

# Resource Summary Report

Generated by [kravitz2](#) on Aug 26, 2026

## ALLMAP

RRID:SCR\_021120

Type: Tool

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### Proper Citation

ALLMAP (RRID:SCR\_021120)

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### Resource Information

**URL:** <https://github.com/tanghaibao/jcvi/wiki/ALLMAPS>

**Proper Citation:** ALLMAP (RRID:SCR\_021120)

**Description:** Software tool for computing scaffold ordering that maximizes colinearity across collection of maps including genetic, physical or comparative maps into final chromosome build. Robust scaffold ordering based on multiple maps. ALLMAPS is robust against common mapping errors, and generates sequences that are maximally concordant with input maps. Used in building high quality genome assemblies.

**Resource Type:** software resource

**Defining Citation:** [DOI:10.1186/s13059-014-0573-1](https://doi.org/10.1186/s13059-014-0573-1)

**Keywords:** Computing scaffold ordering, colinearity across map collection maximization, final chromosome build, robust scaffold ordering, multiple maps, common mapping errors, genome assemblies

**Funding:** Gordon and Betty Moore Foundation ;  
National Science Foundation

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

**Resource Name:** ALLMAP

**Resource ID:** SCR\_021120

**Record Creation Time:** 20220129T080353+0000

**Record Last Update:** 20260815T182652+0000

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### Ratings and Alerts

No rating or validation information has been found for ALLMAP .

No alerts have been found for ALLMAP .

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Mart??n A, et al. (2026) Targeted KRASG12V Degradation in vivo Elicits Lung Adenocarcinoma Regression with Subsequent Relapse from Dysregulated Proteolysis. Cancer research.