

Resource Summary Report

Generated by [kravitz2](#) on Aug 23, 2026

Coselens

RRID:SCR_022578

Type: Tool

Proper Citation

Coselens (RRID:SCR_022578)

Resource Information

URL: <https://github.com/ggruenhagen3/coselens>

Proper Citation: Coselens (RRID:SCR_022578)

Description: Software R package to detect gene level differential selection between two groups of samples.Used for calculation of excess of non synonymous mutations between two groups.

Synonyms: COnditional SElection on the Excess of NonSynonymous Substitutions

Resource Type: software resource, software toolkit

Defining Citation: [DOI:10.1101/2022.01.10.475617](https://doi.org/10.1101/2022.01.10.475617)

Keywords: detect gene level differential selection, selection between two groups of samples, calculation of excess mutation, non synonymous mutations,

Funding: Spanish Ministry of Science

Availability: Free, Available for download, Freely available

Resource Name: Coselens

Resource ID: SCR_022578

Record Creation Time: 20220726T050157+0000

Record Last Update: 20260821T194227+0000

Ratings and Alerts

No rating or validation information has been found for Coselens.

No alerts have been found for Coselens.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Olafsson S, et al. (2026) A meta-analysis identifies driver genes and characterizes the molecular epidemiology of colorectal cancer. Scientific reports, 16(1).

Iranzo J, et al. (2023) Protocol for comparing gene-level selection on coding mutations between two groups of samples with Coselens. STAR protocols, 4(1), 102117.

Iranzo J, et al. (2022) Pervasive conditional selection of driver mutations and modular epistasis networks in cancer. Cell reports, 40(8), 111272.