

Resource Summary Report

Generated by SPARC SAWG on Sep 18, 2026

HTSJDK

RRID:SCR_024036

Type: Tool

Proper Citation

HTSJDK (RRID:SCR_024036)

Resource Information

URL: <http://samtools.github.io/htsjdk/>

Proper Citation: HTSJDK (RRID:SCR_024036)

Description: Software implementation of unified Java library for accessing common file formats, such as SAM and VCF, used for high-throughput sequencing data. There are also an number of useful utilities for manipulating HTS data.

Synonyms: htsjdk

Resource Type: software application, software resource

Keywords: accessing common file formats, SAM, VCF, manipulating HTS data,

Availability: Free, Available for download, Freely available,

Resource Name: HTSJDK

Resource ID: SCR_024036

Alternate URLs: <https://sources.debian.org/src/htsjdk/>, <https://github.com/samtools/htsjdk>

License: MIT license/ Apache License v2.0/ LGPL

Record Creation Time: 20230824T050211+0000

Record Last Update: 20260912T200307+0000

Ratings and Alerts

No rating or validation information has been found for HTSJDK.

No alerts have been found for HTSJDK.

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 [SPARC SAWG](#) .

van Rengs WMJ, et al. (2026) Wild tomato genome assemblies reveal structural variants and repeat content act as recombination barriers. Nature communications, 17(1).

Simmons SK, et al. (2026) Experimental and computational methods for allelic imbalance analysis from single-nucleus RNA-seq data. Genome biology, 27(1).

Wen X, et al. (2025) Deciphering splicing heterogeneity at single-cell resolution by SCSES. Nature communications, 16(1), 9459.

Simmons SK, et al. (2024) Experimental and Computational Methods for Allelic Imbalance Analysis from Single-Nucleus RNA-seq Data. bioRxiv : the preprint server for biology.