

Resource Summary Report

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LoRDEC

RRID:SCR_015814

Type: Tool

Proper Citation

LoRDEC (RRID:SCR_015814)

Resource Information

URL: <http://www.atgc-montpellier.fr/lordec/>

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Description: Software that performs hybrid error correction for long, PacBio reads. LoRDEC can correct insertions, deletions, and substitutions in PacBio reads.

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

Defining Citation: [PMID:25165095](#)

Keywords: hybrid error correction, pacbio read, long error correction, real-time sequencing, bio.tools

Funding: Academy of Finland 267591;
ANR Colib'read ANR-12-BS02-0008

Availability: Free, Available for download

Resource Name: LoRDEC

Resource ID: SCR_015814

Alternate IDs: biotools:lordec

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

License: CeCILL A license

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260801T190520+0000

Ratings and Alerts

No rating or validation information has been found for LoRDEC.

No alerts have been found for LoRDEC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 206 mentions in open access literature.

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

Yan Y, et al. (2025) Comprehensive full-Length transcriptomic resource for wing dimorphism in English green aphid, *Sitobion avenae*. *Scientific data*, 12(1), 1034.

He H, et al. (2025) Chromosome-level genome assembly of *Monolepta hieroglyphica*, two-spotted leaf beetle (Coleoptera: Chrysomelidae). *Scientific data*, 12(1), 1.

Brunelli L, et al. (2025) Genetic and phenotypic stability of *Lactocaseibacillus paracasei* DG (DSM 34154) over 10 years of industrial production. *Applied and environmental microbiology*, 91(5), e0239424.

Li J, et al. (2025) Full-length transcriptome analysis of male and female gonads in Japanese Eel (*Anguilla japonica*). *BMC genomics*, 26(1), 89.

Hegedüs B, et al. (2025) Morphogenesis, starvation, and light responses in a mushroom-forming fungus revealed by long-read sequencing and extensive expression profiling. *Cell genomics*, 5(6), 100853.

Tonon E, et al. (2025) Chromosomal-level assembly of *Magnusiomyces clavatus*: novel genetic insights on an emerging fungal pathogen. *G3 (Bethesda, Md.)*, 15(11).

Li Y, et al. (2025) Skeleton-Forming Responses of Reef-Building Corals under Ocean Acidification. *Research (Washington, D.C.)*, 8, 0736.

Zhang B, et al. (2025) Transcriptome-wide analysis of AlbHLH gene family in *Atractylodes lancea* (Thunb.) DC and functional exploration of AlbHLH3 in regulating terpenoid biosynthesis. *BMC plant biology*, 25(1), 1551.

Park H, et al. (2025) Chromosome-level genome of *Zoysia sinica* in the intertidal zone reveals genomic insights into waterlogging stress adaptation. *The plant genome*, 18(3), e70070.

Peng Y, et al. (2024) Characterization and analysis of multi-organ full-length transcriptomes in *Sphaeropteris brunoniana* and *Alsophila latebrosa* highlight secondary metabolism and chloroplast RNA editing pattern of tree ferns. *BMC plant biology*, 24(1), 73.

Bai Y, et al. (2024) Color components determination and full-length comparative transcriptomic analyses reveal the potential mechanism of carotenoid synthesis during *Paphiopedilum armeniacum* flowering. *PeerJ*, 12, e16914.

Zhang W, et al. (2024) Transcriptome analysis reveals the regulatory mechanism of myofiber development in male and female black Muscovy duck at different ages. *Frontiers in veterinary science*, 11, 1484102.

Wang L, et al. (2024) Multiple strategies, including 6mA methylation, affecting plant alternative splicing in allopolyploid peanut. *Plant biotechnology journal*, 22(6), 1681.

Liu S, et al. (2024) The *Chrysosplenium sinicum* genome provides insights into adaptive evolution of shade plants. *Communications biology*, 7(1), 1004.

Zhang T, et al. (2024) Comparative transcriptomic analysis delineates adaptation strategies of *Rana kukunoris* toward cold stress on the Qinghai-Tibet Plateau. *BMC genomics*, 25(1), 363.

Searle PC, et al. (2024) Heterochronic shift in gene expression leads to ontogenetic morphological divergence between two closely related polyploid species. *iScience*, 27(4), 109566.

Jiao N, et al. (2024) Genome-wide characterization of post-transcriptional processes related to wood formation in *Dalbergia odorifera*. *BMC genomics*, 25(1), 372.

Wang Y, et al. (2024) Full-length single-molecule sequencing uncovers novel insight into the global landscape of the cold stress response in trifoliate orange (*Citrus trifoliata*). *Frontiers in plant science*, 15, 1506414.

Hou Z, et al. (2024) Mitochondrial genome insights into the spatio-temporal distribution and genetic diversity of *Dendrobium hancockii* Rolfe (Orchidaceae). *Frontiers in plant science*, 15, 1469267.

Lin CY, et al. (2024) Chromosome-level genome assemblies of 2 hemichordates provide new insights into deuterostome origin and chromosome evolution. *PLoS biology*, 22(6), e3002661.