

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 21, 2026

Evolutionary Rate Covariation

RRID:SCR_015669

Type: Tool

Proper Citation

Evolutionary Rate Covariation (RRID:SCR_015669)

Resource Information

URL: http://csb.pitt.edu/erc_analysis/Methods.php

Proper Citation: Evolutionary Rate Covariation (RRID:SCR_015669)

Description: Web-based statistical application that measures correlated rates across a phylogeny, allowing for extraction of genes with similar evolutionary histories. It can identify new functional connections between genes.

Abbreviations: ERC

Synonyms: ERC: Evolutionary Rate Covariation, Evolutionary Rate Covariation (ERC) Analysis, Evolutionary Rate Covariation (ERC)

Resource Type: data analysis software, data processing software, software application, software resource, web application

Defining Citation: [PMID:25679399](#), [PMID:24453993](#), [PMID:22287101](#)

Keywords: statistical software, correlation, phylogeny, gene extraction, genetic evolutionary history, covariation, group analysis

Availability: Freely available, Free, Available for download

Resource Name: Evolutionary Rate Covariation

Resource ID: SCR_015669

Record Creation Time: 20220129T080326+0000

Record Last Update: 20260919T195310+0000

Ratings and Alerts

No rating or validation information has been found for Evolutionary Rate Covariation.

No alerts have been found for Evolutionary Rate Covariation.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Francette AM, et al. (2026) Evolutionary analysis of transcription elongation factors reveals conserved and lineage-specific regulatory domains. PLoS biology, 24(6), e3003855.

Himmelstein DS, et al. (2017) Systematic integration of biomedical knowledge prioritizes drugs for repurposing. eLife, 6.