# **Resource Summary Report**

Generated by <u>dkNET</u> on May 18, 2025

# **CSDeconv**

RRID:SCR\_000016 Type: Tool

**Proper Citation** 

CSDeconv (RRID:SCR\_000016)

#### **Resource Information**

URL: http://crab.rutgers.edu/~dslun/csdeconv/index.html

Proper Citation: CSDeconv (RRID:SCR\_000016)

**Description:** Software application that maps transcription factor binding sites from ChIP-seq data to high resolution using a blind deconvolution approach.

Abbreviations: CSDeconv

**Resource Type:** software application, software resource, data analysis software, data processing software

Defining Citation: PMID:20028542

**Keywords:** sequence analysis software, transcription factor binding site, chip-seq, blind deconvolution, transcription binding, bio.tools

Funding:

Availability: Public, Open source

Resource Name: CSDeconv

Resource ID: SCR\_000016

Alternate IDs: OMICS\_00436, biotools:csdeconv

Alternate URLs: https://bio.tools/csdeconv

Record Creation Time: 20220129T080159+0000

#### **Ratings and Alerts**

No rating or validation information has been found for CSDeconv.

No alerts have been found for CSDeconv.

### Data and Source Information

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We have not found any literature mentions for this resource.