Resource Summary Report

Generated by NIF on Aug 28, 2026

nsSNPAnalyzer

RRID:SCR_010780
Type: Tool

Proper Citation

nsSNPAnalyzer (RRID:SCR_010780)

Resource Information

URL: http://snpanalyzer.uthsc.edu/

Proper Citation: nsSNPAnalyzer (RRID:SCR_010780)

Description: A tool to predict whether a nonsynonymous single nucleotide polymorphism (nsSNP) has a phenotypic effect.

Abbreviations: nsSNPAnalyzer

Synonyms: nsSNPAnalyzer: predicting disease-associated nonsynonymous single nucleotide polymorphisms

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

Keywords: bio.tools

Resource Name: nsSNPAnalyzer

Resource ID: SCR_010780

Alternate IDs: OMICS_00156, biotools:nssnpanalyzer

Alternate URLs: https://bio.tools/nssnpanalyzer

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260821T193927+0000

Ratings and Alerts

No rating or validation information has been found for nsSNPAnalyzer.

No alerts have been found for nsSNPAnalyzer.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 50 mentions in open access literature.

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

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).

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.

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.

Song SN, et al. (2026) Endothelial NOX4?driven oxidative stress inhibition reverses HtrA1 deficiency?induced blood?brain barrier disruption and cognitive impairment. International journal of molecular medicine, 58(1).

Baba H, et al. (2025) Functional and structural analysis of missense variants in the human PDCD1 Gene. Journal of public health in Africa, 16(4), 1348.

Koh HYK, et al. (2024) Machine learning optimized DriverDetect software for high precision prediction of deleterious mutations in human cancers. Scientific reports, 14(1), 22618.

Chandrasekaran FP, et al. (2024) Molecular dynamics simulations involving different ?-propeller mutations reported in Swiss and French patients correlate with their disease phenotypes. Scientific reports, 14(1), 24133.

Roy AS, et al. (2024) A computational approach for structural and functional analyses of disease-associated mutations in the human CYLD gene. Genomics & informatics, 22(1), 4.

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.

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.

Sola D, et al. (2023) Novel polymorphisms in the prion protein gene (PRNP) and stability of the resultant prion protein in different horse breeds. Veterinary research, 54(1), 94.

Benamri I, et al. (2022) An in silico analysis of rpoB mutations to affect Chlamydia trachomatis sensitivity to rifamycin. Journal, genetic engineering & biotechnology, 20(1), 146.

Singh P, et al. (2021) Computational modeling and bioinformatic analyses of functional mutations in drug target genes in Mycobacterium tuberculosis. Computational and structural biotechnology journal, 19, 2423.

Peres KC, et al. (2021) Clinical utility of TGFB1 and its receptors (TGFBR1 and TGFBR2) in thyroid nodules: evaluation based on single nucleotide polymorphisms and mRNA analysis. Archives of endocrinology and metabolism, 65(2), 172.

Alhaidan Y, et al. (2021) CRISPR/Cas9 ADCY7 Knockout Stimulates the Insulin Secretion Pathway Leading to Excessive Insulin Secretion. Frontiers in endocrinology, 12, 657873.

Bug DS, et al. (2021) Towards Understanding the Pathogenicity of DROSHA Mutations in Oncohematology. Cells, 10(9).

Rashid MU, et al. (2020) Prevalence of RECQL germline variants in Pakistani early-onset and familial breast cancer patients. Hereditary cancer in clinical practice, 18(1), 25.

Singh A, et al. (2020) Exploring the effect of nsSNPs in human YPEL3 gene in cellular senescence. Scientific reports, 10(1), 15301.

Ibrahim O, et al. (2020) Exploring Neuronal Vulnerability to Head Trauma Using a Whole Exome Approach. Journal of neurotrauma, 37(17), 1870.

Khalid Z, et al. (2020) Effects of Single-Nucleotide Polymorphisms in Calmodulin-Dependent Protein Kinase Kinase 2 (CAMKK2): A Comprehensive Study. Computational and mathematical methods in medicine, 2020, 7419512.