

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.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8320 mentions in open access literature.

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

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.