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).

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.

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.

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).

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

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.

Zhang Z, et al. (2020) Next generation sequencing of RB1gene for the molecular diagnosis of ethnic minority with retinoblastoma in Yunnan. BMC medical genetics, 21(1), 230.

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.