

Resource Summary Report

Generated by T1D on Aug 2, 2026

Exonerate

RRID:SCR_016088

Type: Tool

Proper Citation

Exonerate (RRID:SCR_016088)

Resource Information

URL: <https://www.ebi.ac.uk/about/vertebrate-genomics/software/exonerate>

Proper Citation: Exonerate (RRID:SCR_016088)

Description: Software package for sequence alignment of pairwise sequence comparison. Exonerate can be used to align sequences using many alignment models, exhaustive dynamic programming, or a variety of heuristics., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Resource Type: image analysis software, software toolkit, alignment software, software application, data processing software, software resource

Defining Citation: [PMID:15713233](https://pubmed.ncbi.nlm.nih.gov/15713233/)

Keywords: sequence, alignment, pairwise, comparison, dynamic, programming, heuristic, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Exonerate

Resource ID: SCR_016088

Alternate IDs: biotools:exonerate

Alternate URLs: <https://bio.tools/exonerate>

License: GPL

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260801T190527+0000

Ratings and Alerts

No rating or validation information has been found for Exonerate.

No alerts have been found for Exonerate.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 374 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Jiang D, et al. (2025) The telomere-to-telomere genome of flowering cherry (*Prunus campanulata*) reveals genomic evolution of the subgenus *Cerasus*. *GigaScience*, 14.

Zhang R, et al. (2025) Chromosomal level genome assembly of medicinal plant *Rosa laevigata*. *Scientific data*, 12(1), 716.

Mo S, et al. (2025) Rapid Evolution of Host Repertoire and Geographic Range in a Young and Diverse Genus of Montane Butterflies. *Systematic biology*, 74(1), 141.

Liu F, et al. (2025) The telomere-to-telomere gapless genome of grass carp provides insights for genetic improvement. *GigaScience*, 14.

Policarpo M, et al. (2025) Multiple Horizontal Transfers of Immune Genes Between Distantly Related Teleost Fishes. *Molecular biology and evolution*, 42(5).

Hu Y, et al. (2025) Highly contiguous genome of the medicinal plant *Sarcandra glabra* (Thunb.) Nakai. *Scientific data*, 12(1), 1508.

Xiang N, et al. (2025) Chromosomal level genome assembly of medicinal plant *Chrysosplenium macrophyllum*. *Scientific data*, 12(1), 1224.

Wang Q, et al. (2025) Loss of olfaction reduces caterpillar performance and increases susceptibility to a natural enemy. *eLife*, 14.

Cheng L, et al. (2025) Genome assembly of *Stewartia sinensis* reveals origin and evolution of orphan genes in Theaceae. *Communications biology*, 8(1), 354.

Stankiewicz KH, et al. (2025) Genomic comparison of the temperate coral *Astrangia poculata* with tropical corals yields insights into winter quiescence, innate immunity, and sexual reproduction. *G3 (Bethesda, Md.)*, 15(4).

Tenger-Trolander A, et al. (2025) Genomic Resources for the Scuttle Fly *Megaselia abdita*: A Model Organism for Comparative Developmental Studies in Flies. *bioRxiv : the preprint server for biology*.

Paulo DF, et al. (2025) Functional genomics implicates ebony in the black pupae phenotype of tephritid fruit flies. *Communications biology*, 8(1), 60.

Lai Y, et al. (2025) Genome assembly of the grassland caterpillar *Gynaephora qinghaiensis*. *Scientific data*, 12(1), 158.

Liao J, et al. (2025) A high-quality chromosome-level genome assembly of Pacific whiteleg shrimp (*Penaeus vannamei*). *Scientific data*, 12(1), 340.

Zou X, et al. (2025) Chromosome-level genome assembly of the pine wood nematode carrier *Arhopalus unicolor*. *Scientific data*, 12(1), 111.

García-Muñoz A, et al. (2025) Evaluating the Assembly Strategy of a Fungal Genome from Metagenomic Data: *Solorina crocea* (Peltigerales, Ascomycota) as a Case Study. *Journal of fungi* (Basel, Switzerland), 11(8).

Tang M, et al. (2025) A facultative plasminogen-independent thrombolytic enzyme from *Sipunculus nudus*. *Nature communications*, 16(1), 3852.

Liu H, et al. (2025) A telomere-to-telomere gapless genome reveals SIPRR1 control of circadian rhythm and photoperiodic flowering in tomato. *GigaScience*, 14.

Nakamura Y, et al. (2025) Distribution of estrogen sulfotransferase genes in tunas and their relatives. *BMC research notes*, 18(1), 308.

Li Y, et al. (2025) Chromosome-level genome assembly assisting for dissecting mechanism of anthocyanin regulation in kiwifruit (*Actinidia arguta*). *Molecular horticulture*, 5(1), 18.