

Resource Summary Report

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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

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: 20260729T044355+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

Usage and Citation Metrics

We found 111 mentions in open access literature.

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

Li Z, et al. (2025) Phase-separated NDF-FACT condensates facilitate transcription elongation on chromatin. *Nature cell biology*, 27(11), 1938.

Kumar K, et al. (2025) Protocol for analyzing chromatin dynamics in macrophage-internalized *Candida glabrata* cells using micrococcal nuclease digestion. *STAR protocols*, 6(3), 104050.

Huang S, et al. (2025) Super-enhancer-mediated circRNAs exhibit high splicing circularization diversity and transcriptional activity. *Nucleic acids research*, 53(11).

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.

Wu H, et al. (2025) Single-cell Micro-C profiles 3D genome structures at high resolution and characterizes multi-enhancer hubs. *Nature genetics*, 57(7), 1777.

Singh AK, et al. (2025) The WAC-downWAC domain in the yeast ISW2 nucleosome remodeling complex forms a structural module essential for ISW2 function but not cell viability. *Epigenetics & chromatin*, 18(1), 30.

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

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

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

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.

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

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

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

195(1), 640.

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

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.

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.

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.

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.