

Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

[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: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on July 31, 2025. Software application that maps transcription factor binding sites from ChIP-seq data to high resolution using a blind deconvolution approach.

Abbreviations: CSDeconv

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

Defining Citation: [PMID:20028542](#)

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

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: CSDeconv

Resource ID: SCR_000016

Alternate IDs: OMICS_00436, biotools:csdeconv

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

Record Creation Time: 20220129T080159+0000

Record Last Update: 20260905T132952+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.