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

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

Defining Citation: PMID:23193289

Funding:

Resource Name: PANTHER Evolutionary analysis of coding SNPs

Resource ID: SCR_005145

Alternate IDs: OMICS_00135

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250425T055433+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 91 mentions in open access literature.

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

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.

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.

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.

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.

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

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).

Nohara F, et al. (2022) MCAD deficiency caused by compound heterozygous pathogenic variants in ACADM. Human genome variation, 9(1), 2.

Vidal OM, et al. (2022) ADGRL3 genomic variation implicated in neurogenesis and ADHD links functional effects to the incretin polypeptide GIP. Scientific reports, 12(1), 15922.

Prado MJ, et al. (2022) Variant predictions in congenital adrenal hyperplasia caused by mutations in CYP21A2. Frontiers in pharmacology, 13, 931089.

Udosen B, et al. (2021) In-silico analysis reveals druggable single nucleotide polymorphisms in angiotensin 1 converting enzyme involved in the onset of blood pressure. BMC research notes, 14(1), 457.

Lira SS, et al. (2021) A comprehensive in silico investigation into the nsSNPs of Drd2 gene predicts significant functional consequences in dopamine signaling and pharmacotherapy. Scientific reports, 11(1), 23212.

Gong T, et al. (2021) Computational and Mass Spectrometry-Based Approach Identify Deleterious Non-Synonymous Single Nucleotide Polymorphisms (nsSNPs) in JMJD6. Molecules (Basel, Switzerland), 26(15).

Gupta R, et al. (2021) Computational Analysis Indicates That PARP1 Acts as a Histone Deacetylases Interactor Sharing Common Lysine Residues for Acetylation, Ubiquitination, and SUMOylation in Alzheimer's and Parkinson's Disease. ACS omega, 6(8), 5739.

Cheng C, et al. (2021) The VANGL1 P384R variant cause both neural tube defect and Klippel-Feil syndrome. Molecular genetics & genomic medicine, 9(7), e1710.

Suleman M, et al. (2021) Mutational Landscape of Pirin and Elucidation of the Impact of Most Detrimental Missense Variants That Accelerate the Breast Cancer Pathways: A Computational Modelling Study. Frontiers in molecular biosciences, 8, 692835.

Khoruddin NA, et al. (2021) Pathogenic nsSNPs that increase the risks of cancers among the Orang Asli and Malays. Scientific reports, 11(1), 16158.