

Resource Summary Report

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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: 20260829T182939+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.