Resource Summary Report

Generated by <u>NIF</u> on Apr 22, 2025

Tuxedo

RRID:SCR_013194 Type: Tool

Proper Citation

Tuxedo (RRID:SCR_013194)

Resource Information

URL: http://sourceforge.net/projects/tuxe/

Proper Citation: Tuxedo (RRID:SCR_013194)

Description: Software that manages the RNA-sequencing pipeline based on the TopHat suite of software automatically.

Abbreviations: Tuxedo

Synonyms: Tuxedo: Automated RNA-sequencing Pipeline Script

Resource Type: software resource

Funding:

Resource Name: Tuxedo

Resource ID: SCR_013194

Alternate IDs: OMICS_01415

Record Creation Time: 20220129T080314+0000

Record Last Update: 20250420T014636+0000

Ratings and Alerts

No rating or validation information has been found for Tuxedo.

No alerts have been found for Tuxedo.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 93 mentions in open access literature.

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

Thadtapong N, et al. (2024) Enhancing effect of natural adjuvant, panduratin A, on antibacterial activity of colistin against multidrug-resistant Acinetobacter baumannii. Scientific reports, 14(1), 9863.

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.

Greig LC, et al. (2024) BEAM: A combinatorial recombinase toolbox for binary gene expression and mosaic genetic analysis. Cell reports, 43(8), 114650.

Paton AJ, et al. (2024) Camouflage or Coincidence? Investigating the Effects of Spatial and Temporal Environmental Features on Feral Cat Morphology in Tasmania. Ecology and evolution, 14(11), e70530.

Hahn EE, et al. (2024) Century-old chromatin architecture revealed in formalin-fixed vertebrates. Nature communications, 15(1), 6378.

Kalaipandian S, et al. (2023) Transcriptome Analysis of Heat Shock Factor C2a Over-Expressing Wheat Roots Reveals Ferroptosis-like Cell Death in Heat Stress Recovery. International journal of molecular sciences, 24(4).

Naseem MT, et al. (2023) NHA1 is a cation/proton antiporter essential for the waterconserving functions of the rectal complex in Tribolium castaneum. Proceedings of the National Academy of Sciences of the United States of America, 120(13), e2217084120.

Yazar V, et al. (2023) Impaired ATF3 signaling involves SNAP25 in SOD1 mutant ALS patients. Scientific reports, 13(1), 12019.

Su SH, et al. (2023) Brachypodium distachyon Seedlings Display Accession-Specific Morphological and Transcriptomic Responses to the Microgravity Environment of the International Space Station. Life (Basel, Switzerland), 13(3).

Norris MH, et al. (2023) Beyond the spore, the exosporium sugar anthrose impacts vegetative Bacillus anthracis gene regulation in cis and trans. Scientific reports, 13(1), 5060.

Pritchett EM, et al. (2023) Chicken pituitary transcriptomic responses to acute heat stress. Molecular biology reports, 50(6), 5233.

Dobbs OG, et al. (2023) Epigenetic instability caused by absence of CIZ1 drives transformation during quiescence cycles. BMC biology, 21(1), 175.

Vujovic A, et al. (2023) In Vivo Screening Unveils Pervasive RNA-Binding Protein Dependencies in Leukemic Stem Cells and Identifies ELAVL1 as a Therapeutic Target. Blood cancer discovery, 4(3), 180.

Matern MS, et al. (2023) Transcriptional dynamics of delaminating neuroblasts in the mouse otic vesicle. Cell reports, 42(6), 112545.

James ND, et al. (2022) TUXEDO: A phase I/II trial of cetuximab with chemoradiotherapy in muscle-invasive bladder cancer. BJU international, 131(1), 63.

Moore EC, et al. (2022) The Evolution of Widespread Recombination Suppression on the Dwarf Hamster (Phodopus) X Chromosome. Genome biology and evolution, 14(6).

Paslaru L, et al. (2022) Comparative RNA-Sequencing Analysis Reveals High Complexity and Heterogeneity of Transcriptomic and Immune Profiles in Hepatocellular Carcinoma Tumors of Viral (HBV, HCV) and Non-Viral Etiology. Medicina (Kaunas, Lithuania), 58(12).

Laitinen P, et al. (2022) Nuclear microRNA-466c regulates Vegfa expression in response to hypoxia. PloS one, 17(3), e0265948.

Kaashyap M, et al. (2022) Comprehensive transcriptomic analysis of two RIL parents with contrasting salt responsiveness identifies polyadenylated and non-polyadenylated flower IncRNAs in chickpea. Plant biotechnology journal, 20(7), 1402.

Bandopadhyay S, et al. (2022) SIRT6 promotes mitochondrial fission and subsequent cellular invasion in ovarian cancer. FEBS open bio, 12(9), 1657.