

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 2, 2026

NucHunter

RRID:SCR_010894

Type: Tool

Proper Citation

NucHunter (RRID:SCR_010894)

Resource Information

URL: <http://epigen.molgen.mpg.de/nuchunter/>

Proper Citation: NucHunter (RRID:SCR_010894)

Description: Software for inferring nucleosome positions with their histone mark annotation from ChIP data. It is a versatile tool that can be used to predict positioned nucleosomes from one or multiple ChIP-seq bam files and it can be also used in conjunction with a control experiment.

Abbreviations: NucHunter

Resource Type: software resource

Defining Citation: [PMID:23981350](#)

Resource Name: NucHunter

Resource ID: SCR_010894

Alternate IDs: OMICS_00509

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260801T190400+0000

Ratings and Alerts

No rating or validation information has been found for NucHunter.

No alerts have been found for NucHunter.

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](#) .

Hui-Yuen J, et al. (2023) B lymphocytes in treatment-naïve paediatric patients with lupus are epigenetically distinct from healthy children. *Lupus science & medicine*, 10(1).

Schuyler RP, et al. (2016) Distinct Trends of DNA Methylation Patterning in the Innate and Adaptive Immune Systems. *Cell reports*, 17(8), 2101.

Veluchamy A, et al. (2015) An integrative analysis of post-translational histone modifications in the marine diatom *Phaeodactylum tricornutum*. *Genome biology*, 16(1), 102.

Mammana A, et al. (2015) Chromatin segmentation based on a probabilistic model for read counts explains a large portion of the epigenome. *Genome biology*, 16(1), 151.