Resource Summary Report

Generated by Kravitz on Sep 10, 2026

PredictSNP

RRID:SCR_006327
Type: Tool

Proper Citation

PredictSNP (RRID:SCR_006327)

Resource Information

URL: http://loschmidt.chemi.muni.cz/predictsnp/

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Description: Consensus classifier tool that combines six of the top performing tools for the prediction of the effects of mutation on protein function. The obtained results are provided together with annotations extracted from the Protein Mutant Database and the UniProt database. A stand-alone version is also available.

Abbreviations: PredictSNP

Synonyms: PredictSNP - Consensus classifier for prediction of disease-related mutations

Resource Type: analysis service resource, data analysis service, production service resource, service resource, software resource

Defining Citation: PMID:24453961

Keywords: single nucleotide polymorphism, classifier, prediction, mutation, protein function, FASEB list

Availability: Free for academic use

Resource Name: PredictSNP

Resource ID: SCR_006327

Alternate IDs: OMICS_02218

Record Creation Time: 20220129T080235+0000

Record Last Update: 20260905T132551+0000

Ratings and Alerts

No rating or validation information has been found for PredictSNP.

No alerts have been found for PredictSNP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 148 mentions in open access literature.

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

Rietmann SJ, et al. (2026) GJB6 missense variant in a Labrador Retriever with paw pad hyperkeratosis. Animal genetics, 57(1), e70075.

Wu C, et al. (2026) Molecular Mechanisms of CLCN5 Missense Mutations in Dent Disease Type 1: A Comprehensive Computational Analysis and Clinical Correlations in a Chinese Cohort. Journal of cellular and molecular medicine, 30(6), e71108.

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.

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.

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).

Ezahedi FE, et al. (2026) Tracing SARS-CoV-2 Evolution in Algeria: Insights from 2020 to 2023. Viruses, 18(2).

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.

Esdaile E, et al. (2025) A de novo FBN1 variant likely causes congenital bilateral ectopia lentis in a crossbred horse. Scientific reports, 15(1), 37238.

Simonini C, et al. (2025) Neurodegenerative and neuroinflammatory changes in SOD1-ALS patients receiving tofersen. Scientific reports, 15(1), 11034.

Habib O, et al. (2025) Structural and immunological impacts of TOLLIP nsSNPs: A computational biology approach to drug discovery and immune system modulation. PloS

one, 20(11), e0328573.

Kong AS, et al. (2025) In-silico analysis of nsSNPs in BCL-2 family proteins: Implications for colorectal cancer pathogenesis and therapeutics. Biochemistry and biophysics reports, 42, 101957.

Hossain MM, et al. (2025) Computational prediction of high-risk non-synonymous SNPs in human ApoE and their structural impact on amyloid-? interaction in Alzheimer's disease pathogenesis. PloS one, 20(9), e0331339.

Akçe?me B, et al. (2025) Identification of deleterious non-synonymous single nucleotide polymorphisms in the mRNA decay activator ZFP36L2. RNA biology, 22(1), 1.

Kucukvardar S, et al. (2025) A novel MAP7D1 mutation causes mitotic defects and RPS14 accumulation in Shwachman-Diamond syndrome patient cells. Disease models & mechanisms, 18(8).

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.

Hosseini Faradonbeh SM, et al. (2025) Structural insights into SOD1: from in silico and molecular dynamics to experimental analyses of ALS-associated E49K and R115G mutants. Frontiers in molecular biosciences, 12, 1532375.

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).

Jin Y, et al. (2025) Clinical Characteristics and Genetic Variants in Children with PAX2 Mutation-Associated Disorders. Medicina (Kaunas, Lithuania), 61(6).

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.

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.