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: production service resource, data analysis service, analysis 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: 20260804T043147+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 ASWG .

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.

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.

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.

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.

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

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.

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.

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.

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.

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.

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.

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.

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.

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.

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

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.

Blomquist MR, et al. (2025) Glioblastoma resistance to EGFR antibody-drug conjugate is driven by transcriptional reprogramming and TEK-induced EGFR suppression. Journal of translational medicine, 23(1), 1153.

Sheng H, et al. (2025) Clinical characteristics, genetic spectrum and therapeutic effects of 51 male patients with idiopathic hypogonadotropic hypogonadism from southern China. Orphanet journal of rare diseases, 20(1), 574.