

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: software application, data processing software, algorithm resource, data analysis software, 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: Swiss National Science Foundation ;
Marie Curie International Outgoing Fellowship

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 7284 mentions in open access literature.

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

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.

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).

García JF, et al. (2026) Intraspecies sequence-graph analysis of the *Phytophthora theobromicola* genome reveals a dynamic structure and variable effector repertoires. *G3 (Bethesda, Md.)*, 16(1).

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.

Richmond JQ, et al. (2026) A chromosome-level reference genome assembly for Gilbert's skink *Plestiodon gilberti*. *The Journal of heredity*, 117(1), 115.

Gao C, et al. (2026) High-Quality Genome Assembly of *Diplocarpon coronariae* Unveils LTR Retrotransposon-Driven Structural Dynamics in Fungi Evolution. *Molecular ecology resources*, 26(1), e70070.

Johns J, et al. (2026) A near chromosome-level assembly of the serpentine endemic columbine, *Aquilegia eximia*. *The Journal of heredity*, 117(1), 85.

Wang B, et al. (2026) The expansion of culturable opportunistic pathogens and antibiotic resistance in mouse gut following antibiotic exposure. *Microbiology spectrum*, 14(1), e0110425.

Shi M, et al. (2026) Genomic architecture and evolution of heterostyly: new insights from *Cordia subcordata* (Boraginaceae). *Molecular biology and evolution*, 43(1).

Kulikov N, et al. (2026) The Chromosome-Scale Genome Assembly of the Redlip Blenny, *Ophioblennius macclurei* (Blenniidae). *Genome biology and evolution*, 18(1).

Mantzana-Oikonomaki V, et al. (2026) Pigments, Chromatophore Structure, and Gene Expression Underlying Colour Polytypy of a Panamanian Poison Frog. *Molecular ecology*, 35(1), e70214.

Lv X, et al. (2026) *Blautia coccoides*-derived metabolite trimethylamine-N-oxide exacerbates Alzheimer's disease progression via targeting HIF1 α signaling. *Gut microbes*, 18(1), 2605768.

Sun T, et al. (2026) Conserved spatial patterning of gene expression in independent lineages of C4 plants. *The New phytologist*, 249(1), 24.

Hirase S, et al. (2026) Ancestral Origin and Structural Characteristics of Non-Syntenic Homologous Chromosomes in Abalones (*Haliotis*). *Molecular ecology resources*, 26(1), e70057.

Tagirdzhanova G, et al. (2026) Chromosome-level genome assembly of the photobiont microalga *Trebouxia* sp. 'A48' from the lichen *Xanthoria parietina*. *The New phytologist*, 249(2), 1036.

Contreras-Moreira B, et al. (2026) The PanOryza pangene catalog of Asian cultivated rice. *Genome research*, 36(1), 226.

Wang YH, et al. (2026) Insights into dill (*Anethum graveolens*) flavor formation via integrative analysis of chromosomal-scale genome, metabolome and transcriptome. *Journal of advanced research*, 79, 847.

Sperschneider J, et al. (2026) The fungal pathogen *Rhizoctonia solani* AG-8 has 2 nuclear haplotypes that differ in abundance. *G3 (Bethesda, Md.)*, 16(1).

Luo Z, et al. (2026) Host adaptation and genome evolution of the broad host range fungal rust pathogen, *Austropuccinia psidii*. *G3 (Bethesda, Md.)*, 16(1).

Ganesh A, et al. (2026) The Karnataka Individual Genome Project expands the human reference landscape to include South Asia. *HGG advances*, 7(1), 100516.