Resource Summary Report

Generated by RRID 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 RRID .

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

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

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

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.

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.

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.

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

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.

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).

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.