Resource Summary Report

Generated by NIF on Apr 27, 2025

DANPOS2

RRID:SCR_015527
Type: Tool

Proper Citation

DANPOS2 (RRID:SCR_015527)

Resource Information

URL: https://sites.google.com/site/danposdoc/

Proper Citation: DANPOS2 (RRID:SCR_015527)

Description: Software toolkit with various functions for the analysis of nucleosome and protein occupancy by sequencing.

Synonyms: DANPOS

Resource Type: software toolkit, software resource

Keywords: nucleosome analysis, protein analysis, protein occupancy, bio.tools

Funding:

Availability: Available for download, Different versions are available for download

Resource Name: DANPOS2

Resource ID: SCR_015527

Alternate IDs: biotools:danpos

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

Record Creation Time: 20220129T080326+0000

Record Last Update: 20250426T060500+0000

Ratings and Alerts

No rating or validation information has been found for DANPOS2.

No alerts have been found for DANPOS2.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 106 mentions in open access literature.

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

Jia X, et al. (2025) Exploring vimentin's role in breast cancer via PICK1 alternative polyadenylation and the miR-615-3p-PICK1 interaction. BioFactors (Oxford, England), 51(1), e2147.

Tam PLF, et al. (2024) Cell-type differential targeting of SETDB1 prevents aberrant CTCF binding, chromatin looping, and cis-regulatory interactions. Nature communications, 15(1), 15.

Liao Y, et al. (2024) Protocol to analyze immune cells in the tumor microenvironment by transcriptome using machine learning. STAR protocols, 5(1), 102684.

Ju J, et al. (2024) Cell-free DNA end characteristics enable accurate and sensitive cancer diagnosis. Cell reports methods, 4(10), 100877.

Jing X, et al. (2024) Creating a bacterium that forms eukaryotic nucleosome core particles. Nature communications, 15(1), 8283.

Shi G, et al. (2024) DNA polymerase ? subunit Pol32 binds histone H3-H4 and couples nucleosome assembly with Okazaki fragment processing. Science advances, 10(32), eado1739.

Xu M, et al. (2024) A repressive H3K36me2 reader mediates Polycomb silencing. Nature communications, 15(1), 7287.

Pavlu S, et al. (2024) Core promoterome of barley embryo. Computational and structural biotechnology journal, 23, 264.

Blanco-Touriñán N, et al. (2024) The plant POLYMERASE-ASSOCIATED FACTOR1 complex links transcription and H2B monoubiquitination genome wide. Plant physiology, 195(1), 640.

Yu J, et al. (2024) A replisome-associated histone H3-H4 chaperone required for epigenetic inheritance. Cell, 187(18), 5010.

Wang Y, et al. (2024) Determinant of m6A regional preference by transcriptional dynamics. Nucleic acids research, 52(7), 3510.

Li Y, et al. (2024) Multimodal epigenetic sequencing analysis (MESA) of cell-free DNA for non-invasive colorectal cancer detection. Genome medicine, 16(1), 9.

Bu L, et al. (2024) CHD6 eviction of promoter nucleosomes maintains housekeeping transcriptional program in prostate cancer. Molecular therapy. Nucleic acids, 35(4), 102397.

Xu L, et al. (2023) TAZ2 truncation confers overactivation of p300 and cellular vulnerability to HDAC inhibition. Nature communications, 14(1), 5362.

Schwartz U, et al. (2023) Changes in adenoviral chromatin organization precede early gene activation upon infection. The EMBO journal, 42(19), e114162.

Wang X, et al. (2023) The N-terminus of Spt16 anchors FACT to MCM2-7 for parental histone recycling. Nucleic acids research, 51(21), 11549.

Barrientos-Moreno M, et al. (2023) Transcription and FACT facilitate the restoration of replication-coupled chromatin assembly defects. Scientific reports, 13(1), 11397.

Lyu X, et al. (2023) Regulation of CTCF loop formation during pancreatic cell differentiation. Nature communications, 14(1), 6314.

Gao X, et al. (2023) Low RNA stability signifies strong expression regulatability of tumor suppressors. Nucleic acids research, 51(21), 11534.

Haase MAB, et al. (2023) DASH/Dam1 complex mutants stabilize ploidy in histone-humanized yeast by weakening kinetochore-microtubule attachments. The EMBO journal, 42(8), e112600.