

# Resource Summary Report

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## [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:** 20260829T182059+0000

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## Ratings and Alerts

No rating or validation information has been found for ChIPMunk.

No alerts have been found for ChIPMunk.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

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.