

Resource Summary Report

Generated by NIF on May 14, 2025

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.

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

Defining Citation: [PMID:15713233](#)

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

Funding:

Availability: Free, Available for download

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: 20250513T061729+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 345 mentions in open access literature.

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

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.

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

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

Li L, et al. (2025) A Chromosomal-level genome assembly and annotation of fat greenling (*Hexagrammos otakii*). *Scientific data*, 12(1), 78.

Matthews MC, et al. (2025) A combined recombinase polymerase amplification CRISPR/Cas12a assay for detection of *Fusarium oxysporum* f. sp. *cubense* tropical race 4. *Scientific reports*, 15(1), 2436.

Tao L, et al. (2024) Chromosome-level genome assembly of the threatened resource plant *Cinnamomum chago*. *Scientific data*, 11(1), 447.

Wang M, et al. (2024) Annotation of 2,507 *Saccharomyces cerevisiae* genomes. *Microbiology spectrum*, 12(4), e0358223.

Brainard SH, et al. (2024) The first two chromosome-scale genome assemblies of American hazelnut enable comparative genomic analysis of the genus *Corylus*. *Plant biotechnology journal*, 22(2), 472.

Decker SH, et al. (2024) Boring systematics: A genome skinned phylogeny of ctenostome bryozoans and their endolithic family Penetrantiidae with the description of one new species. *Ecology and evolution*, 14(4), e11276.

Hafezi Y, et al. (2024) The *Drosophila melanogaster* Y-linked gene, WDY, is required for sperm to swim in the female reproductive tract. *Communications biology*, 7(1), 90.

He J, et al. (2024) A chromosome-level genome assembly for *Onobrychis viciifolia* reveals gene copy number gain underlying enhanced proanthocyanidin biosynthesis. *Communications biology*, 7(1), 19.

Mukhametzyanova L, et al. (2024) Activation of recombinases at specific DNA loci by zinc-finger domain insertions. *Nature biotechnology*.

Li M, et al. (2024) Chromosome-level genome assembly of *Aquilaria yunnanensis*. *Scientific data*, 11(1), 790.

Cao S, et al. (2024) Gapless genome assembly and epigenetic profiles reveal gene regulation of whole-genome triplication in lettuce. *GigaScience*, 13.

Langdon QK, et al. (2024) Swordtail fish hybrids reveal that genome evolution is surprisingly predictable after initial hybridization. *PLoS biology*, 22(8), e3002742.

Wang H, et al. (2024) The genomes of *Dahlia pinnata*, *Cosmos bipinnatus*, and *Bidens alba* in tribe Coreopsideae provide insights into polyploid evolution and inulin biosynthesis. *GigaScience*, 13.

Kim B, et al. (2024) Chromosome-level genome assembly of Korean holoparasitic plants, *Orobanche coerulescens*. *Scientific data*, 11(1), 714.

Kiang AL, et al. (2024) Insights into genomic sequence diversity of the SAG surface antigen superfamily in geographically diverse *Eimeria tenella* isolates. *Scientific reports*, 14(1), 26251.

Rabeh K, et al. (2024) Genome-wide identification of SSR markers from coding regions for endangered *Argania spinosa* L. skeels and construction of SSR database: AsSSRdb. *Database : the journal of biological databases and curation*, 2024.