

Resource Summary Report

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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: 20260801T190417+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 [ASWG](#) .

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.