Resource Summary Report

Generated by NIF on May 15, 2025

SeqtrimNEXT

RRID:SCR_011845
Type: Tool

Proper Citation

SeqtrimNEXT (RRID:SCR_011845)

Resource Information

URL: http://www.scbi.uma.es/ingebiol/session/new/seqtrimnext

Proper Citation: SeqtrimNEXT (RRID:SCR_011845)

Description: A customizable and distributed pre-processing software for NGS (Next Generation Sequencing) biological data.The old version for Sanger sequences, Seqtrim, has been discontinued.

Abbreviations: SeqtrimNEXT

Synonyms: Seqtrim

Resource Type: software resource

Keywords: bio.tools

Funding:

Resource Name: SeqtrimNEXT

Resource ID: SCR_011845

Alternate IDs: biotools:seqtrim, OMICS_01093

Alternate URLs: https://bio.tools/seqtrim

Record Creation Time: 20220129T080307+0000

Record Last Update: 20250420T014600+0000

Ratings and Alerts

No rating or validation information has been found for SeqtrimNEXT.

No alerts have been found for SeqtrimNEXT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 28 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Lavado-Benito C, et al. (2024) GacA reduces virulence and increases competitiveness in planta in the tumorigenic olive pathogen Pseudomonas savastanoi pv. savastanoi. Frontiers in plant science, 15, 1347982.

Vela-Corcia D, et al. (2024) Cyclo(Pro-Tyr) elicits conserved cellular damage in fungi by targeting the [H+]ATPase Pma1 in plasma membrane domains. Communications biology, 7(1), 1253.

Pérez-Lorente AI, et al. (2023) Sporulation Activated via ?W Protects Bacillus from a Tse1 Peptidoglycan Hydrolase Type VI Secretion System Effector. Microbiology spectrum, 11(2), e0504522.

Berlanga-Clavero MV, et al. (2022) Bacillus subtilis biofilm matrix components target seed oil bodies to promote growth and anti-fungal resistance in melon. Nature microbiology, 7(7), 1001.

Qi M, et al. (2021) cDNA-detector: detection and removal of cDNA contamination in DNA sequencing libraries. BMC bioinformatics, 22(1), 611.

Molina-Santiago C, et al. (2021) Chemical interplay and complementary adaptative strategies toggle bacterial antagonism and co-existence. Cell reports, 36(4), 109449.

Moreno-Pérez A, et al. (2021) HrpL Regulon of Bacterial Pathogen of Woody Host Pseudomonas savastanoi pv. savastanoi NCPPB 3335. Microorganisms, 9(7).

Elvira González L, et al. (2021) Persistent Southern Tomato Virus (STV) Interacts with Cucumber Mosaic and/or Pepino Mosaic Virus in Mixed- Infections Modifying Plant Symptoms, Viral Titer and Small RNA Accumulation. Microorganisms, 9(4).

Arce-Leal ÁP, et al. (2020) Gene Expression Profile of Mexican Lime (Citrus aurantifolia) Trees in Response to Huanglongbing Disease caused by Candidatus Liberibacter asiaticus.

Microorganisms, 8(4).

Cámara-Almirón J, et al. (2020) Dual functionality of the amyloid protein TasA in Bacillus physiology and fitness on the phylloplane. Nature communications, 11(1), 1859.

Ramírez-Zapata D, et al. (2020) Two Homologues of the Global Regulator Csr/Rsm Redundantly Control Phaseolotoxin Biosynthesis and Virulence in the Plant Pathogen Pseudomonas amygdali pv. phaseolicola 1448A. Microorganisms, 8(10).

Arce-Leal ÁP, et al. (2020) De novo assembly and functional annotation of Citrus aurantifolia transcriptome from Candidatus Liberibacter asiaticus infected and non-infected trees. Data in brief, 29, 105198.

González-Gordo S, et al. (2019) Nitric oxide-dependent regulation of sweet pepper fruit ripening. Journal of experimental botany, 70(17), 4557.

Herrera-Uribe J, et al. (2018) Regulatory role of microRNA in mesenteric lymph nodes after Salmonella Typhimurium infection. Veterinary research, 49(1), 9.

García-Gutiérrez Á, et al. (2018) Glutamate synthases from conifers: gene structure and phylogenetic studies. BMC genomics, 19(1), 65.

Labella AM, et al. (2018) Transcriptomic Profiles of Senegalese Sole Infected With Nervous Necrosis Virus Reassortants Presenting Different Degree of Virulence. Frontiers in immunology, 9, 1626.

Seoane P, et al. (2018) TransFlow: a modular framework for assembling and assessing accurate de novo transcriptomes in non-model organisms. BMC bioinformatics, 19(Suppl 14), 416.

Zafra A, et al. (2017) Identification and Functional Annotation of Genes Differentially Expressed in the Reproductive Tissues of the Olive Tree (Olea europaea L.) through the Generation of Subtractive Libraries. Frontiers in plant science, 8, 1576.

Carmona R, et al. (2017) Automated identification of reference genes based on RNA-seq data. Biomedical engineering online, 16(Suppl 1), 65.

Seoane-Zonjic P, et al. (2016) Establishing gene models from the Pinus pinaster genome using gene capture and BAC sequencing. BMC genomics, 17, 148.