

Resource Summary Report

Generated by [nidm-terms](#) on Aug 9, 2026

ALLMAP

RRID:SCR_021120

Type: Tool

Proper Citation

ALLMAP (RRID:SCR_021120)

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: 20260808T190208+0000

Ratings and Alerts

No rating or validation information has been found for ALLMAP .

No alerts have been found for ALLMAP .

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 [nidm-terms](#) .

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