

Resource Summary Report

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

ChIPMunk

RRID:SCR_001191

Type: Tool

Proper Citation

ChIPMunk (RRID:SCR_001191)

Resource Information

URL: <http://autosome.ru/ChIPMunk/>

Proper Citation: ChIPMunk (RRID:SCR_001191)

Description: DNA motif discovery software adapted for ChIP-Seq data. It is an iterative algorithm that combines greedy optimization with bootstrapping and uses coverage profiles as motif positional preferences. It does not require truncation of long DNA segments and it is practical for processing up to tens of thousands of data sequences

Abbreviations: ChIPMunk

Resource Type: software resource

Defining Citation: [PMID:20736340](#)

Keywords: chip-seq, java, binding, motif, dna, bio.tools

Funding: Russian Federal Agency for Science and Innovation State Contract 02.531.11.9003;

Russian Federal Agency for Science and Innovation State Contract 02.740.11.5008;

Russian Fund for Basic Research Project 10-04-92663

Availability: Free, Available for download, Freely available

Resource Name: ChIPMunk

Resource ID: SCR_001191

Alternate IDs: biotools:chipmunk, OMICS_02140

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

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260905T132430+0000

Ratings and Alerts

No rating or validation information has been found for ChIPMunk.

No alerts have been found for ChIPMunk.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Datta V, et al. (2018) Detection of cooperatively bound transcription factor pairs using ChIP-seq peak intensities and expectation maximization. PloS one, 13(7), e0199771.

Kulakovskiy IV, et al. (2016) HOCOMOCO: expansion and enhancement of the collection of transcription factor binding sites models. Nucleic acids research, 44(D1), D116.