Resource Summary Report

Generated by Kravitz on Sep 10, 2026

Segtools

RRID:SCR_004394
Type: Tool

Proper Citation

Segtools (RRID:SCR_004394)

Resource Information

URL: http://noble.gs.washington.edu/proj/segtools/

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Description: Segtools is a Python package designed to put genomic segmentations back in the context of the genome! Using R for graphics, Segtools provides a number of modules to analyze a segmentation in various ways and help you interpret its biological relevance. Segmentations should be in BED4+ or GFF format, with the "name" field of each line used specifying the segment label of that line. The Segtools commands allow you to compare the properties of the segment labels with one another.

Resource Type: software resource, source code

Defining Citation: PMID:22029426

Resource Name: Segtools

Resource ID: SCR_004394

Alternate IDs: nlx_40271

Record Creation Time: 20220129T080224+0000

Record Last Update: 20260905T133325+0000

Ratings and Alerts

No rating or validation information has been found for Segtools.

No alerts have been found for Segtools.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Holub E, et al. (2026) Effects of thymidylate synthase inhibitors differ in genomic uracilation and mutagenic potential. Life science alliance, 9(4).

Mendez M, et al. (2026) Segzoo: a turnkey system that summarizes genome annotations. Bioinformatics (Oxford, England), 42(5).

Zhang L, et al. (2019) Tumor-derived extracellular vesicles inhibit osteogenesis and exacerbate myeloma bone disease. Theranostics, 9(1), 196.

Richard G, et al. (2017) Dosage compensation and sex-specific epigenetic landscape of the X chromosome in the pea aphid. Epigenetics & chromatin, 10, 30.

Buske OJ, et al. (2011) Exploratory analysis of genomic segmentations with Segtools. BMC bioinformatics, 12, 415.