

Resource Summary Report

Generated by T1D on Aug 2, 2026

4D Nucleome

RRID:SCR_016925

Type: Tool

Proper Citation

4D Nucleome (RRID:SCR_016925)

Resource Information

URL: <https://www.4dnucleome.org>

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Description: Research project to understand the principles underlying nuclear organization in space and time, the role nuclear organization plays in gene expression and cellular function, and how changes in nuclear organization affect normal development and diseases. Portal provides free access to datasets, software packages, and protocols to advance biomedical research of nuclear architecture. Aims to develop and apply approaches to map the structure and dynamics of the human and mouse genomes.

Synonyms: 4D Nucleome Network; 4DN Web Portal, The 4D nucleome project, 4DN Portal

Resource Type: portal, data or information resource, project portal

Defining Citation: [PMID:28905911](https://pubmed.ncbi.nlm.nih.gov/28905911/)

Keywords: nuclear, organization, gene, expression, cellular, function, normal, development, disease, map, structure, human, mouse, genome

Funding: NIH Common Fund

Availability: Public

Resource Name: 4D Nucleome

Resource ID: SCR_016925

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260801T190842+0000

Ratings and Alerts

No rating or validation information has been found for 4D Nucleome .

No alerts have been found for 4D Nucleome .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Zhou S, et al. (2025) Cancer-associated snaR-A noncoding RNA interacts with core splicing machinery and disrupts processing of mRNA subpopulations. Nature communications, 16(1), 10460.

Zhou S, et al. (2024) Cancer-associated snaR-A noncoding RNA interacts with core splicing machinery and disrupts processing of mRNA subpopulations. bioRxiv : the preprint server for biology.

Wen X, et al. (2024) Single-cell multiplex chromatin and RNA interactions in ageing human brain. Nature, 628(8008), 648.

Perdyan A, et al. (2024) Chromosomal positioning and epigenetic architecture influence DNA methylation patterns triggered by galactic cosmic radiation. Scientific reports, 14(1), 1324.

Xu J, et al. (2024) A comprehensive benchmarking with interpretation and operational guidance for the hierarchy of topologically associating domains. Nature communications, 15(1), 4376.

Stear BJ, et al. (2024) Petagraph: A large-scale unifying knowledge graph framework for integrating biomolecular and biomedical data. Scientific data, 11(1), 1338.

Race AM, et al. (2023) Visualization and data exploration of chromosome conformation capture data using Voronoi diagrams with v3c-viz. Scientific reports, 13(1), 22020.

Jimenez Gonzalez A, et al. (2023) Zebrafish regulatory genomic resources for disease modelling and regeneration. Disease models & mechanisms, 16(8).

Buckberry S, et al. (2023) Transient naive reprogramming corrects hiPS cells functionally and epigenetically. Nature, 620(7975), 863.

Ng M, et al. (2023) Myeloid leukemia vulnerabilities embedded in long noncoding RNA locus MYNRL15. iScience, 26(10), 107844.

, et al. (2022) 3DGenBench: a web-server to benchmark computational models for 3D Genomics. Nucleic acids research, 50(W1), W4.

Xie L, et al. (2022) BRD2 compartmentalizes the accessible genome. *Nature genetics*, 54(4), 481.

Pandey N, et al. (2021) Improving Chromatin-Interaction Prediction Using Single-Cell Open-Chromatin Profiles and Making Insight Into the Cis-Regulatory Landscape of the Human Brain. *Frontiers in genetics*, 12, 738194.

Bartlett DA, et al. (2021) High-throughput single-cell epigenomic profiling by targeted insertion of promoters (TIP-seq). *The Journal of cell biology*, 220(12).

Lee JY, et al. (2021) Misexpression of genes lacking CpG islands drives degenerative changes during aging. *Science advances*, 7(51), eabj9111.

Li B, et al. (2021) CRISPR-SE: a brute force search engine for CRISPR design. *NAR genomics and bioinformatics*, 3(1), lqab013.

Lee BH, et al. (2021) Molecular and computational approaches to map regulatory elements in 3D chromatin structure. *Epigenetics & chromatin*, 14(1), 14.

Stanfill AG, et al. (2021) Enhancing Research Through the Use of the Genotype-Tissue Expression (GTEx) Database. *Biological research for nursing*, 23(3), 533.

Bedwell GJ, et al. (2021) rigrag: high-resolution mapping of genic targeting preferences during HIV-1 integration in vitro and in vivo. *Nucleic acids research*, 49(13), 7330.

Krietenstein N, et al. (2020) Ultrastructural Details of Mammalian Chromosome Architecture. *Molecular cell*, 78(3), 554.