

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 31, 2026

TopDom

RRID:SCR_016964

Type: Tool

Proper Citation

TopDom (RRID:SCR_016964)

Resource Information

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

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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 processing software, software toolkit, data analysis software, software resource, software application

Defining Citation: [PMID:26704975](#)

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

Funding: NHLBI U01 HL108634;
NIDDK U54 DK107981;
NSF CAREER 0747475;
NSF CAREER 1150287;
Arnold and Mabel Beckman foundation ;
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 10 mentions in open access literature.

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

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.

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

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.

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),

