Resource Summary Report

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SNAP - Effects of Single Amino Acid Substitutions on Protein Function

RRID:SCR_010786
Type: Tool

Proper Citation

SNAP - Effects of Single Amino Acid Substitutions on Protein Function (RRID:SCR_010786)

Resource Information

URL: https://rostlab.org/services/snap/

Proper Citation: SNAP - Effects of Single Amino Acid Substitutions on Protein Function (RRID:SCR_010786)

Description: A method for evaluating effects of single amino acid substitutions on protein function.

Abbreviations: SNAP

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

Defining Citation: PMID:17526529

Availability: Acknowledgement requested

Resource Name: SNAP - Effects of Single Amino Acid Substitutions on Protein Function

Resource ID: SCR_010786

Alternate IDs: OMICS_00162

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260903T235052+0000

Ratings and Alerts

No rating or validation information has been found for SNAP - Effects of Single Amino Acid Substitutions on Protein Function.

No alerts have been found for SNAP - Effects of Single Amino Acid Substitutions on Protein Function.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 38 mentions in open access literature.

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

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.

Li Y, et al. (2024) Very important pharmacogenetic variants landscape and potential clinical relevance in the Zhuang population from Yunnan province. Scientific reports, 14(1), 7495.

Zhu HY, et al. (2024) PemK's Arg24 is a crucial residue for PemIK toxin-antitoxin system to induce the persistence of Weissella cibaria against ciprofloxacin stress. Frontiers in microbiology, 15, 1402319.

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.

Kumari S, et al. (2023) Identification and characterization of putative biomarkers and therapeutic axis in Glioblastoma multiforme microenvironment. Frontiers in cell and developmental biology, 11, 1236271.

Behairy MY, et al. (2022) HBD-2 variants and SARS-CoV-2: New insights into inter-individual susceptibility. Frontiers in immunology, 13, 1008463.

Kanwal A, et al. (2022) RGS3 and IL1RAPL1 missense variants implicate defective neurotransmission in early-onset inherited schizophrenias. Journal of psychiatry & neuroscience : JPN, 47(6), E379.

Ali MZ, et al. (2022) In Silico Analysis Identified Putative Pathogenic Missense nsSNPs in Human SLITRK1 Gene. Genes, 13(4).

Ebrahim E, et al. (2022) Association of Cytotoxic T-Lymphocyte Antigen-4 Gene Polymorphism with Type 1 Diabetes Mellitus: In silico Analysis of Biological Features of CTLA-4 Protein on Ethiopian Population. Diabetes, metabolic syndrome and obesity : targets and therapy, 15, 2733.

Suleman M, et al. (2022) Sequence-structure functional implications and molecular simulation of high deleterious nonsynonymous substitutions in IDH1 revealed the mechanism of drug resistance in glioma. Frontiers in pharmacology, 13, 927570.

Behairy MY, et al. (2022) In silico analysis of missense variants of the C1qA gene related to infection and autoimmune diseases. Journal of Taibah University Medical Sciences, 17(6), 1074.

Gupta N, et al. (2022) Computational and Structural Analysis to Assess the Pathogenicity of Bardet-Biedl Syndrome Related Missense Variants Identified in Bardet-Biedl Syndrome 10 Gene (BBS10). ACS omega, 7(42), 37654.

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.

Shahrokhi SZ, et al. (2021) The effect of A1298c polymorphism of the MTHFR gene on anti-Müllerian hormone levels: experimental and Web-based analysis. Journal of clinical laboratory analysis, 35(9), e23948.

Ray M, et al. (2021) Essential interpretations of bioinformatics in COVID-19 pandemic. Meta gene, 27, 100844.

Saih A, et al. (2021) Computational Analysis of Missense Variants in the Human Transmembrane Protease Serine 2 (TMPRSS2) and SARS-CoV-2. BioMed research international, 2021, 9982729.

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.

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

Emadi E, et al. (2020) Predicting the most deleterious missense nsSNPs of the protein isoforms of the human HLA-G gene and in silico evaluation of their structural and functional consequences. BMC genetics, 21(1), 94.

Zhang W, et al. (2020) Update analysis on the association between Methionine synthase rs1805087 A/G variant and risk of prostate cancer. Scientific reports, 10(1), 13384.