Resource Summary Report

Generated by NIF on Apr 28, 2025

PROVEAN

RRID:SCR_002182
Type: Tool

Proper Citation

PROVEAN (RRID:SCR_002182)

Resource Information

URL: http://provean.jcvi.org/

Proper Citation: PROVEAN (RRID:SCR_002182)

Description: A software tool which predicts whether an amino acid substitution or indel has an impact on the biological function of a protein.

Abbreviations: PROVEAN

Synonyms: Protein Variation Effect Analyzer

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

Defining Citation: PMID:23056405

Keywords: amino acid substitution, indel, function, protein, amino acid, substitution, protein variant, genome variant, next-generation sequencing, insertion, deletion

Funding: NIH ;
NHGRI 5R01HG004701-04

Availability: GNU General Public License, v3

Resource Name: PROVEAN

Resource ID: SCR_002182

Alternate IDs: OMICS_01849

Record Creation Time: 20220129T080212+0000

Record Last Update: 20250428T052926+0000

Ratings and Alerts

No rating or validation information has been found for PROVEAN.

No alerts have been found for PROVEAN.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2083 mentions in open access literature.

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

Ranji P, et al. (2025) Four putative pathogenic ARHGAP29 variants in patients with non-syndromic orofacial clefts (NsOFC). European journal of human genetics : EJHG, 33(1), 38.

Kesdiren E, et al. (2025) Heterozygous variants in the teashirt zinc finger homeobox 3 (TSHZ3) gene in human congenital anomalies of the kidney and urinary tract. European journal of human genetics : EJHG, 33(1), 44.

Huang X, et al. (2025) Mutation spectra and genotype?phenotype analysis of congenital hypothyroidism in a neonatal population. Biomedical reports, 22(2), 30.

Kamal MM, et al. (2025) Investigating the functional and structural effect of non-synonymous single nucleotide polymorphisms in the cytotoxic T-lymphocyte antigen-4 gene: An in-silico study. PloS one, 20(1), e0316465.

Kokuryo T, et al. (2025) Whole-genome Sequencing Analysis of Bile Tract Cancer Reveals Mutation Characteristics and Potential Biomarkers. Cancer genomics & proteomics, 22(1), 34.

Al-Hamed MH, et al. (2025) Genetics of Primary Adrenal Insufficiency Beyond CAH in Saudi Arabian Population. Molecular genetics & genomic medicine, 13(1), e70052.

Zhao W, et al. (2025) GoFCards: an integrated database and analytic platform for gain of function variants in humans. Nucleic acids research, 53(D1), D976.

Jian Z, et al. (2025) Prevalence and molecular characteristics of colistin-resistant isolates among carbapenem-resistant Klebsiella pneumoniae in Central South China: a multicenter

study. Annals of clinical microbiology and antimicrobials, 24(1), 1.

Purev C, et al. (2025) Understanding molecular mechanisms of vertebral number of variations on Mongolian sheep using candidate genes analysis. Animal bioscience, 38(2), 247.

Katsonis P, et al. (2025) Meta-EA: a gene-specific combination of available computational tools for predicting missense variant effects. Nature communications, 16(1), 159.

Petrovic Pajic S, et al. (2025) Atypical Leber Hereditary Optic Neuropathy (LHON) Associated with a Novel MT-CYB:m.15309T>C(Ile188Thr) Variant. Genes, 16(1).

Waqar S, et al. (2025) Arsenic efflux and bioremediation potential of Klebsiella oxytoca via the arsB gene. PloS one, 20(1), e0307918.

Zhang D, et al. (2025) Association between ABCB4 variants and intrahepatic cholestasis of pregnancy. Scientific reports, 15(1), 3300.

Van den Bossche V, et al. (2025) PPAR?-mediated lipid metabolism reprogramming supports anti-EGFR therapy resistance in head and neck squamous cell carcinoma. Nature communications, 16(1), 1237.

Meng L, et al. (2025) Heterozygous pathogenic STT3A variation leads to dominant congenital glycosylation disorders and functional validation in zebrafish. Orphanet journal of rare diseases, 20(1), 46.

Lawrence ES, et al. (2024) Functional EPAS1/HIF2A missense variant is associated with hematocrit in Andean highlanders. Science advances, 10(6), eadj5661.

Guerrini-Rousseau L, et al. (2024) Neurofibromatosis type 1 mosaicism in patients with constitutional mismatch repair deficiency. Journal of medical genetics, 61(2), 158.

Almakhari M, et al. (2024) In-silico identification of deleterious non-synonymous SNPs of TBX1 gene: Functional and structural impact towards 22q11.2DS. PloS one, 19(6), e0298092.

Zhou Y, et al. (2024) Variant analysis and PGT-M of OTC gene in a Chinese family with ornithine carbamoyltransferase deficiency. BMC pregnancy and childbirth, 24(1), 491.

Li R, et al. (2024) Less is more: CRISPR/Cas9-based mutations in DND1 gene enhance tomato resistance to powdery mildew with low fitness costs. BMC plant biology, 24(1), 763.