Resource Summary Report

Generated by ASWG on Aug 3, 2026

SNPnexus

RRID:SCR_005192
Type: Tool

Proper Citation

SNPnexus (RRID:SCR_005192)

Resource Information

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

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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: production service resource, data analysis service, service resource, analysis 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: 20260803T040418+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 155 mentions in open access literature.

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

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.

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.

You D, et al. (2025) A genome-wide cross-trait analysis characterizes the shared genetic architecture between lung and gastrointestinal diseases. Nature communications, 16(1), 3032.

Satria RD, et al. (2025) Bioinformatic and genomic analysis identifies C allele of APOE rs7412 as the most prominent variant limiting extreme human longevity. Scientific reports, 15(1), 21688.

Menon S, et al. (2025) Meta-analysis and in-silico functional characterization of the SNCA variant rs356220 in Parkinson's disease. Scientific reports, 15(1), 23358.

Mishra BH, et al. (2025) Genetic crossroads of cardiovascular disease and its comorbidities: toward holistic therapeutic strategies. BMC medical genomics, 19(1), 1.

Minnai F, et al. (2025) A genome-wide association study of European advanced cancer patients treated with opioids identifies regulatory variants on chromosome 20 associated

with pain intensity. European journal of pain (London, England), 29(1), e4764.

Oh S, et al. (2025) Association of APOC1 with cortical atrophy during conversion to Alzheimer's disease. GeroScience, 47(6), 6665.

Kendall C, et al. (2025) Archaic adaptive introgression in modern human reproductive genes. Communications biology, 8(1), 1365.

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

Zhang X, et al. (2025) Machine Learning Based Early Diagnosis of ADHD with SHAP Value Interpretation: A Retrospective Observational Study. Neuropsychiatric disease and treatment, 21, 1075.

Payva F, et al. (2025) Systems biology approach delineates critical pathways associated with papillary thyroid cancer: a multi-omics data analysis. Thyroid research, 18(1), 15.

Raj APMS, et al. (2025) Genetic signatures of exceptional longevity: a comprehensive analysis of coding region single nucleotide polymorphisms (SNPs) in centenarians and supercentenarians. Human genomics, 19(1), 115.

Erdogan O, et al. (2025) EnSCAN: ENsemble Scoring for prioritizing CAusative variaNts across multiplatform GWASs for late-onset alzheimer's disease. BioData mining, 18(1), 20.

Abou Warda AE, et al. (2025) Genetic polymorphisms in SLC5A2 are associated with clinical outcomes and dapagliflozin response in heart failure patients. Frontiers in pharmacology, 16, 1539870.

Jibon MDK, et al. (2025) In-silico analysis of deleterious non-synonymous SNPs in the human AVPR1a gene linked to autism. BMC genomics, 26(1), 492.

Haydar S, et al. (2025) A Genome-Wide Association Study of Taste Liking in the Danish Population. The Journal of nutrition, 155(8), 2591.

Zhu M, et al. (2025) Common genetic variation influencing the human lung imaging phenotypes. Nature communications, 16(1), 9551.

Tariq EB, et al. (2025) CD36 and SR-B1 polymorphisms exhibit distinct association patterns in active and latent tuberculosis. Journal of medical microbiology, 74(12).