

Resource Summary Report

Generated by [NIF](#) on Aug 31, 2026

BUSCO

RRID:SCR_015008

Type: Tool

Proper Citation

BUSCO (RRID:SCR_015008)

Resource Information

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

Proper Citation: BUSCO (RRID:SCR_015008)

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 [NIF](#) .

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.

She J, et al. (2026) DOO: integrated multi-omics resources for deep ocean organisms. Nucleic acids research, 54(D1), D1031.

Yunusbaev U, et al. (2026) The Evolution and Origin of Allotetraploid Aegilops geniculata Revealed by the Homoeolog-Resolved Genome Assembly. Plant biotechnology journal, 24(3), 1866.

Chen Z, et al. (2026) Evaluating Probe Design for Phylogenomics Across Taxonomic Scales: First Steps for Applying Ultraconserved Elements in an Understudied Class (Mollusca: Polyplacophora). Molecular ecology resources, 26(1), e70076.

Hu H, et al. (2026) Structural variation drives rhizome innovation and adaptive divergence in sister Medicago species. Journal of integrative plant biology, 68(2), 406.

Sahoo RK, et al. (2026) Genome assembly and protein structure modeling reveal key molecular features of divergent wmk homologs in Wolbachia. Microbiology spectrum, 14(2), e0289325.

Wood JC, et al. (2026) Chromosome-scale genome assembly for yellow wood sorrel, Oxalis stricta. G3 (Bethesda, Md.), 16(3).

Helmy M, et al. (2026) High-quality mouse reference genomes reveal the structural complexity of the murine protein-coding landscape. *Cell genomics*, 6(2), 101074.

Park S, et al. (2026) Structural variation and evolutionary dynamics of plastid genomes in the subgenus *Lychnis* (*Silene*, *Caryophyllaceae*): insights from genome rearrangements and substitution rates. *BMC plant biology*, 26(1), 266.

Ji R, et al. (2026) GdbMTB: a manually curated genomic database of magnetotactic bacteria. *Database : the journal of biological databases and curation*, 2026.

Dhakad P, et al. (2026) Comparative gene annotation and orthology assignments across 301 species of *Drosophilidae*. *bioRxiv : the preprint server for biology*.

Baker HK, et al. (2026) The genome assemblies of the Tui chub, *Siphateles bicolor*, and Arroyo chub, *Gila orcuttii*. *The Journal of heredity*, 117(4), 843.

Alshwairikh YA, et al. (2026) The transcriptomics and differential gene expression of freezing and thawing in a freeze-tolerant vertebrate. *BMC genomics*, 27(1), 167.

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.

Li FQ, et al. (2026) Transcriptomic Resource of *Trissolcus cultratus*: A Key Biological Control Agent for *Halyomorpha halys*. *Scientific data*, 13(1).

Wijesundara UK, et al. (2026) Chromosome-Scale Haplotype Genome Assemblies for the Australian Mango 'Kensington Pride' and a Wild Relative, *Mangifera laurina*, Provide Insights Into Anthracnose-Resistance and Volatile Compound Biosynthesis Genes. *Plant biotechnology journal*, 24(5), 3172.

Jarrell AF, et al. (2026) Building genomic resources to facilitate the study and use of *Solanum microdontum*, a wild relative of cultivated potato. *G3 (Bethesda, Md.)*, 16(1).

Zhou W, et al. (2026) Comparative analysis of gene family evolution demonstrates expansion of digestive, immunity and olfactory functions in the black soldier fly (*Hermetia illucens*) lineage. *Heredity*, 135(3), 187.