

Resource Summary Report

Generated by [dkNET](#) on Sep 21, 2026

TopDom

RRID:SCR_016964

Type: Tool

Proper Citation

TopDom (RRID:SCR_016964)

Resource Information

URL: <http://zhoulab.usc.edu/TopDom/>

Proper Citation: TopDom (RRID:SCR_016964)

Description: Software tool to identify Topological Domains, which are basic building blocks of genome structure. Detects topological domains in a linear time., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: TOPDOM

Synonyms: TOPological DOMains, Topological Domains, TopDom_v0.0.2, TopDom_v0.0.1

Resource Type: data analysis software, data processing software, software application, software resource, software toolkit

Defining Citation: [PMID:26704975](#)

Keywords: identify, topological, domain, genome, structure, linear, time, data, analysis

Funding: Arnold and Mabel Beckman foundation ;
NHLBI U01 HL108634;
NIDDK U54 DK107981;
NSF CAREER 0747475;
NSF CAREER 1150287;
Pew Charitable Trusts

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: TopDom

Resource ID: SCR_016964

Record Creation Time: 20220129T080332+0000

Ratings and Alerts

No rating or validation information has been found for TopDom.

No alerts have been found for TopDom.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

D??az-Velis L, et al. (2025) Metagenomic and ribosomal transcript profiles of diabetic foot osteomyelitis in Hispanic patients: underestimated bacteria in biofilm persistence. *Frontiers in cellular and infection microbiology*, 15, 1729196.

Jin W, et al. (2024) Disorganized chromatin hierarchy and stem cell aging in a male patient of atypical laminopathy-based progeria mandibuloacral dysplasia type A. *Nature communications*, 15(1), 10046.

Okonechnikov K, et al. (2023) 3D genome mapping identifies subgroup-specific chromosome conformations and tumor-dependency genes in ependymoma. *Nature communications*, 14(1), 2300.

Osman N, et al. (2022) Exploring the effects of genetic variation on gene regulation in cancer in the context of 3D genome structure. *BMC genomic data*, 23(1), 13.

Tammer L, et al. (2022) Gene architecture directs splicing outcome in separate nuclear spatial regions. *Molecular cell*, 82(5), 1021.

Kaushal A, et al. (2022) Essential role of Cp190 in physical and regulatory boundary formation. *Science advances*, 8(19), eabl8834.

Arnould C, et al. (2021) Loop extrusion as a mechanism for formation of DNA damage repair foci. *Nature*, 590(7847), 660.

Liu X, et al. (2021) Time-dependent effect of 1,6-hexanediol on biomolecular condensates and 3D chromatin organization. *Genome biology*, 22(1), 230.

Liu Y, et al. (2021) Monocytic THP-1 cells diverge significantly from their primary counterparts: a comparative examination of the chromosomal conformations and transcriptomes. *Hereditas*, 158(1), 43.

Salviato E, et al. (2021) Leveraging three-dimensional chromatin architecture for effective reconstruction of enhancer-target gene regulatory interactions. *Nucleic acids research*, 49(17), e97.

Kakui Y, et al. (2020) Fission yeast condensin contributes to interphase chromatin organization and prevents transcription-coupled DNA damage. *Genome biology*, 21(1), 272.