Resource Summary Report

Generated by NIF on Sep 18, 2026

PathoMAN

RRID:SCR_026552
Type: Tool

Proper Citation

PathoMAN (RRID:SCR_026552)

Resource Information

URL: https://pathoman.mskcc.org/

Proper Citation: PathoMAN (RRID:SCR_026552)

Description: Web application to automate germline genomic variant curation from clinical sequencing based on ACMG guidelines. Aggregates multiple tracks of genomic, protein and disease specific information from public sources.

Abbreviations: PathoMAN

Synonyms: Pathogenicity of Mutation Analyzer

Resource Type: software resource, web application

Defining Citation: PMID:30787465

Keywords: Aggregates multiple tracks, automate germline genomic variant curation, clinical sequencing, genomic, protein, disease specific information, public sources,

Funding: NCI P30CA008748;
NCI P50CA221745;
NCI R21CA029533

Availability: Free, Freely available,

Resource Name: PathoMAN

Resource ID: SCR_026552

Record Creation Time: 20250311T060327+0000

Record Last Update: 20260912T200507+0000

Ratings and Alerts

No rating or validation information has been found for PathoMAN.

No alerts have been found for PathoMAN.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Ghasemnejad T, et al. (2026) Comprehensive evaluation of ACMG/AMP-based variant classification tools. Bioinformatics (Oxford, England), 42(2).

Conry M, et al. (2026) Multiple myeloma risk linked to DNA damage response genes. Journal of hematology & oncology, 19(1), 10.

Guan B, et al. (2022) Identification of Germline Mutations in Upper Tract Urothelial Carcinoma With Suspected Lynch Syndrome. Frontiers in oncology, 12, 774202.