

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/>

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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, data analysis service, production service resource, service resource, software 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: 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: 20260912T195537+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 [SPARC SAWG](#) .

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.

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).

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.

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).

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.

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

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).

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.

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

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