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: software resource, production service resource, service resource, data analysis service, analysis service 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: 20260803T040553+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 29 mentions in open access literature.

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

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.

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.

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.

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.

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.

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.

Basir A, et al. (2019) Methionine Synthase Reductase-A66G and -C524T Single Nucleotide Polymorphisms and Prostate Cancer: A Case-Control Trial. Asian Pacific journal of cancer prevention : APJCP, 20(5), 1445.

Wang Q, et al. (2019) Computational Screening and Analysis of Lung Cancer Related Non-Synonymous Single Nucleotide Polymorphisms on the Human Kirsten Rat Sarcoma Gene. Molecules (Basel, Switzerland), 24(10).

Pereira GRC, et al. (2019) In silico analysis and molecular dynamics simulation of human superoxide dismutase 3 (SOD3) genetic variants. Journal of cellular biochemistry, 120(3), 3583.

Nejati M, et al. (2018) Lipoprotein lipase gene polymorphisms as risk factors for stroke: a computational and meta-analysis. Iranian journal of basic medical sciences, 21(7), 701.

Hassan MM, et al. (2016) Bioinformatics Approach for Prediction of Functional Coding/Noncoding Simple Polymorphisms (SNPs/Indels) in Human BRAF Gene. Advances in bioinformatics, 2016, 2632917.

Raygan F, et al. (2016) Angiotensinogen-M235T as a risk factor for myocardial infarction in Asian populations: a genetic association study and a bioinformatics approach. Croatian medical journal, 57(4), 351.

Arai Y, et al. (2015) Retinitis Pigmentosa with EYS Mutations Is the Most Prevalent Inherited Retinal Dystrophy in Japanese Populations. Journal of ophthalmology, 2015, 819760.

Hagen CM, et al. (2015) Private mitochondrial DNA variants in danish patients with hypertrophic cardiomyopathy. PloS one, 10(4), e0124540.