

Resource Summary Report

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ChIPMonk

RRID:SCR_002975

Type: Tool

Proper Citation

ChIPMonk (RRID:SCR_002975)

Resource Information

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

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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

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Record Last Update: 20260801T190222+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 [PRECISE-TBI](#) .

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.