

Resource Summary Report

Generated by [ASWG](#) on Aug 2, 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: 20260801T190334+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 217 mentions in open access literature.

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

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

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.

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

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.

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*.

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.

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

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.

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.

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*.

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.

Nijboer TCW, et al. (2023) Identification of candidate genes for developmental colour agnosia in a single unique family. *PloS one*, 18(9), e0290013.

Asaad M, et al. (2023) Loss-of-function mutations in MYO15A and OTOF cause non-syndromic hearing loss in two Yemeni families. *Human genomics*, 17(1), 42.

Lourenço RA, et al. (2023) BRCA1 VUS: A functional analysis to differentiate pathogenic from benign variants identified in clinical diagnostic panels for breast cancer. *Molecular medicine reports*, 28(1).

Zheng J, et al. (2023) RAF1 mutation leading to hypertrophic cardiomyopathy in a Chinese family with a history of sudden cardiac death: A diagnostic insight into Noonan syndrome. *Molecular genetics & genomic medicine*, 12(1), e2290.

AlGhamdi NA, et al. (2022) Emerging of composition variations of SARS-CoV-2 spike protein and human ACE2 contribute to the level of infection: in silico approaches. *Journal of biomolecular structure & dynamics*, 40(6), 2635.