

Resource Summary Report

Generated by T1D on Aug 4, 2026

MIP Scaffolder

RRID:SCR_005072

Type: Tool

Proper Citation

MIP Scaffolder (RRID:SCR_005072)

Resource Information

URL: <http://www.cs.helsinki.fi/u/lmsalmel/mip-scaffolder/>

Proper Citation: MIP Scaffolder (RRID:SCR_005072)

Description: A software program for scaffolding contigs produced by fragment assemblers using mate pair data such as those generated by ABI SOLiD or Illumina Genome Analyzer.

Abbreviations: MIP Scaffolder

Resource Type: software resource

Keywords: scaffolding, bio.tools

Resource Name: MIP Scaffolder

Resource ID: SCR_005072

Alternate IDs: OMICS_00044, biotools:mip_scaffolder

Alternate URLs: https://bio.tools/mip_scaffolder

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260801T190253+0000

Ratings and Alerts

No rating or validation information has been found for MIP Scaffolder.

No alerts have been found for MIP Scaffolder.

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 [T1D](#) .

El-Metwally S, et al. (2013) Next-generation sequence assembly: four stages of data processing and computational challenges. PLoS computational biology, 9(12), e1003345.