Resource Summary Report

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

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: 20260728T043343+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 46 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

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.

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.

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.

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).

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

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.

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.

Karthikeyan V, et al. (2020) Estimation of varicocele associated human ARG2 and NOS1 proteins and computational analysis on the effect of its nsSNPs. International journal of biological macromolecules, 164, 735.

Alzahrani FA, et al. (2020) Investigating the pathogenic SNPs in BLM helicase and their biological consequences by computational approach. Scientific reports, 10(1), 12377.

Palomo L, et al. (2020) Spanish Guidelines for the use of targeted deep sequencing in myelodysplastic syndromes and chronic myelomonocytic leukaemia. British journal of haematology, 188(5), 605.

Michels M, et al. (2019) Determining the pathogenicity of CFTR missense variants: Multiple comparisons of in silico predictors and variant annotation databases. Genetics and molecular biology, 42(3), 560.