

# Resource Summary Report

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

## BINOCh

RRID:SCR\_002778

Type: Tool

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### Proper Citation

BINOCh (RRID:SCR\_002778)

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### 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., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on January 15,2026.

**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

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** BINOCh

**Resource ID:** SCR\_002778

**Alternate IDs:** OMICS\_00500

**Record Creation Time:** 20220129T080215+0000

**Record Last Update:** 20260905T132453+0000

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## Ratings and Alerts

No rating or validation information has been found for BINOCh.

No alerts have been found for BINOCh.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [RRID](#) .

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.