Resource Summary Report

Generated by RRID on Apr 9, 2025

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: software application, data analysis software, software resource, data processing software, algorithm resource

Defining Citation: DOI: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

Record Last Update: 20250409T061240+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 5901 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Polinski JM, et al. (2025) Chromosome-level reference genome for the Jonah crab, Cancer borealis. G3 (Bethesda, Md.), 15(1).

Liu Z, et al. (2025) Genome architecture of the allotetraploid wild grass Aegilops ventricosa reveals its evolutionary history and contributions to wheat improvement. Plant communications, 6(1), 101131.

Schöneberg Y, et al. (2025) Three Novel Spider Genomes Unveil Spidroin Diversification and Hox Cluster Architecture: Ryuthela nishihirai (Liphistiidae), Uloborus plumipes (Uloboridae) and Cheiracanthium punctorium (Cheiracanthiidae). Molecular ecology resources, 25(1), e14038.

Ragasa LRP, et al. (2025) Comparative genomics reveals putative copper tolerance genes in a Fusarium oxysporum strain. G3 (Bethesda, Md.), 15(1).

Gauthier J, et al. (2025) Chromosome-Scale Genomes of the Flightless Caterpillar Hunter Beetles Calosoma tepidum and Calosoma wilkesii From British Columbia (Coleoptera: Carabidae). Genome biology and evolution, 17(1).

Florean M, et al. (2025) Independent evolution of plant natural products: Formation of benzoxazinoids in Consolida orientalis (Ranunculaceae). The Journal of biological chemistry,

301(1), 108019.

Liu F, et al. (2025) Uneven distribution of prokaryote-derived horizontal gene transfer in fungi: a lifestyle-dependent phenomenon. mBio, 16(1), e0285524.

Li R, et al. (2025) Photosymbiosis shaped animal genome architecture and gene evolution as revealed in giant clams. Communications biology, 8(1), 7.

He H, et al. (2025) Chromosome-level genome assembly of Monolepta hieroglyphica, two-spotted leaf beetle (Coleoptera: Chrysomelidae). Scientific data, 12(1), 1.

Lei Y, et al. (2025) Population sequencing of cherry accessions unravels the evolution of Cerasus species and the selection of genetic characteristics in edible cherries. Molecular horticulture, 5(1), 6.

Kim MS, et al. (2025) Discovery of 15-deoxynaphthomycins activating the antioxidant NRF2-ARE pathway from Streptomyces sp. N50 via genome mining, global regulator introduction, and molecular networking. Microbial cell factories, 24(1), 14.

Cruz-Laufer AJ, et al. (2025) Adaptive evolution of stress response genes in parasites aligns with host niche diversity. BMC biology, 23(1), 10.

Clancy SM, et al. (2025) The Calicophoron daubneyi genome provides new insight into mechanisms of feeding, eggshell synthesis and parasite-microbe interactions. BMC biology, 23(1), 11.

Elizondo-Reyna E, et al. (2025) Insights from a Genome-Wide Study of Pantoea agglomerans UADEC20: A Promising Strain for Phosphate Solubilization and Exopolysaccharides Production. Current issues in molecular biology, 47(1).

Wang X, et al. (2025) Chromosome-level haplotype-resolved genome of the tropical loach (Oreonectes platycephalus). Scientific data, 12(1), 29.

D'aes J, et al. (2025) Metagenomics-based tracing of genetically modified microorganism contaminations in commercial fermentation products. Food chemistry. Molecular sciences, 10, 100236.

Wang Y, et al. (2025) A high-quality chromosome-scale genome assembly of the Cherokee rose (Rosa laevigata). Scientific data, 12(1), 132.

Ma C, et al. (2025) Chromosome-level Genome Assembly and Annotation of the Arctic Moss Ptychostomum knowltonii. Genome biology and evolution, 17(1).

Liu R, et al. (2025) Chromosome-level reference genome and annotation of the Arctic fish Anisarchus medius. Scientific data, 12(1), 68.

Chudhary A, et al. (2025) Characterization of chemosensory genes in the subterranean pest Gryllotalpa Orientalis based on genome assembly and transcriptome comparison. BMC genomics, 26(1), 33.