Resource Summary Report

Generated by PRECISE-TBI on Sep 19, 2026

Condel

RRID:SCR_008584
Type: Tool

Proper Citation

Condel (RRID:SCR_008584)

Resource Information

URL: http://bg.upf.edu/condel/home

Proper Citation: Condel (RRID:SCR_008584)

Description: A method to assess the outcome of nonsynonymous SNVs using a consensus deleteriousness score that combines various tools (e.g. SIFT, Polyphen2, MutationAssessor).

Abbreviations: Condel

Synonyms: CONsensus DELeteriousness score of missense SNVs

Resource Type: software resource

Resource Name: Condel

Resource ID: SCR_008584

Alternate IDs: OMICS_00146

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260912T195706+0000

Ratings and Alerts

No rating or validation information has been found for Condel.

No alerts have been found for Condel.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 222 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Rafi MO, et al. (2026) Predicting the Impact of Deleterious Single-Nucleotide Polymorphisms in the p47ING1a Isoform of Human ING1 Gene. Genetics research, 2026(1), e2859448.

Molnar C, et al. (2026) PUMA-induced apoptosis drives bone marrow failure and genomic instability in telomerase-deficient mice. Cell death and differentiation, 33(1), 38.

Ferrer M, et al. (2026) Clinical and molecular characterization of a novel pathogenic AIFM1 E336K mutation connecting mitochondrial dysfunction and neurodegeneration. Cell communication and signaling : CCS, 24(1).

Tang J, et al. (2026) Reduced activity of two LPL C-terminal variants, p.Glu396Val and novel p.Trp417Cys: a clinical, biochemical and structural study. Frontiers in physiology, 17, 1820368.

Nappi A, et al. (2025) BayesRVAT enhances rare-variant association testing through Bayesian aggregation of functional annotations. Genome research, 35(12), 2682.

Wang Q, et al. (2025) A Novel Missense Variant in SORBS2 Is Causative With Familial Alzheimer's Disease. CNS neuroscience & therapeutics, 31(2), e70256.

Helderman NC, et al. (2025) Clinical syndromes linked to biallelic germline variants in MCM8 and MCM9. HGG advances, 6(4), 100480.

Pawar AS, et al. (2025) Leukemia mutated proteins PHF6 and PHIP form a chromatin complex that represses acute myeloid leukemia stemness. Genes & development.

Felício D, et al. (2025) Missense variant in TTBK2 kinase domain causes loss of function and impaired protein phosphorylation. Scientific reports, 16(1), 2501.

Kong AS, et al. (2025) In-silico analysis of nsSNPs in BCL-2 family proteins: Implications for colorectal cancer pathogenesis and therapeutics. Biochemistry and biophysics reports, 42, 101957.

Fan W, et al. (2024) Computational analysis of the deleterious non-synonymous single nucleotide polymorphisms (nsSNPs) in TYR gene impacting human tyrosinase protein and the protein stability. PloS one, 19(11), e0308927.

Wang Z, et al. (2024) VarCards2: an integrated genetic and clinical database for ACMG-AMP variant-interpretation guidelines in the human whole genome. Nucleic acids research, 52(D1), D1478.

Martínez-Hernández A, et al. (2024) CFTR pathogenic variants spectrum in a cohort of Mexican patients with cystic fibrosis. Heliyon, 10(7), e28984.

Rashid M, et al. (2024) High-throughput sequencing and in-silico analysis confirm pathogenicity of novel MSH3 variants in African American colorectal cancer. Neoplasia (New York, N.Y.), 49, 100970.

Pawar AS, et al. (2024) Leukemia-mutated proteins PHF6 and PHIP form a chromatin complex that represses acute myeloid leukemia stemness. bioRxiv : the preprint server for biology.

Koh HYK, et al. (2024) Machine learning optimized DriverDetect software for high precision prediction of deleterious mutations in human cancers. Scientific reports, 14(1), 22618.

Martin-Morales L, et al. (2023) Germline gain-of-function MMP11 variant results in an aggressive form of colorectal cancer. International journal of cancer, 152(2), 283.

Chang L, et al. (2023) An alpha-helix variant p.Arg156Pro in LMNA as a cause of hereditary dilated cardiomyopathy: genetics and bioinfomatics exploration. BMC medical genomics, 16(1), 229.

Prakash S, et al. (2023) Cross-Protection Induced by Highly Conserved Human B, CD4+, and CD8+ T Cell Epitopes-Based Coronavirus Vaccine Against Severe Infection, Disease, and Death Caused by Multiple SARS-CoV-2 Variants of Concern. bioRxiv : the preprint server for biology.

Gonzalez B, et al. (2023) High-throughput sequencing analysis of nuclear-encoded mitochondrial genes reveals a genetic signature of human longevity. GeroScience, 45(1), 311.