# **Resource Summary Report**

Generated by dkNET on Apr 23, 2025

## **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

Funding:

Availability: GNU General Public License, v2 or later

Resource Name: ChIPMonk

Resource ID: SCR 002975

Alternate IDs: OMICS 02043, nif-0000-30159

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

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

Record Last Update: 20250420T014133+0000

### Ratings and Alerts

No rating or validation information has been found for ChIPMonk.

No alerts have been found for ChIPMonk.

#### Data and Source Information

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 4 mentions in open access literature.

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

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.