

Resource Summary Report

Generated by [NIF](#) on Aug 10, 2026

[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

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: 20260808T185924+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 18 mentions in open access literature.

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

Jiang M, et al. (2026) Coleaf, an image recognition-driven approach facilitates the genome-wide association study with tea leaf morphology. *Plant methods*, 22(1).

Zhang T, et al. (2026) Proteogenomic characterization delineates clinically relevant subtypes of advanced differentiated thyroid cancer. *Cell reports. Medicine*, 7(3), 102661.

Zheng C, et al. (2026) Genetic diversity analysis and core collection construction of *Macadamia* spp. from Yunnan using fourfold degenerate SNP sites. *BMC plant biology*, 26(1).

Zhou C, et al. (2025) Genetic Diversity and Population Structure of the Chinese Three-Keeled Pond Turtle (*Mauremys reevesii*). *International journal of molecular sciences*, 26(12).

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.

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

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.

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 ATG125 protects against sucrose-induced gastrocnemius muscle atrophy by rescuing Akt signaling and improving mitochondrial dysfunction in young adult mice. *Molecular medicine reports*, 25(2).

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.

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

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) Genotype-by-sequencing of three geographically distinct populations of Olympia oysters, *Ostrea lurida*. *Scientific data*, 4, 170130.