Resource Summary Report

Generated by Kravitz on Sep 16, 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: 20260912T195723+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 335 mentions in open access literature.

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

Jenni R, et al. (2026) Novel genetic variants identification and immune profiling in ataxia telangiectasia patients. Journal of translational medicine, 24(1).

Khan A, et al. (2026) Computational hybrid framework integrating clinical-mutation profiling and physics-based simulations to predict structural tolerance of Bruton tyrosine kinase (BTK) and sustained ARQ 531 binding. Current research in structural biology, 11, 100186.

Sivakumar R, et al. (2026) In silico prioritisation of EDN1 missense variants identifies mature endothelin-1 substitutions with predicted receptor-binding effects. BMC genomics, 27(1).

Iqbal MW, et al. (2026) Exploring Deleterious Nonsynonymous SNPs in the ACADM Gene: Insights Into Medium-Chain Acyl-CoA Dehydrogenase Deficiency (MCADD) via In Silico Analysis. Genetics research, 2026, 6682668.

Azmi MB, et al. (2026) Computational identification of rare pathogenic genomic variants in esophageal cancer markers: Transcript-level analysis, sequence-based insights, and structural-functional impacts of non-synonymous SNPs. Biochemistry and biophysics reports, 45, 102503.

Islam N, et al. (2026) Single nucleotide polymorphisms affecting galantamine binding to acetylcholinesterase in Alzheimer's disease: a structural bioinformatics study. Journal of computer-aided molecular design, 40(1).

Ishaq S, et al. (2026) Pathogenic KRAS variants disrupt structure and dynamics: Insights from integrated computational analyses. PloS one, 21(2), e0341219.

Nila NN, et al. (2026) Comprehensive analysis of the deleterious nonsynonymous, non-coding SNPs and cancer variants of human aldo-keto reductase type 1 (AKR1C1) protein and their probable association with disease risk and progression: a computational study. Biochemistry and biophysics reports, 45, 102502.

Huang J, et al. (2026) A 20 Bp Indel of HNF4A Is Associated with Piglet Growth Partially by Regulating Its Transcription. Animals : an open access journal from MDPI, 16(12).

Xu Y, et al. (2026) Integrated mapping resolves pathogenicity of 11 CYP21A2 variants in congenital adrenal hyperplasia. Journal of the Endocrine Society, 10(7), bvag127.

Sage EE, et al. (2026) Structural modeling and docking analysis of canonical and novel resistance-associated missense mutations in Sudanese Escherichia coli. Scientific reports, 16(1).

Mubarak SMH, et al. (2026) Decoding the impact of nsSNP variants on BCL6 function through integrated computational analysis. Current research in structural biology, 11, 100180.

Harini R, et al. (2026) Identification of high-risk SNPs in SLC22A transporter genes: their potential role in PCOS and metformin uptake. BMC genomic data, 27(1).

Naveed M, et al. (2026) Potential of Bacillus paramycoides hydrolase to degrade propiconazole. Arhiv za higijenu rada i toksikologiju, 77(1), 9.

Priya M, et al. (2026) Computational Prediction of Deleterious SNPs in the GALNS Gene Implicated in Morquio A Syndrome (MPS IVA). ACS omega, 11(7), 11183.

Abass Eltaib Ahmed H, et al. (2026) Low Frequency of Pathogenic Variants in BRCA1 Exons 11/20 and BRCA2 Exon 11 Suggests Divergent Mutational Hotspots in Sudanese Breast Cancer Patients: A Case-Control Study. Breast cancer : basic and clinical research, 20, 11782234261455512.

Abdelazim AA, et al. (2026) Computational analysis and validation of UGT1A1/4 missense variants impacting tecovirimat metabolism in monkeypox patients. Frontiers in systems biology, 6, 1821230.

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.

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.