

# Resource Summary Report

Generated by T1D on Jul 29, 2026

## ChIPMonk

RRID:SCR\_002975

Type: Tool

### Proper Citation

ChIPMonk (RRID:SCR\_002975)

### Resource Information

**URL:** <http://www.bioinformatics.babraham.ac.uk/projects/chipmonk/>

**Proper Citation:** ChIPMonk (RRID:SCR\_002975)

**Description:** Software tool to visualize and analyse ChIP-on-chip array data. Main features: \* Import of data from Nimblegen arrays (other formats can be added if people send us examples) \* Normalization of data (both per array and per probe) \* Various data plotting options to assess data quality and the effectiveness of normalization \* Creation of data groups for visualization and analysis \* Visualization of data against an annotated genome. \* Statistical analysis of data to find probes of interest \* Creation of reports containing probes, data and genome annotation Note: This project is no longer being developed, but critical bug fixes will still be provided

**Abbreviations:** ChIPMonk

**Resource Type:** software resource

**Keywords:** java, chip, chip-on-chip, plotting, normalization, visualization, genome, annotation, probe, array, analysis

**Availability:** Free, Available for download, Freely available

**Resource Name:** ChIPMonk

**Resource ID:** SCR\_002975

**Alternate IDs:** OMICS\_02043, nif-0000-30159

**Alternate URLs:** <http://www.bioinformatics.bbsrc.ac.uk/projects/chipmonk/>

**License:** GNU General Public License, v2 or later

**Record Creation Time:** 20220129T080216+0000

**Record Last Update:** 20260725T190535+0000

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## Ratings and Alerts

No rating or validation information has been found for ChIPMonk.

No alerts have been found for ChIPMonk.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 4 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

Legge D, et al. (2022) The epithelial splicing regulator ESRP2 is epigenetically repressed by DNA hypermethylation in Wilms tumour and acts as a tumour suppressor. *Molecular oncology*, 16(3), 630.

Charlet J, et al. (2017) Genome-wide DNA methylation analysis identifies MEGF10 as a novel epigenetically repressed candidate tumor suppressor gene in neuroblastoma. *Molecular carcinogenesis*, 56(4), 1290.

Fiorino A, et al. (2016) Retina-derived POU domain factor 1 coordinates expression of genes relevant to renal and neuronal development. *The international journal of biochemistry & cell biology*, 78, 162.

Dallosso AR, et al. (2009) Frequent long-range epigenetic silencing of protocadherin gene clusters on chromosome 5q31 in Wilms' tumor. *PLoS genetics*, 5(11), e1000745.