

# Resource Summary Report

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## **BUSCO**

RRID:SCR\_015008

Type: Tool

### Proper Citation

BUSCO (RRID:SCR\_015008)

### Resource Information

**URL:** <http://busco.ezlab.org/>

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**Description:** Software tool to quantitatively measure genome assembly and annotation completeness based on evolutionarily informed expectations of gene content.

**Synonyms:** BUSCO v2, Benchmarking Universal Single-Copy Orthologs (BUSCO), Benchmarking Universal Single-Copy Orthologs, BUSCO v1

**Resource Type:** algorithm resource, data analysis software, data processing software, software application, software resource

**Defining Citation:** [DOI:10.1093/bioinformatics/btv351](https://doi.org/10.1093/bioinformatics/btv351)

**Keywords:** genome assembly, annotation completeness, quantitative method, bio.tools

**Funding:** Marie Curie International Outgoing Fellowship ;  
Swiss National Science Foundation

**Availability:** Free, Available for download, Freely available

**Resource Name:** BUSCO

**Resource ID:** SCR\_015008

**Alternate IDs:** biotools:busco

**Alternate URLs:** <https://gitlab.com/ezlab/busco>, <https://bio.tools/busco>,  
<https://sources.debian.org/src/busco/>

**License:** GNU GPL

**Record Creation Time:** 20220129T080323+0000

## Ratings and Alerts

No rating or validation information has been found for BUSCO.

No alerts have been found for BUSCO.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 8320 mentions in open access literature.

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

Zeng L, et al. (2026) Functional genomics reveals key gene families and molecular pathways for extreme cold survival in the khapra beetle. *BMC biology*, 24(1).

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

Liu P, et al. (2026) Discovery of mannose as an alternative non-nutrient-deficient regulator of lipid accumulation in microalgae. *Journal of advanced research*, 79, 239.

Pennington LK, et al. (2026) A reference genome for Colusa grass, *Neostapfia colusana*, a threatened and endangered California vernal pool plant. *The Journal of heredity*, 117(3), 459.

Adedokun AA, et al. (2026) Exploring the First Draft Genome of the Oribatid Mite, *Oppia nitens*: A Standardized Model Invertebrate in Soil Ecotoxicology. *Genome biology and evolution*, 18(2).

Qiu B, et al. (2026) Arms races between selfish genetic elements and their host defence in termites. *Nature communications*, 17(1), 1702.

Zhang X, et al. (2026) Integrative transcriptomic and metabolomic analysis of *Drynaria roosii* reveals genes involved in the biosynthesis of medicinal compounds. *Scientific reports*, 16(1).

Postma A, et al. (2026) Genome and transcriptome-based identification and expression profiling of chemosensory gene families across developmental stages and tissues in *Sirex noctilio* (Hymenoptera: Siricidae). *Insect molecular biology*, 35(3), 270.

Penaranda C, et al. (2026) Genomic comparison and phenotypic characterization of *Pseudomonas aeruginosa* isolates across environmental and diverse clinical isolation sites. *mSystems*, 11(3), e0136225.

Dong Z, et al. (2026) Fungal photobiont and microbiome genome composition in the *Cladonia uncialis* tripartite symbiosis. *Scientific data*, 13(1).

Mdyogolo S, et al. (2026) A high-quality chromosome level genome assembly of the South African indigenous Nguni goat (*Capra hircus*). *Scientific data*, 13(1).

Abrecht M, et al. (2026) A chromosome-level genome assembly for the beach-spawning California grunion, *Leuresthes tenuis*. *The Journal of heredity*, 117(4), 856.

Mu D, et al. (2026) The genome of the medicinal plant *Uncaria rhynchophylla* provides new insights into monoterpenoid indole alkaloid metabolism and its molecular regulatory mechanism. *Molecular horticulture*, 6(1), 9.

Kuang Z, et al. (2026) Genomic insights into chromosomal fusion and its evolutionary implications for zokors. *Molecular biology and evolution*, 43(2).

Dong H, et al. (2026) The genome of *Phlebotomus chinensis*, the primary vector of visceral leishmaniasis in China: insights from chromosome-level assembly and comparative analysis. *Infectious diseases of poverty*, 15(1), 20.

Krah FS, et al. (2026) Population Genomics of a Rare and a Common Wood-Inhabiting Fungal Species Across Europe. *Molecular ecology*, 35(3), e70260.

García-García I, et al. (2026) De novo transcriptome assembly of the silver fir, *Abies alba* Mill. *Scientific data*, 13(1).

Sessi IR, et al. (2026) First whole-genome assembly of the Galápagos Petrel (*Pterodroma phaeopygia*) using Oxford Nanopore sequencing to advance conservation genomics in a critically endangered seabird. *G3 (Bethesda, Md.)*, 16(3).

Corre P, et al. (2026) Energy metabolism and adaptation to hypoxia in the non-photosynthetic green alga *Leontynka*. *BMC biology*, 24(1).

Wijaya SC, et al. (2026) Linking metagenomic insight to cultivable microbes: isolation of a vitamin B12-producing *Sphingomonad* from Indonesian tempeh. *BMC microbiology*, 26(1), 127.