Resource Summary Report

Generated by T1D on Aug 8, 2026

CAROL

RRID:SCR_001800
Type: Tool

Proper Citation

CAROL (RRID:SCR_001800)

Resource Information

URL: http://www.sanger.ac.uk/science/tools/carol

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Description: Software application that is a combined functional annotation score of non-synonymous coding variants. A major challenge in interpreting whole-exome data is predicting which of the discovered variants are deleterious or neutral. To address this question in silico, they have developed a score called Combined Annotation scoRing toOL (CAROL), which combines information from two bioinformatics tools: PolyPhen-2 and SIFT, in order to improve the prediction of the effect of non-synonymous coding variants. The combination of annotation tools can help improve automated prediction of whole-genome/exome non-synonymous variant functional consequences. (entry from Genetic Analysis Software) The software should run on any UNIX or GNU/Linux system.

Abbreviations: CAROL

Synonyms: Combined Annotation scoRing toOL

Resource Type: software resource, software application

Defining Citation: PMID:22261837

Keywords: gene, genetic, genomic, r, prediction, non-synonymous coding variant

Availability: Free, Available for download, Freely available

Resource Name: CAROL

Resource ID: SCR_001800

Alternate IDs: nlx_154254, OMICS_00143

Old URLs: http://www.sanger.ac.uk/resources/software/carol/

License: Creative Commons

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260808T190451+0000

Ratings and Alerts

No rating or validation information has been found for CAROL.

No alerts have been found for CAROL.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Minsinger KD, et al. (2025) Examinee Nondisclosure of Relevant Medical Information During Transportation-Related Regulatory Examinations: A Case Series. Journal of occupational and environmental medicine, 67(5), e336.

Williamson D, et al. (2022) Medulloblastoma group 3 and 4 tumors comprise a clinically and biologically significant expression continuum reflecting human cerebellar development. Cell reports, 40(5), 111162.

Toma C, et al. (2018) An examination of multiple classes of rare variants in extended families with bipolar disorder. Translational psychiatry, 8(1), 65.

Schiff ER, et al. (2018) Rare coding variant analysis in a large cohort of Ashkenazi Jewish families with inflammatory bowel disease. Human genetics, 137(9), 723.

de la Campa EÁ, et al. (2017) Development of pathogenicity predictors specific for variants that do not comply with clinical guidelines for the use of computational evidence. BMC genomics, 18(Suppl 5), 569.

Tsang H, et al. (2017) Resources for Interpreting Variants in Precision Genomic Oncology Applications. Frontiers in oncology, 7, 214.

Kloss-Brandstätter A, et al. (2015) Validation of Next-Generation Sequencing of Entire Mitochondrial Genomes and the Diversity of Mitochondrial DNA Mutations in Oral Squamous Cell Carcinoma. PloS one, 10(8), e0135643.

Ritchie GR, et al. (2014) Computational approaches to interpreting genomic sequence variation. Genome medicine, 6(10), 87.

Wain LV, et al. (2014) Whole exome re-sequencing implicates CCDC38 and cilia structure and function in resistance to smoking related airflow obstruction. PLoS genetics, 10(5), e1004314.

Bang SY, et al. (2014) Targeted exon sequencing fails to identify rare coding variants with large effect in rheumatoid arthritis. Arthritis research & therapy, 16(5), 447.

Champion MD, et al. (2013) The evolutionary history of amino acid variations mediating increased resistance of S. aureus identifies reversion mutations in metabolic regulators. PloS one, 8(2), e56466.