

# Resource Summary Report

Generated by [dkNET](#) on Sep 3, 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:** 20260903T004057+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 [dkNET](#) .

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