

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 1, 2026

## [QTrim](#)

RRID:SCR\_011842

Type: Tool

### Proper Citation

QTrim (RRID:SCR\_011842)

### Resource Information

**URL:** <http://hiv.sanbi.ac.za/software/qtrim>

**Proper Citation:** QTrim (RRID:SCR\_011842)

**Description:** A next generation sequence quality trimming tool.

**Abbreviations:** QTrim

**Resource Type:** software resource

**Resource Name:** QTrim

**Resource ID:** SCR\_011842

**Alternate IDs:** OMICS\_01089

**Record Creation Time:** 20220129T080307+0000

**Record Last Update:** 20260725T190723+0000

### Ratings and Alerts

No rating or validation information has been found for QTrim.

No alerts have been found for QTrim.

### Data and Source Information

**Source:** [SciCrunch Registry](#)

### Usage and Citation Metrics

We found 6 mentions in open access literature.

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

MacLeod IJ, et al. (2021) PANDAA intentionally violates conventional qPCR design to enable durable, mismatch-agnostic detection of highly polymorphic pathogens. *Communications biology*, 4(1), 227.

Tian R, et al. (2020) Gene Expression Profiling Indicated Diverse Functions and Characteristics of Core Genes in Pea Aphid. *Insects*, 11(3).

Zarars??z G, et al. (2017) A comprehensive simulation study on classification of RNA-Seq data. *PloS one*, 12(8), e0182507.

Plasil M, et al. (2016) The major histocompatibility complex in Old World camelids and low polymorphism of its class II genes. *BMC genomics*, 17, 167.

Menon R, et al. (2016) Comparative analysis of SNP candidates in disparate milk yielding river buffaloes using targeted sequencing. *PeerJ*, 4, e2147.

Austin CM, et al. (2015) Whole Genome Sequencing of the Asian Arowana (*Scleropages formosus*) Provides Insights into the Evolution of Ray-Finned Fishes. *Genome biology and evolution*, 7(10), 2885.