**HTSeq**

RRID:SCR_005514  
Type: Tool

**Proper Citation**

HTSeq (RRID:SCR_005514)

**Resource Information**

**URL:** [http://htseq.readthedocs.io/en/release_0.9.1/](http://htseq.readthedocs.io/en/release_0.9.1/)

**Proper Citation:** HTSeq (RRID:SCR_005514)

**Description:** THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 28, 2023. Software Python package that provides infrastructure to process data from high-throughput sequencing assays. While the main purpose of HTSeq is to allow you to write your own analysis scripts, customized to your needs, there are also a couple of stand-alone scripts for common tasks that can be used without any Python knowledge.

**Abbreviations:** HTSeq

**Synonyms:** HTSeq: Analysing high-throughput sequencing data with Python

**Resource Type:** standalone software, software resource, software application, authoring tool, data processing software

**Defining Citation:** DOI:10.1093/bioinformatics/btu638

**Keywords:** python, high-throughput sequencing assay, bio.tools

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** HTSeq

**Resource ID:** SCR_005514

**Alternate IDs:** biotools:htseq, OMICS_01053
Alternate URLs: https://bio.tools/htseq

Old URLs: http://www-huber.embl.de/users/anders/HTSeq/, https://sources.debian.org/src/python3-htseq/

Record Creation Time: 20220129T080230+0000

Record Last Update: 20240616T053402+0000

Ratings and Alerts

No rating or validation information has been found for HTSeq.

No alerts have been found for HTSeq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7557 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.


Kellett DO, et al. (2024) Transcriptional response of the heart to vagus nerve stimulation. Physiological genomics, 56(2), 167.

Talvi S, et al. (2024) Embigin deficiency leads to delayed embryonic lung development and high neonatal mortality in mice. iScience, 27(2), 108914.


Carrick BH, et al. (2024) PUF partner interactions at a conserved interface shape the RNA-binding landscape and cell fate in Caenorhabditis elegans. Developmental cell, 59(5), 661.

Griffiths JA, et al. (2024) Peripheral neuronal activation shapes the microbiome and alters gut physiology. Cell reports, 43(4), 113953.


Wen J, et al. (2024) Time-series transcriptome reveals inflammatory signature in monocytes and neutrophils following acute heat exposure in mine rescuers. Physiological reports, 12(3), e15946.


