

Resource Summary Report

Generated by [nidm-terms](#) on Sep 23, 2026

AHA

RRID:SCR_012090

Type: Tool

Proper Citation

AHA (RRID:SCR_012090)

Resource Information

URL: <https://github.com/PacificBiosciences/Bioinformatics-Training/wiki/AHA>

Proper Citation: AHA (RRID:SCR_012090)

Description: Contigs from a draft assembly generated by a different assembler can be joined using PacBio long reads.

Resource Type: software resource

Defining Citation: [PMID:22750883](#)

Keywords: standalone software

Availability: GNU General Public License

Resource Name: AHA

Resource ID: SCR_012090

Alternate IDs: OMICS_05096

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260919T195224+0000

Ratings and Alerts

No rating or validation information has been found for AHA.

No alerts have been found for AHA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Laehnemann D, et al. (2016) Denoising DNA deep sequencing data-high-throughput sequencing errors and their correction. Briefings in bioinformatics, 17(1), 154.