

Resource Summary Report

Generated by [RRID](#) on Aug 13, 2026

HTStream

RRID:SCR_018354

Type: Tool

Proper Citation

HTStream (RRID:SCR_018354)

Resource Information

URL: <https://ibest.github.io/HTStream/>

Proper Citation: HTStream (RRID:SCR_018354)

Description: Software tool as quality control and processing pipeline for High Throughput Sequencing data. Uses tab delimited fastq format that allows for streaming from application to application. Interoperable with other standard Linux tools., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Resource Type: data processing software, software resource, software application

Keywords: Next Generation Sequencing, data processing, quality control, data preprocessing

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: HTStream

Resource ID: SCR_018354

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260813T055207+0000

Ratings and Alerts

No rating or validation information has been found for HTStream.

No alerts have been found for HTStream.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Mao X, et al. (2026) Cytoplasmic mRNA decay by the antiviral nuclease RNase L promotes transcriptional repression. *Cell reports*, 45(3), 117028.

Morgens DW, et al. (2025) Enhancers and genome conformation provide complex transcriptional control of a herpesviral gene. *Molecular systems biology*, 21(1), 30.

Ariza-Suarez D, et al. (2025) Association genetics and genomic prediction for resistance to root rot in a diverse collection of *Pisum sativum* L. *BMC plant biology*, 26(1), 131.

Andrews KR, et al. (2024) Comparative genomic analysis identifies potential adaptive variation in *Mycoplasma ovipneumoniae*. *Microbial genomics*, 10(8).

Ramirez MD, et al. (2024) Cellular-resolution gene expression mapping reveals organization in the head ganglia of the gastropod, *Berghia stephanieae*. *The Journal of comparative neurology*, 532(6), e25628.

Morgens DW, et al. (2023) Coding and non-coding elements comprise a regulatory network controlling transcription in Kaposi's sarcoma-associated herpesvirus. *bioRxiv : the preprint server for biology*.

Sadovnikova A, et al. (2022) Transcriptomic changes underlying glucocorticoid-induced suppression of milk production by dairy cows. *Frontiers in genetics*, 13, 1072853.

Pandolfo M, et al. (2022) MetaPhage: an Automated Pipeline for Analyzing, Annotating, and Classifying Bacteriophages in Metagenomics Sequencing Data. *mSystems*, 7(5), e0074122.

Jenner BN, et al. (2022) Pathotypes of *Fusarium oxysporum* f. sp. *fragariae* express discrete repertoires of accessory genes and induce distinct host transcriptional responses during root infection. *Environmental microbiology*, 24(10), 4570.

Andrews KR, et al. (2021) A new mouse SNP genotyping assay for speed congenics: combining flexibility, affordability, and power. *BMC genomics*, 22(1), 378.

Magdesian KG, et al. (2020) A De Novo MITF Deletion Explains a Novel Splashed White Phenotype in an American Paint Horse. *The Journal of heredity*, 111(3), 287.

Johansson ??, et al. (2020) Detection and Genetic Characterization of Viruses Present in Free-Ranging Snow Leopards Using Next-Generation Sequencing. *Frontiers in veterinary science*, 7, 645.

Andrews KR, et al. (2020) Wireworm (Coleoptera: Elateridae) genomic analysis reveals putative cryptic species, population structure, and adaptation to pest control. *Communications biology*, 3(1), 489.