Resource Summary Report

Generated by dkNET on May 20, 2025

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: production service resource, data analysis service, service resource, analysis service resource

Defining Citation: PMID:19514061

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

Funding:

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: 20250519T204702+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 56 mentions in open access literature.

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

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).

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.

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

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.

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

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).

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.

Hwang IT, et al. (2020) Role of NPR2 mutation in idiopathic short stature: Identification of two novel mutations. Molecular genetics & genomic medicine, 8(3), e1146.

Palomo L, et al. (2020) Spanish Guidelines for the use of targeted deep sequencing in myelodysplastic syndromes and chronic myelomonocytic leukaemia. British journal of haematology, 188(5), 605.

Alzahrani FA, et al. (2020) Investigating the pathogenic SNPs in BLM helicase and their biological consequences by computational approach. Scientific reports, 10(1), 12377.

Mustafa MI, et al. (2020) Extensive In Silico Analysis of ATL1 Gene?:?Discovered Five Mutations That May Cause Hereditary Spastic Paraplegia Type 3A. Scientifica, 2020, 8329286.

Mustafa MI, et al. (2019) In Silico Genetics Revealing 5 Mutations in CEBPA Gene Associated With Acute Myeloid Leukemia. Cancer informatics, 18, 1176935119870817.