Resource Summary Report

Generated by RRID on Apr 8, 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: alignment software, software application, software toolkit, data processing software, image analysis software, software resource

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: 20250407T220308+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 RRID.

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 skimmed 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.