

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/>

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 [RRID](#) .

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.