

# Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

## Scythe

RRID:SCR\_011844

Type: Tool

### Proper Citation

Scythe (RRID:SCR\_011844)

### Resource Information

**URL:** <https://github.com/vsbuffalo/scythe>

**Proper Citation:** Scythe (RRID:SCR\_011844)

**Description:** Scythe uses a Naive Bayesian approach to classify contaminant substrings in sequence reads.

**Abbreviations:** Scythe

**Synonyms:** Scythe - A Bayesian adapter trimmer

**Resource Type:** software resource

**Resource Name:** Scythe

**Resource ID:** SCR\_011844

**Alternate IDs:** OMICS\_01091

**Alternate URLs:** <https://sources.debian.org/src/scythe/>

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

**Record Last Update:** 20260801T190432+0000

### Ratings and Alerts

No rating or validation information has been found for Scythe.

No alerts have been found for Scythe.

### Data and Source Information

## Usage and Citation Metrics

We found 174 mentions in open access literature.

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

Cavicchio L, et al. (2025) Swine influenza surveillance in Italy uncovers regional and farm-based genetic clustering. *Frontiers in microbiology*, 16, 1607204.

Verma R, et al. (2025) Commentary: a review of technical considerations for planning an RNA-Sequencing experiment. *BMC genomics*, 26(1), 918.

Mazzetto E, et al. (2025) Infectivity in full-term placenta of Zika viruses with different lipid profiles. *Virus research*, 352, 199518.

Marchese M, et al. (2025) CLN5 deficiency impairs glucose uptake and uncovers PHGDH as a potential biomarker in Batten disease. *Molecular psychiatry*, 30(10), 4591.

Festa F, et al. (2025) A multi-disciplinary approach to identify spillover interfaces of bat coronaviruses to pig farms in Italy. *PloS one*, 20(10), e0332117.

Frascarelli G, et al. (2025) The evolutionary history of the common bean (*Phaseolus vulgaris*) revealed by chloroplast and nuclear genomes analysis. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 138(2), 47.

Xue H, et al. (2025) The Genomic Basis of the Tristylous Floral Polymorphism: Evidence for a Role of Gene Duplications in a Region of Restricted Recombination. *Molecular biology and evolution*, 42(8).

Vaiasicca S, et al. (2024) Transcriptomic analysis reveals the anti-cancer effect of gestational mesenchymal stem cell secretome. *Stem cells translational medicine*, 13(7), 693.

Achiro JM, et al. (2024) Aging differentially alters the transcriptome and landscape of chromatin accessibility in the male and female mouse hippocampus. *Frontiers in molecular neuroscience*, 17, 1334862.

Kim H, et al. (2024) Unacylated Ghrelin Protects Against Age-Related Loss of Muscle Mass and Contractile Dysfunction in Skeletal Muscle. *Aging cell*, 23(12), e14323.

Albizzati E, et al. (2024) Mecp2 knock-out astrocytes affect synaptogenesis by interleukin 6 dependent mechanisms. *iScience*, 27(3), 109296.

Kohlhase DR, et al. (2024) GmGLU1 and GmRR4 contribute to iron deficiency tolerance in soybean. *Frontiers in plant science*, 15, 1295952.

Marcolungo L, et al. (2024) Haematococcus lacustris genome assembly and annotation reveal diploid genetic traits and stress-induced gene expression patterns. *Algal research*, 80, 103567.

Eme L, et al. (2023) Inference and reconstruction of the heimdallarchaeial ancestry of eukaryotes. *Nature*, 618(7967), 992.

Nwagbo I, et al. (2023) Genomic Analysis of Infectious Bursal Disease Virus in Nigeria: Identification of Unique Mutations of Yet Unknown Biological Functions in Both Segments A and B. *Vaccines*, 11(4).

Brundu S, et al. (2023) Mutated axon guidance gene PLXNB2 sustains growth and invasiveness of stem cells isolated from cancers of unknown primary. *EMBO molecular medicine*, 15(3), e16104.

Monti M, et al. (2023) Impaired activation of plasmacytoid dendritic cells via toll-like receptor 7/9 and STING is mediated by melanoma-derived immunosuppressive cytokines and metabolic drift. *Frontiers in immunology*, 14, 1227648.

Wang Z, et al. (2023) Chromosome-level genome assembly and population genomics of *Robinia pseudoacacia* reveal the genetic basis for its wide cultivation. *Communications biology*, 6(1), 797.

Cana A, et al. (2023) Emergence and Persistent Circulation of Highly Pathogenic Avian Influenza Virus A (H5N8) in Kosovo, May 2021-May 2022. *Microorganisms*, 11(9).

Meseko C, et al. (2023) The Evolution of Highly Pathogenic Avian Influenza A (H5) in Poultry in Nigeria, 2021-2022. *Viruses*, 15(6).