

Resource Summary Report

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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: production service resource, data analysis service, analysis 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: 20260804T043259+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 140 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.

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.

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.

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.

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.

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.

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).

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.

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).

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.

Nguyen TN, et al. (2024) A novel missense variant located within the zinc finger domain of the GLI3 gene was identified in a Vietnamese pedigree with index finger polydactyly. *Molecular genetics & genomic medicine*, 12(6), e2468.

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.

Chen J, et al. (2024) Identification of Pathogenic Missense Mutations of NF1 Using Computational Approaches. *Journal of molecular neuroscience* : MN, 74(4), 94.

Tanshee RR, et al. (2024) A comprehensive in silico investigation into the pathogenic SNPs in the RTEL1 gene and their biological consequences. *PloS one*, 19(9), e0309713.

Yang X, et al. (2024) Genotypic and phenotypic spectrum of maple syrup urine disease in Zhejiang of China. *QJM : monthly journal of the Association of Physicians*, 117(10), 717.

Ashok G, et al. (2024) Transcriptomic, mutational and structural bioinformatics approaches to explore the therapeutic role of FAP in predominant cancer types. *Discover oncology*, 15(1), 699.