Resource Summary Report

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

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: Free, Available for download, Freely available

Resource Name: PROVEAN

Resource ID: SCR_002182

Alternate IDs: OMICS_01849

License: GNU General Public License, v3

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260819T044032+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 2380 mentions in open access literature.

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

Xi J, et al. (2026) Global developmental delay and focal seizures in individuals with de novo truncating MACF1 variants. Human genomics, 20(1), 38.

Alimoradi E, et al. (2026) Identification of a Novel Missense Homozygous Variant in LINS1 in Two Distinct Iranian Families With Consanguineous Marriage. Molecular genetics & genomic medicine, 14(2), e70184.

Akkus N, et al. (2026) Whole Exome Sequencing in Patients With Developmental Delay/Intellectual Disability (DD/ID), Epilepsy and the First Turkish Patient Diagnosed With BCL11A-Related Intellectual Disability. Molecular genetics & genomic medicine, 14(1), e70180.

Ofori-Minta K, et al. (2026) Clinicogenomic Insights for Progression-Free Survival in Prostate Cancer. International journal of environmental research and public health, 23(2).

Jiang Z, et al. (2026) Clinical and Genetic Characteristics of a Chinese Occult Maculopathy Cohort. Translational vision science & technology, 15(3), 32.

Liu J, et al. (2026) Whole-exome sequencing increases variant detection compared to karyotyping and CMA in an unselected FGR cohort. Scientific reports, 16(1).

Yang Q, et al. (2026) Novel Compound Heterozygous Variants in the COG5 Gene Causing Fetal Hydrops and Skeletal Dysplasia. Molecular genetics & genomic medicine, 14(4), e70215.

Shi X, et al. (2026) Novel GJC2 and OBSCN variants co-segregating in a Chinese primary lymphedema pedigree. Orphanet journal of rare diseases, 21(1), 17.

Fatima AE, et al. (2026) Mutation screening of ??-crystallin gene in congenital cataract patients from North India. Indian journal of ophthalmology, 74(2), 196.

Plengvidhya N, et al. (2026) Targeted analysis of whole exome sequencing in Thai patients with neonatal diabetes. Human genetics, 145(1), 11.

Han C, et al. (2026) Whole-exome sequencing for the genetic diagnosis of early-onset high myopia and associated hereditary eye disorders. BMC medical genomics, 19(1).

Al Alwan I, et al. (2026) Familial glucocorticoid deficiency due to a novel TXNRD2 variant: expanding the spectrum of a rare genetic cause. Frontiers in endocrinology, 17, 1834727.

de Freitas LM, et al. (2026) Investigation of Pharmacogenomic Variants in the CYP (P450) Family in Native American Populations of the Brazilian Amazon. International journal of genomics, 2026, 5804093.

Sun H, et al. (2026) Eight-year follow-up of phenotypic progression in a Chinese XLRP pedigree with a novel RP2 gene mutation. Frontiers in genetics, 17, 1783270.

Gao J, et al. (2026) Genetic heterogeneity correlated with phenotypic variability in 6 Chinese families with Alport syndrome. Frontiers in genetics, 17, 1840344.

Altintas Kazar G, et al. (2026) In Silico Identification and Structural Characterization of High-Risk Missense SNVs in the Human IL23R Gene Relevant to Inflammatory Bowel Disease. Genes, 17(6).

Harini R, et al. (2026) Identification of high-risk SNPs in SLC22A transporter genes: their potential role in PCOS and metformin uptake. BMC genomic data, 27(1).

Rafi MO, et al. (2026) Predicting the Impact of Deleterious Single-Nucleotide Polymorphisms in the p47ING1a Isoform of Human ING1 Gene. Genetics research, 2026(1), e2859448.

Sever EA, et al. (2026) Novel pathogenic variant in ARMC4 identified by whole exome sequencing in a Turkish family with primary ciliary dyskinesia. Frontiers in molecular biosciences, 13, 1815627.

Kurnaz E, et al. (2026) Genetic Analyses in a Cohort of Pediatric Patients with Congenital Hypothyroidism Based on Congenital Hypothyroidism Consensus Guideline. Hormone research in paediatrics, 99(1), 23.