Resource Summary Report

Generated by PRECISE-TBI on Jul 31, 2026

PhD-SNP

RRID:SCR_010782
Type: Tool

Proper Citation

PhD-SNP (RRID:SCR_010782)

Resource Information

URL: http://snps.biofold.org/phd-snp/phd-snp.html

Proper Citation: PhD-SNP (RRID:SCR_010782)

Description: It is based a SVM-based classifier.

Abbreviations: PhD-SNP

Synonyms: Predictor of human Deleterious Single Nucleotide Polymorphisms

Resource Type: software resource

Defining Citation: PMID:16895930

Resource Name: PhD-SNP

Resource ID: SCR_010782

Alternate IDs: OMICS_00158

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260725T190702+0000

Ratings and Alerts

No rating or validation information has been found for PhD-SNP.

No alerts have been found for PhD-SNP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 293 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Khan A, et al. (2025) Exploring the Dynamic Interplay of Deleterious Variants on the RAF1-RAP1A Binding in Cancer: Conformational Analysis, Binding Free Energy, and Essential Dynamics. Proteins, 93(3), 684.

Shaon MA, et al. (2025) Genetic and computational analysis of AKR1C4 gene rs17134592 polymorphism in breast cancer among the Bangladeshi population. Scientific reports, 15(1), 27526.

Majeed S, et al. (2025) Identification of candidate nsSNPs of the human FNDC5 gene and their structural and functional consequences using in silico analysis. Scientific reports, 15(1), 7681.

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.

Shaon MA, et al. (2025) Aldo-keto reductase family 1 member C3 (AKR1C3) gene polymorphism (rs12529) is associated with breast cancer in Bangladeshi population: A case-control study and computational investigation. PloS one, 20(6), e0318079.

Sarker DK, et al. (2025) Exploring the impact of deleterious missense nonsynonymous single nucleotide polymorphisms in the DRD4 gene using computational approaches. Scientific reports, 15(1), 3150.

Abdelazim AA, et al. (2025) In-silico screening and analysis of missense SNPs in human CYP3A4/5 affecting drug-enzyme interactions of FDA-approved COVID-19 antiviral drugs. Scientific reports, 15(1), 2153.

Bayraktar M, et al. (2025) Association Between FABP3 and FABP4 Genes with Changes in Milk Composition and Fatty Acid Profiles in the Native Southern Yellow Cattle Breed. Veterinary sciences, 12(9).

Sharif M, et al. (2025) Decoding pathogenic MMP9 variants in rheumatoid arthritis using computational and molecular dynamics approaches. Scientific reports, 15(1), 33743.

Begum R, et al. (2025) Insights Into Genetic Variations of the OCT1 Gene in Metformin Poor Responders Among Bangladeshi Type 2 Diabetic Patients. Advances in pharmacological and pharmaceutical sciences, 2025, 8568658.

El Houdi M, et al. (2025) Association study of the JAK/STAT signaling pathway with susceptibility to COVID-19 in moroccan patient and in-silico analysis of rare variants. Virus research, 351, 199509.

Hossain S, et al. (2025) In silico evaluation of missense SNPs in cancer-associated Cystatin A protein and their potential to disrupt Cathepsin B interaction. Heliyon, 11(3), e42478.

Malik S, et al. (2025) Comprehensive structural and functional analyses of RAD50 nsSNPs: from prediction to impact assessment. Frontiers in bioinformatics, 5, 1535482.

Mahmoud AA, et al. (2025) The impact of mutations on TP53 protein and MicroRNA expression in HNSCC: Novel insights for diagnostic and therapeutic strategies. PloS one, 20(5), e0307859.

Hossen MA, et al. (2025) Computational investigation unveils pathogenic LIG3 non-synonymous mutations and therapeutic targets in acute myeloid leukemia. PloS one, 20(6), e0320550.

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.

Jacinto J, et al. (2025) Exploring skeletal disorders in cattle and sheep: a WGS-based framework for diagnosis and classification. Genetics, selection, evolution : GSE, 57(1), 51.

Arachchige NDS, et al. (2025) Comprehensive bioinformatics analysis of selected germline variants of uncertain significance identified in a cohort of Sri Lankan hereditary breast cancer patients. Human genomics, 19(1), 12.

Iqbal MW, et al. (2025) Exploring deleterious non-synonymous SNPs in FUT2 gene, and implications for norovirus susceptibility and gut microbiota composition. Scientific reports, 15(1), 10395.

Elnageeb ME, et al. (2025) Computational prediction of the pathogenic variants of arachidonate 5-lipoxygenase activating protein using Molecular Dynamics simulation. PloS one, 20(7), e0329126.