R21 genes affect survival of patients with immunotherapy-treated lung cancer. Journal for immunotherapy of cancer, 13(9).

Van Syoc EP, et al. (2025) Gut fungi are associated with human genetic variation and disease risk. PLoS biology, 23(9), e3003339.

Hafeez KS, et al. (2025) Integrating polygenic and methylation risk scores for pleural mesothelioma risk stratification. International journal of cancer.

Wang Y, et al. (2025) Genome-wide association study identified novel loci and gene-environment interaction for refractive error in children. NPJ genomic medicine, 10(1), 44.