Resource Summary Report

Generated by dkNET on Apr 30, 2025

ConDeTri

RRID:SCR_011838 Type: Tool

Proper Citation

ConDeTri (RRID:SCR_011838)

Resource Information

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

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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,

Funding:

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

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 64 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

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).

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.

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

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.

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.

Sävilammi 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.

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.

Mäkinen H, et al. (2018) Modularity Facilitates Flexible Tuning of Plastic and Evolutionary Gene Expression Responses during Early Divergence. Genome biology and evolution, 10(1), 77.

Fogelqvist J, et al. (2018) Analysis of the hybrid genomes of two field isolates of the soilborne fungal species Verticillium longisporum. BMC genomics, 19(1), 14.