

Resource Summary Report

Generated by SPARC SAWG on Jul 29, 2026

FastUniq

RRID:SCR_000682

Type: Tool

Proper Citation

FastUniq (RRID:SCR_000682)

Resource Information

URL: <http://sourceforge.net/projects/fastuniq/>

Proper Citation: FastUniq (RRID:SCR_000682)

Description: A software tool for removal of de novo duplicates in paired short DNA sequences.

Resource Type: software resource

Defining Citation: [DOI:10.1371/journal.pone.0052249](https://doi.org/10.1371/journal.pone.0052249)

Keywords: de novo, dna, sequence, duplicate,

Availability: Free, Available for download, Freely available

Resource Name: FastUniq

Resource ID: SCR_000682

Alternate IDs: OMICS_01044

Record Creation Time: 20220129T080202+0000

Record Last Update: 20260725T190448+0000

Ratings and Alerts

No rating or validation information has been found for FastUniq.

No alerts have been found for FastUniq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Voelker J, et al. (2021) A high-quality draft genome for *Melaleuca alternifolia* (tea tree): a new platform for evolutionary genomics of myrtaceous terpene-rich species. *GigaByte* (Hong Kong, China), 2021, gigabyte28.

Baek S, et al. (2018) Draft genome sequence of wild *Prunus yedoensis* reveals massive inter-specific hybridization between sympatric flowering cherries. *Genome biology*, 19(1), 127.

Yang W, et al. (2017) The draft genome sequence of a desert tree *Populus pruinosa*. *GigaScience*, 6(9), 1.