

Resource Summary Report

Generated by [dkNET](#) on Sep 3, 2026

GENERA

RRID:SCR_023113

Type: Tool

Proper Citation

GENERA (RRID:SCR_023113)

Resource Information

URL: <https://github.com/Lcornet/GENERA>

Proper Citation: GENERA (RRID:SCR_023113)

Description: Software toolbox to infer completely reproducible comparative genomic and metabolic analyses on prokaryotes and small eukaryotes.

Synonyms: GEN-ERA toolbox

Resource Type: data or information resource, narrative resource, training material, workflow

Keywords: Genomic, Genome assembly, Phylogeny, Phylogenomic, comparative genomic, metabolic analyses, prokaryotes, eukaryotes

Availability: Free, Available for download, Freely available

Resource Name: GENERA

Resource ID: SCR_023113

License: GNU GPL v3.0

Record Creation Time: 20230116T062750+0000

Record Last Update: 20260829T182824+0000

Ratings and Alerts

No rating or validation information has been found for GENERA.

No alerts have been found for GENERA.

Data and Source Information

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Chen T, et al. (2026) Assessment of dispersion metrics for estimating single-cell transcriptional variability. PLoS computational biology, 22(3), e1014030.

Remmel A, et al. (2025) Recently Evolved, Stage-Specific Genes Are Enriched at Life-Stage Transitions in Flies. Journal of experimental zoology. Part B, Molecular and developmental evolution, 344(7), 428.

Einspanier S, et al. (2025) Co-option of transcription factors drives evolution of quantitative disease resistance against a necrotrophic pathogen. The Plant cell, 37(10).

Sami AA, et al. (2025) The phylotranscriptomic profile of angiosperm seed development follows a reverse hourglass pattern. The Plant cell, 37(12).

Piovani L, et al. (2025) The genomic origin of the unique chaetognath body plan. Nature, 645(8082), 964.

Roces V, et al. (2025) Pra-GE-ATLAS: Empowering Pinus radiata stress and breeding research through a multi-omics database. Journal of integrative plant biology, 67(8), 2028.

Lotharukpong JS, et al. (2024) A transcriptomic hourglass in brown algae. Nature, 635(8037), 129.

Larue GE, et al. (2023) Where the minor things are: a pan-eukaryotic survey suggests neutral processes may explain much of minor intron evolution. Nucleic acids research, 51(20), 10884.

Cornet L, et al. (2022) The GEN-ERA toolbox: unified and reproducible workflows for research in microbial genomics. GigaScience, 12.