

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 19, 2026

PMut

RRID:SCR_010783

Type: Tool

Proper Citation

PMut (RRID:SCR_010783)

Resource Information

URL: <http://mmb.pcb.ub.es/PMut/>

Proper Citation: PMut (RRID:SCR_010783)

Description: A software aimed at the annotation and prediction of pathological mutations.

Abbreviations: PMut

Resource Type: software resource

Defining Citation: [PMID:15390262](#)

Resource Name: PMut

Resource ID: SCR_010783

Alternate IDs: OMICS_00159

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260912T195723+0000

Ratings and Alerts

No rating or validation information has been found for PMut.

No alerts have been found for PMut.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 80 mentions in open access literature.

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

Mayer T, et al. (2025) Alpha-Synuclein as a Potential Biomarker for Inclusion Body Myositis in Blood and Muscle. *Neuropathology and applied neurobiology*, 51(3), e70019.

Wang Y, et al. (2025) Cantilever beam-based piezoelectric micromachined ultrasonic transducer with post processing soft interconnecting strategy for in-air rangefinding. *Microsystems & nanoengineering*, 11(1), 97.

Kuwada E, et al. (2024) Identification of lineage-specific cis-trans regulatory networks related to kiwifruit ripening initiation. *The Plant journal : for cell and molecular biology*, 120(5), 1987.

Tanshee RR, et al. (2024) A comprehensive in silico investigation into the pathogenic SNPs in the RTEL1 gene and their biological consequences. *PloS one*, 19(9), e0309713.

Iqbal S, et al. (2023) An Integrated Computational Analysis of High-Risk SNPs in Angiopoietin-like Proteins (ANGPTL3 and ANGPTL8) Reveals Perturbed Protein Dynamics Associated with Cancer. *Molecules (Basel, Switzerland)*, 28(12).

Xiao YS, et al. (2023) Clinical and whole exome sequencing findings in children from Yunnan Yi minority ethnic group with retinitis pigmentosa: two case reports. *Journal of medical case reports*, 17(1), 226.

Ahsan T, et al. (2022) Missense variants in the TNFA epitopes and their effects on interaction with therapeutic antibodies-in silico analysis. *Journal, genetic engineering & biotechnology*, 20(1), 7.

Choudhury A, et al. (2022) Comparative analysis of web-based programs for single amino acid substitutions in proteins. *PloS one*, 17(5), e0267084.

Chai CY, et al. (2022) Predicting Deleterious Non-Synonymous Single Nucleotide Polymorphisms (nsSNPs) of HRAS Gene and In Silico Evaluation of Their Structural and Functional Consequences towards Diagnosis and Prognosis of Cancer. *Biology*, 11(11).

Chandran SS, et al. (2022) Immunogenicity and therapeutic targeting of a public neoantigen derived from mutated PIK3CA. *Nature medicine*, 28(5), 946.

Ren Q, et al. (2022) Design and 3D FEM Analysis of a Flexible Piezoelectric Micromechanical Ultrasonic Transducer Based on Sc-Doped AlN Film. *Sensors (Basel, Switzerland)*, 22(21).

Mohammadi P, et al. (2021) Whole-exome sequencing identified first homozygous frameshift variant in the COLEC10 gene in an Iranian patient causing 3MC syndrome type 3. *Molecular genetics & genomic medicine*, 9(11), e1834.

AlAjmi MF, et al. (2021) Impact of Deleterious Mutations on Structure, Function and Stability of Serum/Glucocorticoid Regulated Kinase 1: A Gene to Diseases Correlation. *Frontiers in molecular biosciences*, 8, 780284.

Wei C, et al. (2021) Compound heterozygosity of a novel Q73X mutation and a known R141X mutation in CYP11B1 resulting in 11 β -hydroxylase deficiency in a Chinese boy with congenital adrenal hyperplasia. *The Journal of steroid biochemistry and molecular biology*, 211, 105882.

Özkan S, et al. (2021) Towards a New, Endophenotype-Based Strategy for Pathogenicity Prediction in BRCA1 and BRCA2: In Silico Modeling of the Outcome of HDR/SGE Assays for Missense Variants. *International journal of molecular sciences*, 22(12).

Xing D, et al. (2020) Targeted exome sequencing identified a novel USH2A mutation in a Chinese usher syndrome family: a case report. *BMC ophthalmology*, 20(1), 485.

Bigoni S, et al. (2020) Clinical Genetics Can Solve the Pitfalls of Genome-Wide Investigations: Lesson from Mismapping a Loss-of-Function Variant in KANSL1. *Genes*, 11(10).

Hu TM, et al. (2020) Multiple Rare Risk Coding Variants in Postsynaptic Density-Related Genes Associated With Schizophrenia Susceptibility. *Frontiers in genetics*, 11, 524258.

Wu G, et al. (2020) LncRNA DANCR upregulation induced by TUFT1 promotes malignant progression in triple negative breast cancer via miR-874-3p-SOX2 axis. *Experimental cell research*, 396(2), 112331.

Zhang Z, et al. (2020) Next generation sequencing of RB1 gene for the molecular diagnosis of ethnic minority with retinoblastoma in Yunnan. *BMC medical genetics*, 21(1), 230.