

# Resource Summary Report

Generated by [NIF](#) on Sep 9, 2026

## htSeqTools

RRID:SCR\_006614

Type: Tool

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### Proper Citation

htSeqTools (RRID:SCR\_006614)

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### Resource Information

**URL:** <http://www.bioconductor.org/packages/2.14/bioc/html/htSeqTools.html>

**Proper Citation:** htSeqTools (RRID:SCR\_006614)

**Description:** Software tools for quality control, visualization and processing for High-Throughput Sequencing data. These include MDS plots (analogues to PCA), detecting inefficient immuno-precipitation or over-amplification artifacts, tools to identify and test for genomic regions with large accumulation of reads, and visualization of coverage profiles.

**Abbreviations:** htSeqTools

**Resource Type:** software resource

**Keywords:** high-throughput sequencing, chip-seq, rnaseq

**Resource Name:** htSeqTools

**Resource ID:** SCR\_006614

**Alternate IDs:** OMICS\_01233

**Record Creation Time:** 20220129T080237+0000

**Record Last Update:** 20260905T132557+0000

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### Ratings and Alerts

No rating or validation information has been found for htSeqTools.

No alerts have been found for htSeqTools.

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### Data and Source Information

## Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Ospino MC, et al. (2024) Evaluation of multiple displacement amplification for metagenomic analysis of low biomass samples. ISME communications, 4(1), ycae024.

Suñer C, et al. (2022) Macrophage inflammation resolution requires CPEB4-directed offsetting of mRNA degradation. eLife, 11.

Buitrago D, et al. (2021) Impact of DNA methylation on 3D genome structure. Nature communications, 12(1), 3243.

Gonzalez-Pena V, et al. (2021) Accurate genomic variant detection in single cells with primary template-directed amplification. Proceedings of the National Academy of Sciences of the United States of America, 118(24).

Climent-Cantó P, et al. (2020) The embryonic linker histone dBigH1 alters the functional state of active chromatin. Nucleic acids research, 48(8), 4147.

Zhang Q, et al. (2020) Transcriptome Analysis of the Gene Expression Profiles Associated with Fungal Keratitis in Mice Based on RNA-Seq. Investigative ophthalmology & visual science, 61(6), 32.

Pascual R, et al. (2020) mRNA spindle localization and mitotic translational regulation by CPEB1 and CPEB4. RNA (New York, N.Y.), 27(3), 291.

Bayona-Feliu A, et al. (2017) Linker histone H1 prevents R-loop accumulation and genome instability in heterochromatin. Nature communications, 8(1), 283.

Welch R, et al. (2017) Data exploration, quality control and statistical analysis of ChIP-exo/nexus experiments. Nucleic acids research, 45(15), e145.

Daulny A, et al. (2016) The fission yeast CENP-B protein Abp1 prevents pervasive transcription of repetitive DNA elements. Biochimica et biophysica acta, 1859(10), 1314.

Seelke AM, et al. (2016) Individual differences in cortical connections of somatosensory cortex are associated with parental rearing style in prairie voles (*Microtus ochrogaster*). The Journal of comparative neurology, 524(3), 564.