

# Resource Summary Report

Generated by [dkNET](#) on Sep 15, 2026

## JaBba

RRID:SCR\_027134

Type: Tool

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### Proper Citation

JaBba (RRID:SCR\_027134)

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### Resource Information

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

**Proper Citation:** JaBba (RRID:SCR\_027134)

**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 application, software resource

**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:** 20260912T200519+0000

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### Ratings and Alerts

No rating or validation information has been found for JaBba.

No alerts have been found for JaBba.

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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 [dkNET](#) .

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