

Resource Summary Report

Generated by [kravitz2](#) on Sep 18, 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 [kravitz2](#) .

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 bioinformatics 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.