

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://roslab.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).

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.

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.

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.

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.

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.

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.

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.