

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

BUSCOMP

RRID:SCR_021233

Type: Tool

Proper Citation

BUSCOMP (RRID:SCR_021233)

Resource Information

URL: <https://github.com/slimsuite/buscomp>

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Description: Software tool for BUSCO compilation and comparison. Used for assessing completeness in multiple genome assemblies.Used for assembly comparison designed to be robust to differences in assembly size and base calling quality.

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [DOI:10.7490/f1000research.1116972.1](https://doi.org/10.7490/f1000research.1116972.1),
[DOI:10.1101/2021.04.07.438753](https://doi.org/10.1101/2021.04.07.438753)

Keywords: Assessing completeness in multiple genome assemblies, genome assemblies completeness, assemblies completeness assessing

Funding: ARC LP1 60100610;
ARC LP1 80100721

Availability: Free, Available for download, Freely available

Resource Name: BUSCOMP

Resource ID: SCR_021233

License: GNU GPL v3.0

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260905T132936+0000

Ratings and Alerts

No rating or validation information has been found for BUSCOMP.

No alerts have been found for BUSCOMP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Wu L, et al. (2026) Longitudinal Plasma Proteomics Reveals an Immuno-thrombotic Signature That Predicts Radiation Pneumonitis in Lung Cancer. International journal of radiation oncology, biology, physics.

Ballard JWO, et al. (2023) The Australasian dingo archetype: De novo chromosome-length genome assembly, DNA methylome, and cranial morphology. bioRxiv : the preprint server for biology.

Ballard JWO, et al. (2023) The Australasian dingo archetype: de novo chromosome-length genome assembly, DNA methylome, and cranial morphology. GigaScience, 12.

Stuart KC, et al. (2022) Transcript- and annotation-guided genome assembly of the European starling. Molecular ecology resources, 22(8), 3141.