

# Resource Summary Report

Generated by [RRID](#) on Aug 7, 2026

## HaploMaker

RRID:SCR\_021928

Type: Tool

### Proper Citation

HaploMaker (RRID:SCR\_021928)

### Resource Information

**URL:** <https://github.com/mfuzan/HaploMaker>

**Proper Citation:** HaploMaker (RRID:SCR\_021928)

**Description:** Software pipeline for haplotype assembly of diploid genomes using paired end or PacBio reads.

**Resource Type:** software resource

**Keywords:** haplotype assembly, diploid genomes, paired end reads, PacBio reads

**Availability:** Free, Available for download, Freely available

**Resource Name:** HaploMaker

**Resource ID:** SCR\_021928

**Record Creation Time:** 20220421T050137+0000

**Record Last Update:** 20260801T190719+0000

### Ratings and Alerts

No rating or validation information has been found for HaploMaker.

No alerts have been found for HaploMaker.

### 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](#) .

Fruzangohar M, et al. (2022) HaploMaker: An improved algorithm for rapid haplotype assembly of genomic sequences. GigaScience, 11.