

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 30, 2026

## [ABMapper](#)

RRID:SCR\_010242

Type: Tool

### Proper Citation

ABMapper (RRID:SCR\_010242)

### Resource Information

**URL:** <http://hkbic.cuhk.edu.hk/software/abmapper>

**Proper Citation:** ABMapper (RRID:SCR\_010242)

**Description:** A portable, easy-to-use package for spliced alignment, junction site detection, and reads mapping. The core module was written in C++ and wrapped in PERL scripts.

**Abbreviations:** ABMapper

**Synonyms:** ABMapper: A suffix-array based spliced alignment tool

**Resource Type:** software resource

**Resource Name:** ABMapper

**Resource ID:** SCR\_010242

**Alternate IDs:** OMICS\_01238

**Record Creation Time:** 20220129T080257+0000

**Record Last Update:** 20260725T190658+0000

### Ratings and Alerts

No rating or validation information has been found for ABMapper.

No alerts have been found for ABMapper.

### 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 [PRECISE-TBI](#) .

Li MW, et al. (2013) Silicon era of carbon-based life: application of genomics and bioinformatics in crop stress research. International journal of molecular sciences, 14(6), 11444.