**CAROL**

RRID:SCR_001800  
Type: Tool

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**Proper Citation**

CAROL (RRID:SCR_001800)

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**Resource Information**

**URL:** [http://www.sanger.ac.uk/science/tools/carol](http://www.sanger.ac.uk/science/tools/carol)

**Proper Citation:** CAROL (RRID:SCR_001800)

**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

**Resource Name:** CAROL

**Resource ID:** SCR_001800

**Alternate IDs:** nlx_154254, OMICS_00143
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 10 mentions in open access literature.

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

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.


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.

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