Resource Summary Report

Generated by NIF on Apr 8, 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 resource, software application, 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

Record Last Update: 20250407T215123+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.