Resource Summary Report

Generated by T1D on Aug 1, 2026

MutPred

RRID:SCR_010778
Type: Tool

Proper Citation

MutPred (RRID:SCR_010778)

Resource Information

URL: http://mutpred.mutdb.org/

Proper Citation: MutPred (RRID:SCR_010778)

Description: Web application tool developed to classify an amino acid substitution as disease-associated or neutral in human.

Abbreviations: MutPred

Resource Type: software resource, web application

Keywords: bio.tools

Resource Name: MutPred

Resource ID: SCR_010778

Alternate IDs: biotools:mutpred, OMICS_00154

Alternate URLs: https://bio.tools/mutpred

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260731T042836+0000

Ratings and Alerts

No rating or validation information has been found for MutPred.

No alerts have been found for MutPred.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 409 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Mareckova K, et al. (2026) Functional Impact Score of Mitochondrial Variants and Its Relationship With Functional Connectivity of the Brain: Potential Origins of Premature Aging in Young Adulthood. Human brain mapping, 47(1), e70447.

Ncir WB, et al. (2026) First LDLRAP1 and Recurrent LDLR Mutations in Tunisian Families With Familial Hypercholesterolemia. Journal of cellular and molecular medicine, 30(1), e70997.

Lucaciu SA, et al. (2025) Skin disease-associated GJB4 variants differentially influence connexin stability, cell viability and channel function. The Journal of physiology, 603(15), 4383.

Heimer G, et al. (2025) Biallelic PIGM Coding Variant Causes Intractable Epilepsy and Intellectual Disability Without Thrombotic Events. Clinical genetics, 107(2), 179.

Chen L, et al. (2025) Novel AK-1 gene variants combined with thalassemia causing rare hereditary non-spherocytic hemolytic anemia in a Chinese family. Annals of hematology, 104(3), 2035.

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.

Krause MJ, et al. (2025) Distinct dysregulated pathways in sporadic and Lynch syndrome-associated colorectal cancer offer insights for targeted treatment. FEBS letters, 599(7), 1006.

Majeed S, et al. (2025) Identification of candidate nsSNPs of the human FNDC5 gene and their structural and functional consequences using in silico analysis. Scientific reports, 15(1), 7681.

Heo JY, et al. (2025) PRP: pathogenic risk prediction for rare nonsynonymous single nucleotide variants. Human genetics, 144(6), 679.

Sarachakov A, et al. (2025) MutAnt: mutation annotation tool predicts deleteriousness of missense mutations and improves mutation calling from transcriptomics. Human genetics, 144(11-12), 1245.

Danbaki AS, et al. (2025) Pathogenic FANCC Variants Are Associated with Accessory Breasts in a Sub-Saharan African Multiplex Family. Current issues in molecular biology, 47(11).

Elasbali AM, et al. (2025) A structural genomics approach to investigate Dystrophin mutations and their impact on the molecular pathways of Duchenne muscular dystrophy.

Frontiers in genetics, 16, 1517707.

Nie Y, et al. (2025) Origin and cell type specificity of mitochondrial DNA mutations in C9ORF72 ALS-FTLD human brain organoids. Science advances, 11(10), eadr0690.

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.

Sarker DK, et al. (2025) Exploring the impact of deleterious missense nonsynonymous single nucleotide polymorphisms in the DRD4 gene using computational approaches. Scientific reports, 15(1), 3150.

Gill H, et al. (2025) A clinico-genomic prognostic model for primary myelodysplastic neoplasm in Asia. Blood cancer journal, 15(1), 128.

Yadav M, et al. (2025) Paucity of optineurin gene variants in Indian juvenile open-angle glaucoma patients. Indian journal of ophthalmology, 73(8), 1181.

Ahamed MS, et al. (2025) Bioinformatics-driven identification of pathogenic missense nsSNPs in the human proto-oncogene SRC and cancer susceptibility. Journal, genetic engineering & biotechnology, 23(4), 100618.

Francisco S, et al. (2025) Restoring adapter protein complex 4 function with small molecules: an in silico approach to spastic paraplegia 50. Protein science : a publication of the Protein Society, 34(1), e70006.