

Resource Summary Report

Generated by T1D on Aug 4, 2026

ConDeTri

RRID:SCR_011838

Type: Tool

Proper Citation

ConDeTri (RRID:SCR_011838)

Resource Information

URL: <http://code.google.com/p/condetri/>

Proper Citation: ConDeTri (RRID:SCR_011838)

Description: Software tool as content dependent read trimmer for Illumina data. Content dependent read trimming software for Illumina/Solexa sequencing data.

Abbreviations: ConDeTri

Resource Type: software resource

Defining Citation: [PMID:22039460](#)

Keywords: Solexa sequencing data, Illumina data, data read trimming, read trimmer, sequencing data,

Availability: Free, Available for download, Freely available

Resource Name: ConDeTri

Resource ID: SCR_011838

Alternate IDs: OMICS_01085, biotools:condetri

Alternate URLs: <https://bio.tools/condetri>, <https://sources.debian.org/src/condetri/>, <https://github.com/linneas/condetri/>

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260801T190420+0000

Ratings and Alerts

No rating or validation information has been found for ConDeTri.

No alerts have been found for ConDeTri.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 66 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Prentout D, et al. (2025) Evolution of Sex-Biased Gene Expression During Transitions to Separate Sexes in the *Silene* Genus. *Molecular biology and evolution*, 42(10).

Pinder MIM, et al. (2025) Bamboozle: A Bioinformatic Tool for Identification and Quantification of Intraspecific Barcodes. *Molecular ecology resources*, 25(4), e14067.

Valberg SJ, et al. (2023) Novel Expression of GLUT3, GLUT6 and GLUT10 in Equine Gluteal Muscle Following Glycogen-Depleting Exercise: Impact of Dietary Starch and Fat. *Metabolites*, 13(6).

Pagnossin D, et al. (2023) *Streptococcus canis* genomic epidemiology reveals the potential for zoonotic transfer. *Microbial genomics*, 9(3).

Muyle A, et al. (2021) Dioecy Is Associated with High Genetic Diversity and Adaptation Rates in the Plant Genus *Silene*. *Molecular biology and evolution*, 38(3), 805.

Williams ZJ, et al. (2021) Integrated proteomic and transcriptomic profiling identifies aberrant gene and protein expression in the sarcomere, mitochondrial complex I, and the extracellular matrix in Warmblood horses with myofibrillar myopathy. *BMC genomics*, 22(1), 438.

Chen YC, et al. (2021) A Novel Spo11 Homologue Functions as a Positive Regulator in Cyst Differentiation in *Giardia lamblia*. *International journal of molecular sciences*, 22(21).

Ku CC, et al. (2021) Deletion of *Jdp2* enhances *Slc7a11* expression in *Atoh-1* positive cerebellum granule cell progenitors in vivo. *Stem cell research & therapy*, 12(1), 369.

Seligsohn D, et al. (2021) Genomic analysis of group B *Streptococcus* from milk demonstrates the need for improved biosecurity: a cross-sectional study of pastoralist camels in Kenya. *BMC microbiology*, 21(1), 217.

Crestani C, et al. (2021) The fall and rise of group B *Streptococcus* in dairy cattle: reintroduction due to human-to-cattle host jumps? *Microbial genomics*, 7(9).

Martin C, et al. (2020) Analysis of Pigment-Dispersing Factor Neuropeptides and Their Receptor in a Velvet Worm. *Frontiers in endocrinology*, 11, 273.

Popitsch N, et al. (2020) A-to-I RNA Editing Uncovers Hidden Signals of Adaptive Genome Evolution in Animals. *Genome biology and evolution*, 12(4), 345.

Fruchard C, et al. (2020) Evidence for Dosage Compensation in *Coccinia grandis*, a Plant with a Highly Heteromorphic XY System. *Genes*, 11(7).

Lilley TM, et al. (2020) Population Connectivity Predicts Vulnerability to White-Nose Syndrome in the Chilean Myotis (*Myotis chiloensis*) - A Genomics Approach. *G3 (Bethesda, Md.)*, 10(6), 2117.

Höök L, et al. (2019) Multilayered Tuning of Dosage Compensation and Z-Chromosome Masculinization in the Wood White (*Leptidea sinapis*) Butterfly. *Genome biology and evolution*, 11(9), 2633.

Iguchi A, et al. (2019) Identification of genes encoding ALMT and MATE transporters as candidate aluminum tolerance genes from a typical acid soil plant, *Psychotria rubra* (Rubiaceae). *PeerJ*, 7, e7739.

Velez-Irizarry D, et al. (2019) Genetic control of longissimus dorsi muscle gene expression variation and joint analysis with phenotypic quantitative trait loci in pigs. *BMC genomics*, 20(1), 3.

Sävilampi T, et al. (2019) The Chromosome-Level Genome Assembly of European Grayling Reveals Aspects of a Unique Genome Evolution Process Within Salmonids. *G3 (Bethesda, Md.)*, 9(5), 1283.

Riddell EA, et al. (2019) Thermal cues drive plasticity of desiccation resistance in montane salamanders with implications for climate change. *Nature communications*, 10(1), 4091.

Wu W, et al. (2019) Flax rust infection transcriptomics reveals a transcriptional profile that may be indicative for rust Avr genes. *PloS one*, 14(12), e0226106.