

Resource Summary Report

Generated by [NIF](#) on Oct 20, 2026

ZINBA

RRID:SCR_010868

Type: Tool

Proper Citation

ZINBA (RRID:SCR_010868)

Resource Information

URL: <http://code.google.com/p/zinba/>

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Description: Software to identify genomic regions enriched in a variety of ChIP-seq and related next-generation sequencing experiments (DNA-seq), calling both broad and narrow modes of enrichment across a range of signal-to-noise ratios. ZINBA models and accounts for factors that co-vary with background or experimental signal, such as G/C content, and identifies enrichment in genomes with complex local copy number variations. ZINBA provides a single unified framework for analyzing DNA-seq experiments in challenging genomic contexts.

Abbreviations: ZINBA

Synonyms: zinba - Zero Inflated Negative Binomial Algorithm, Zero Inflated Negative Binomial Algorithm

Resource Type: software resource

Defining Citation: [PMID:21787385](#)

Keywords: bio.tools

Availability: GNU General Public License, v3

Resource Name: ZINBA

Resource ID: SCR_010868

Alternate IDs: biotools:zinba, OMICS_00465

Alternate URLs: <https://bio.tools/zinba>

Record Creation Time: 20220129T080301+0000

Record Last Update: 20261017T202746+0000

Ratings and Alerts

No rating or validation information has been found for ZINBA.

No alerts have been found for ZINBA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.