Resource Summary Report

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reseqtools

RRID:SCR_010806
Type: Tool

Proper Citation

reseqtools (RRID:SCR_010806)

Resource Information

URL: https://code.google.com/p/reseqtools/

Proper Citation: reseqtools (RRID:SCR_010806)

Description: A Toolkit for analyzing next-generation DNA Re-Sequencing data.

Abbreviations: reseqtools

Resource Type: software resource

Keywords: java, unix/linux

Funding:

Availability: GNU General Public License, v2

Resource Name: reseqtools

Resource ID: SCR_010806

Alternate IDs: OMICS_00293

Record Creation Time: 20220129T080300+0000

Record Last Update: 20250214T183138+0000

Ratings and Alerts

No rating or validation information has been found for reseqtools.

No alerts have been found for reseqtools.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Lin L, et al. (2024) Transcriptome data reveals the conservation genetics of Cypripedium forrestii, a plant species with extremely small populations endemic to Yunnan, China. Frontiers in plant science, 15, 1303625.

Zhang Y, et al. (2024) Cytochrome P450 CitCYP97B modulates carotenoid accumulation diversity by hydroxylating ?-cryptoxanthin in Citrus. Plant communications, 5(6), 100847.

Zheng Y, et al. (2024) Diagnostic and predictive significance of the ferroptosis-related gene TXNIP in lung adenocarcinoma stem cells based on multi-omics. Translational oncology, 45, 101926.

Chen FW, et al. (2024) Inactivation of pentraxin 3 suppresses M2-like macrophage activity and immunosuppression in colon cancer. Journal of biomedical science, 31(1), 10.

Ren YY, et al. (2024) Characterization of Single-Cell Cis-regulatory Elements Informs Implications for Cell Differentiation. Genome biology and evolution, 16(11).

Liu H, et al. (2022) Genomic regions controlling yield-related traits in spring wheat: a mini review and a case study for rainfed environments in Australia and China. Genomics, 114(2), 110268.

Yeh CC, et al. (2022) Phytochemical?rich herbal formula ATG?125 protects against sucrose?induced gastrocnemius muscle atrophy by rescuing Akt signaling and improving mitochondrial dysfunction in young adult mice. Molecular medicine reports, 25(2).

Zhang Q, et al. (2021) Frequent germplasm exchanges drive the high genetic diversity of Chinese-cultivated common apricot germplasm. Horticulture research, 8(1), 215.

Xie H, et al. (2021) Identification of QTL related to anther color and hull color by RAD sequencing in a RIL population of Setaria italica. BMC genomics, 22(1), 556.

Wang C, et al. (2020) Donkey genomes provide new insights into domestication and selection for coat color. Nature communications, 11(1), 6014.

Zhao J, et al. (2020) Combined use of gap-PCR and next-generation sequencing improves

thalassaemia carrier screening among premarital adults in China. Journal of clinical pathology, 73(8), 488.

Song B, et al. (2019) Draft genome sequence of Solanum aethiopicum provides insights into disease resistance, drought tolerance, and the evolution of the genome. GigaScience, 8(10).

Zhou C, et al. (2018) Characterization of viral RNA splicing using whole-transcriptome datasets from host species. Scientific reports, 8(1), 3273.

White SJ, et al. (2017) Genotoype-by-sequencing of three geographically distinct populations of Olympia oysters, Ostrea lurida. Scientific data, 4, 170130.