

Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

JaBba

RRID:SCR_027134

Type: Tool

Proper Citation

JaBba (RRID:SCR_027134)

Resource Information

URL: <https://github.com/mskilab-org/JaBbA>

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Description: Software tool to infer junction-balanced genome graphs with high fidelity. Builds genome graph based on junctions and read depth from whole genome sequencing, inferring optimal copy numbers for both vertices (DNA segments) and edges (bonds between segments).

Synonyms: Junction Balance Analysis

Resource Type: software resource, software application

Defining Citation: [PMID:33007263](#)

Keywords: Builds genome graph, junctions and read depth, infer junction-balanced genome graphs, whole genome sequencing, inferring optimal copy numbers, vertices and edges, DNA segments, bonds between segments,

Funding: NCI P01 CA91955;
NCI P30 CA015704

Availability: Free, Available for download, Freely available,

Resource Name: JaBba

Resource ID: SCR_027134

License: MIT license

Record Creation Time: 20250703T065557+0000

Record Last Update: 20260801T191408+0000

Ratings and Alerts

No rating or validation information has been found for JaBba.

No alerts have been found for JaBba.

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](#) .

Micoli G, et al. (2025) Decoding the Genomic and Functional Landscape of Emerging Subtypes in Ovarian Cancer. Cancer discovery, 15(11), 2262.