Resource Summary Report

Generated by NIF on Apr 22, 2025

BINOCh

RRID:SCR_002778
Type: Tool

Proper Citation

BINOCh (RRID:SCR_002778)

Resource Information

URL: http://liulab.dfci.harvard.edu/BINOCh/

Proper Citation: BINOCh (RRID:SCR_002778)

Description: Software that infers the identity of transcription factors used to regulate cell response to stimulus or determine a program of differentiation. It uses genome wide information on enhancer proximal nucleosome occupancy, acquired using ChIP-seq targeting enhancer related histone modifications.

Abbreviations: BINOCh

Synonyms: Binding Inference from Nucleosome Occupancy Changes (BINOCh), BINOCh - Binding Inference from Nucleosome Occupancy Changes, Binding Inference from Nucleosome Occupancy Changes

Resource Type: software resource

Defining Citation: PMID:21551136

Keywords: proximal nucleosome occupancy data, transcription factor determination, differentiation

Funding:

Availability: Open source

Resource Name: BINOCh

Resource ID: SCR_002778

Alternate IDs: OMICS_00500

Record Creation Time: 20220129T080215+0000

Record Last Update: 20250420T014122+0000

Ratings and Alerts

No rating or validation information has been found for BINOCh.

No alerts have been found for BINOCh.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Chen X, et al. (2021) NUCOME: A comprehensive database of nucleosome organization referenced landscapes in mammalian genomes. BMC bioinformatics, 22(1), 321.

Luyten A, et al. (2014) Active enhancers are delineated de novo during hematopoiesis, with limited lineage fidelity among specified primary blood cells. Genes & development, 28(16), 1827.

He HH, et al. (2012) Differential DNase I hypersensitivity reveals factor-dependent chromatin dynamics. Genome research, 22(6), 1015.