

Resource Summary Report

Generated by [RRID](#) on Aug 14, 2026

HAST

RRID:SCR_018247

Type: Tool

Proper Citation

HAST (RRID:SCR_018247)

Resource Information

URL: <https://github.com/BGI-Qingdao/HAST>

Proper Citation: HAST (RRID:SCR_018247)

Description: Software tool for partition stLFR reads based on trio binning using prenatally unique markers. Haplotype resolved assembly for synthetic long reads using Trio-Binning strategy.

Synonyms: Haplotype-resolved Assembly for Synthetic long reads using a Trio-binning strategy

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

Keywords: Partition stLFR reads, stLFR read, trio binning, haplotype resolved assembly, synthetic long read, reads assembly

Availability: Free, Available for download, Freely available

Resource Name: HAST

Resource ID: SCR_018247

License: GNU GPL v3

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260814T043011+0000

Ratings and Alerts

No rating or validation information has been found for HAST.

No alerts have been found for HAST.

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 [RRID](#) .

Xu M, et al. (2021) Accurate haplotype-resolved assembly reveals the origin of structural variants for human trios. Bioinformatics (Oxford, England), 37(15), 2095.