Resource Summary Report

Generated by NIF on Sep 4, 2026

SNPsandGO

RRID:SCR_005788
Type: Tool

Proper Citation

SNPsandGO (RRID:SCR_005788)

Resource Information

URL: http://snps-and-go.biocomp.unibo.it/snps-and-go/

Proper Citation: SNPsandGO (RRID:SCR_005788)

Description: A server for the prediction of single point protein mutations likely to be involved in the insurgence of diseases in humans.

Abbreviations: SNPs&GO

Synonyms: SNPs and GO

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

Defining Citation: PMID:19514061

Keywords: prediction, protein, mutation, disease, single nucleotide polymorphism, bio.tools

Resource Name: SNPsandGO

Resource ID: SCR_005788

Alternate IDs: biotools:snps_go, OMICS_02219

Alternate URLs: https://bio.tools/snps_go

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260904T000144+0000

Ratings and Alerts

No rating or validation information has been found for SNPsandGO.

No alerts have been found for SNPsandGO.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 61 mentions in open access literature.

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

Elasbali AM, et al. (2025) A structural genomics approach to investigate Dystrophin mutations and their impact on the molecular pathways of Duchenne muscular dystrophy. Frontiers in genetics, 16, 1517707.

Shadhin MST, et al. (2025) In silico functional, structural, and pathogenicity assessment of single nucleotide polymorphisms in the human SOX9 gene. Scientific reports, 16(1), 941.

Lucaciu SA, et al. (2025) Skin disease-associated GJB4 variants differentially influence connexin stability, cell viability and channel function. The Journal of physiology, 603(15), 4383.

Ahmed EM, et al. (2024) Computational Analysis of Deleterious nsSNPs in INS Gene Associated with Permanent Neonatal Diabetes Mellitus. Journal of personalized medicine, 14(4).

Ali EW, et al. (2024) Exploring the Structural and Functional Consequences of Deleterious Missense Nonsynonymous SNPs in the EPOR Gene: A Computational Approach. Journal of personalized medicine, 14(11).

Tate NM, et al. (2024) Sequence Analysis of Six Candidate Genes in Miniature Schnauzers with Primary Hypertriglyceridemia. Genes, 15(2).

Elangeeb ME, et al. (2024) Molecular Dynamics Simulation of Kir6.2 Variants Reveals Potential Association with Diabetes Mellitus. Molecules (Basel, Switzerland), 29(8).

Kamal MM, et al. (2024) In silico functional, structural and pathogenicity analysis of missense single nucleotide polymorphisms in human MCM6 gene. Scientific reports, 14(1), 11607.

Nila NN, et al. (2024) Investigating the structural and functional consequences of germline single nucleotide polymorphisms located in the genes of the alternative lengthening of telomere (ALT) pathway. Heliyon, 10(12), e33110.

Maryami F, et al. (2023) In silico Analysis of Two Novel Variants in the Pyruvate Carboxylase (PC) Gene Associated with the Severe Form of PC Deficiency. Iranian biomedical journal, 27(5), 307.

Elangeeb ME, et al. (2023) In Silico Investigation of AKT2 Gene and Protein Abnormalities Reveals Potential Association with Insulin Resistance and Type 2 Diabetes. Current issues in molecular biology, 45(9), 7449.

Elnageeb ME, et al. (2023) In Silico Evaluation of the Potential Association of the Pathogenic Mutations of Alpha Synuclein Protein with Induction of Synucleinopathies. Diseases (Basel, Switzerland), 11(3).

Marchena-Perea EM, et al. (2022) A Large Case-Control Study Performed in Spanish Population Suggests That RECQL5 Is the Only RECQ Helicase Involved in Breast Cancer Susceptibility. Cancers, 14(19).

AlGhamdi NA, et al. (2022) Emerging of composition variations of SARS-CoV-2 spike protein and human ACE2 contribute to the level of infection: in silico approaches. Journal of biomolecular structure & dynamics, 40(6), 2635.

Prado MJ, et al. (2022) Variant predictions in congenital adrenal hyperplasia caused by mutations in CYP21A2. Frontiers in pharmacology, 13, 931089.

Sun H, et al. (2021) Severe brain calcification and migraine headache caused by SLC20A2 and PDGFRB heterozygous mutations in a five-year-old Chinese girl. Molecular genetics & genomic medicine, 9(5), e1670.

Gong T, et al. (2021) Computational and Mass Spectrometry-Based Approach Identify Deleterious Non-Synonymous Single Nucleotide Polymorphisms (nsSNPs) in JMJD6. Molecules (Basel, Switzerland), 26(15).

Yu B, et al. (2021) Mutation of c.244G>T in NR5A1 gene causing 46, XY DSD by affecting RNA splicing. Orphanet journal of rare diseases, 16(1), 370.

Diroma MA, et al. (2021) New Insights Into Mitochondrial DNA Reconstruction and Variant Detection in Ancient Samples. Frontiers in genetics, 12, 619950.

Hasnain MJU, et al. (2020) Computational analysis of functional single nucleotide polymorphisms associated with SLC26A4 gene. PloS one, 15(1), e0225368.