

Resource Summary Report

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PANTHER Evolutionary analysis of coding SNPs

RRID:SCR_005145

Type: Tool

Proper Citation

PANTHER Evolutionary analysis of coding SNPs (RRID:SCR_005145)

Resource Information

URL: <http://www.pantherdb.org/tools/csnpscoreForm.jsp>

Proper Citation: PANTHER Evolutionary analysis of coding SNPs (RRID:SCR_005145)

Description: Data analysis service that estimates the likelihood of a particular nonsynonymous (amino-acid changing) coding SNP to cause a functional impact on the protein. To analyze many SNPs, download the PANTHER Coding Snp Analysis tool from the downloads page.

Abbreviations: cSNP Scoring

Synonyms: Evolutionary analysis of coding SNPs, PANTHER Coding SNP Analysis Tool

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

Defining Citation: [PMID:23193289](#)

Resource Name: PANTHER Evolutionary analysis of coding SNPs

Resource ID: SCR_005145

Alternate IDs: OMICS_00135

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260821T193731+0000

Ratings and Alerts

No rating or validation information has been found for PANTHER Evolutionary analysis of coding SNPs.

No alerts have been found for PANTHER Evolutionary analysis of coding SNPs.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 104 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

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.

John P, et al. (2025) Neurogenic locus notch homolog protein 1 (NOTCH 1) SNP informatics coupled with intrinsically disordered regions and post-translational modifications reveals the complex structural crosstalk of Lung Adenocarcinoma (LUAD). *Frontiers in bioinformatics*, 5, 1641521.

Guo J, et al. (2025) CHEK1 variant is a risk factor for premature ovarian insufficiency by mis-regulating metabolism and inflammation-related genes. *Human genomics*, 19(1), 67.

Abuagla HA, et al. (2025) Impact of nonsynonymous single nucleotide polymorphisms in PROCR gene on protein stability and thrombotic risk: a molecular dynamic approach. *Frontiers in genetics*, 16, 1580993.

Nishihara E, et al. (2025) Nodule-Specific NRF2-Targeted Upregulation in Patients With KEAP1 Mutations and Familial Nontoxic Multinodular Goiter. *The Journal of clinical endocrinology and metabolism*, 110(4), 973.

El Houdi M, et al. (2025) Association study of the JAK/STAT signaling pathway with susceptibility to COVID-19 in moroccan patient and in-silico analysis of rare variants. *Virus research*, 351, 199509.

Shen X, et al. (2025) The tomato gene Ty-6, encoding DNA polymerase delta subunit 1, confers broad resistance to Geminiviruses. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 138(1), 22.

Boeykens F, et al. (2024) Development and validation of animal variant classification guidelines to objectively evaluate genetic variant pathogenicity in domestic animals. *Frontiers in veterinary science*, 11, 1497817.

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.

Shiv R, et al. (2024) Characterization of missense nonsynonymous single-nucleotide polymorphism of runt-related transcription factor-2 gene - An in silico approach. *Indian journal of pharmacology*, 56(3), 198.

Jeong MJ, et al. (2024) First Report of Polymorphisms and Genetic Characteristics of Prion-like Protein Gene (PRND) in Cats. *Animals : an open access journal from MDPI*, 14(23).

Maciel-Cruz EJ, et al. (2024) In-Silico Method for Predicting Pathogenic Missense Variants Using Online Tools: AURKA Gene as a Model. *Iranian journal of biotechnology*, 22(2), e3787.

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.

Wan S, et al. (2024) SPARC Stabilizes ApoE to Induce Cholesterol-Dependent Invasion and Sorafenib Resistance in Hepatocellular Carcinoma. *Cancer research*, 84(11), 1872.

Laskar FS, et al. (2023) An In silico Approach towards Finding the Cancer-Causing Mutations in Human MET Gene. *International journal of genomics*, 2023, 9705159.

Hassan MM, et al. (2023) In Silico Analysis: HLA-DRB1 Gene's Variants and Their Clinical Impact. *Cell transplantation*, 32, 9636897231184473.

Gul R, et al. (2023) Identifying the genetic causes of phenotypically diagnosed Pakistani mucopolysaccharidoses patients by whole genome sequencing. *Frontiers in genetics*, 14, 1128850.

Ma W, et al. (2023) Dermokine mutations contribute to epithelial-mesenchymal transition and advanced melanoma through ERK/MAPK pathways. *PloS one*, 18(7), e0285806.

Hassan MM, et al. (2023) Detection of Nonsynonymous Single Variants in Human HLA-DRB1 Exon 2 Associated with Renal Transplant Rejection. *Medicina (Kaunas, Lithuania)*, 59(6).

Elnageeb ME, et al. (2023) In Silico Evaluation of the Potential Association of the Pathogenic Mutations of Alpha Synuclein Protein with Induction of Synucleinopathies. *Diseases (Basel, Switzerland)*, 11(3).