

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: data analysis service, service resource, production service resource, software 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: 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: 20260801T042522+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 2231 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Guo W, et al. (2026) Pathogenicity of novel GLA gene missense mutations in Fabry disease and the therapeutic impact of migalastat. *Journal of advanced research*, 79, 549.

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.

Kim YS, et al. (2025) Allogenic mitochondria transfer improves cardiac function in iPS-cell-differentiated cardiomyocytes of a patient with Barth syndrome. *Experimental & molecular medicine*, 57(6), 1260.

Zhang B, et al. (2025) Low expression of CADPS predicts poor prognosis in pediatric acute lymphoblastic leukemia without fusion genes. *Biomolecules & biomedicine*, 25(10), 2295.

Ganguly A, et al. (2025) Rare and novel variant load threshold for KIF7, GJA1 and PDE1C genes elevates the risk of severity of congenital heart defects in Down syndrome. *PloS one*, 20(6), e0326566.

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

Wang H, et al. (2025) Identification of Novel USH2A Mutations in a Consanguineous Chinese Family With Usher Syndrome. *Human mutation*, 2025, 6391770.

Ma Z, et al. (2025) Mutation within the transmembrane domain of oxidized low-density lipoprotein receptor 1 influences oxidized low-density lipoprotein-induced signal transduction. *Innate immunity*, 31, 17534259251350447.

Ba T, et al. (2025) Prevalence and Clinical Characteristics of NEUROD1-MODY in Chinese Early-Onset Type 2 Diabetes Mellitus and a Literature Review. *Journal of*

diabetes, 17(4), e70080.

Heo JY, et al. (2025) Assessing the performance of 28 pathogenicity prediction methods on rare single nucleotide variants in coding regions. *BMC genomics*, 26(1), 641.

Faruque M, et al. (2025) Deciphering Deleterious nsSNPs in MUC16's SEA Domain: Structural and Functional Implications in Cancer Metastasis via Computational Analysis. *Journal of cellular and molecular medicine*, 29(11), e70633.

Li X, et al. (2025) Clinical and Molecular Landscape of GLRA2 in X-Linked Early-Onset High Myopia. *Investigative ophthalmology & visual science*, 66(4), 30.

Yang X, et al. (2025) A missense variant in the SOX5 gene (c.221C > T) is associated with intellectual disability. *Orphanet journal of rare diseases*, 20(1), 50.

Luo W, et al. (2025) Identification and Functional Analysis of Novel Mutations in AXIN2 and LRP6 Linked With Non-Syndromic Tooth Agenesis. *Molecular genetics & genomic medicine*, 13(5), e70101.

Zhu H, et al. (2025) Common cis-regulatory variation modifies the penetrance of pathogenic SHROOM3 variants in craniofacial microsomia. *Genome research*, 35(5), 1065.

Wang X, et al. (2025) Effect of newborn genomic screening for lysosomal storage disorders: a cohort study in China. *Genome medicine*, 17(1), 52.

Liu Y, et al. (2025) 18 individual genes underwent variant screening in a northwest Chinese group comprised 83 probands diagnosed with early-onset high myopia. *PloS one*, 20(9), e0329472.

Wang Y, et al. (2025) Ubap1l Knockout Mice Model Recapitulates Retinal Degeneration Phenotype Observed in Patients and Exhibits Irregular Photoreceptor Morphology. *Investigative ophthalmology & visual science*, 66(15), 35.

Chen X, et al. (2025) Identification and characterization of novel PAX4 variants in patients with suspected MODY9. *BMJ open diabetes research & care*, 13(6).